

**SCIENTIFIC PROGRAMME
ABSTRACT BOOK**



#ECE2026Tours

Insect physical ecology : from natural history to bioinspired technology

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Abstract

Physical ecology, often regarded as a sister discipline of chemical ecology, can be defined as the study of interactions between insects and their biotic and abiotic environments from a physical perspective. The work conducted over several decades by my collaborators and myself highlights the necessity of investigating these interactions at spatial scales that are functionally relevant to individual organisms, namely micro- and mesoscales, ranging from micrometers to several centimeters.

Locomotion of whirligig beetles and water striders at the water–air interface, the movement of ants on the granular slopes of antlion pits, or oil collection behavior in bees all reveal gaps or unresolved questions in our fundamental physical understanding. These challenges do not arise from alternative physical laws, but rather from the intermediate scales involved, which do not readily conform to classical limit-based approaches commonly employed in physics.

The study of airflow detection in crickets, mediated by filiform hairs, exemplifies the concept of “matched filters” in response to predator-generated signals, such as those produced by spiders, and underscores the remarkable optimization of sensory systems. Furthermore, the sparse and efficient neural processing observed in the terminal abdominal ganglion of crickets demonstrates the potential of bioinspired strategies for reducing energy consumption in neuromorphic computing systems, with notable analogies to visual processing mechanisms involved in looming detection.

Finally, the olfactory-mediated search for sex pheromones in moths is examined, encompassing the processes of pheromone release, atmospheric transport in both molecular and aerosol forms, and subsequent detection by structurally complex antennae coupled with active olfactory mechanisms. This research represents a paradigmatic example of interdisciplinary collaboration, involving ecologists, fluid dynamicists, theoretical and computational physicists, materials scientists, and atmospheric chemists and leads to bioinspired developments in far ranging fields, from agroecology to anti-terrorism. It further illustrates that chemical ecology is, in many instances, inherently physicochemical in nature.

Can herbivore-induced plant volatiles really be exploited for crop protection?

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Abstract

Natural enemies of herbivorous pests often use plant-provided signals to locate plants that carry potential prey. Particularly intriguing are so-called herbivore-induced plant volatiles (HIPVs), which various plants release in large quantities only when they are attacked by insects. New field evidence shows the importance of HIPVs for the recruitment of natural enemies, and I will present evidence that we too can utilize these highly specific plant-produced signals for the real-time detection of agricultural pests. We successfully employed odour sensors to accurately distinguish healthy plants from plants that are under attack by insects or are infected by pathogens. We envision that, in the near future, such odour sensors can be placed on robotic rovers and allow farmers to determine the presence of specific pests on their crops and then take action before these pests do serious harm.

Deciphering mechanisms of service plants involved in the disruption of the host plant recognition by a specialist insect herbivore

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Abstract

Monocultures are known to favor proliferation of specialist pests but remain common. The overreliance on chemical pesticides for pest control has led to significant environmental and human health concerns, as well as the rapid emergence of resistant populations. These challenges beg for more sustainable agroecological strategies relying on the disruption of the target host plant recognition, including crop diversification and, in particular, the use of service plants.

In specialist insect herbivores, semiochemicals - perceived both at a distance and upon contact - play a key role throughout the host selection process. However, the mechanisms involved in the disruption of this behavior in complex environments, comprising both host and non-host service plants, remain largely unexplored.

This study will focus on the cabbage root fly, *Delia radicum*, a major pest of Brassicaceae. Four non-host plant species and one artificial plant were associated with a host plant, *Brassica oleraceae* L., to assess their influence on its selection behavior. Results indicate that this behavior depends on both the nature of the association and its duration. Pot marigold (*Calendula officinalis*) and French marigold (*Tagetes patula*) disrupted the different stages of the host recognition. They influenced not only the location of broccoli, but also post-landing behavior, ultimately reducing oviposition.

These findings suggest the involvement of chemical signals emitted by specific non-host plants, potentially through repellent or masking volatile compounds and/or allelopathic effect. A better understanding of these cues will support the targeted selection of service plants to enhance the agroecological control of *D. radicum*.

Semiochemicals for enhanced biological control: a lot of promise but no payoff

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Mike FURLONG

Abstract

Semiochemicals, such as methyl salicylate, that attract natural enemies, are often promoted as providing a mechanism to improve biological control. Although claims of demonstrated success are often made, the promised advent of applications to improve pest management has not eventuated. We critically review the published literature on the use of methyl salicylate, to improve the biological control of insect pests of plants. The results are mixed. Demonstrating outcomes in what are essentially small plot trials is one thing, but if experiments are conducted at a scale smaller than relevant crop fields, such claims are misleading and provide no support to assertions of improved pest management. Critically, the question of the source of the natural enemies that will be manipulated for large field scale applications of semiochemicals across multiple farms is not addressed. Adoption of new pest management approaches based on the improved understanding of how semiochemicals modify the behaviours of arthropod pests and their natural enemies needs more than hyperbole and small-scale studies that simply demonstrate that some natural enemies are attracted to a lure.

What's my age again? Assessing the impact of stink bug egg mass age on host recognition by egg parasitoids *Trissolcus basalis* and *Trissolcus japonicus* (Hymenoptera: Scelionidae)

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Abstract

Wasps, from the genus *Trissolcus*, are egg parasitoids that are commonly used in biological control programs targeting stink bugs. They navigate a complex environment, relying on a diverse array of biochemical and ecological cues to locate their hosts. Through this endeavour, these parasitoid wasps have to discriminate between young and old eggs as development is only achieved in the latter. In this study, we evaluated the ability of two parasitoid wasps, *Trissolcus japonicus* and *Trissolcus basalis*, on utilising short-range cues and, more specifically, volatile organic compounds emitted by stink bug egg masses to locate their hosts. We hypothesised that (1) stink bug eggs (i.e., *Halyomorpha halys* and *Nezara viridula*) emit short-range cues that are exploited by egg parasitoids (i.e., *T. japonicus* and *T. basalis*) to locate their hosts in addition to insect chemical footprints; (2) *Trissolcus* spp. Have the ability to differentiate young eggs from older ones to increase their fitness (3) based on changes in the chemical profiles of the egg masses according to their age. Our behavioural assays suggested that *T. japonicus* did not respond to stink bug footprints, whereas *T. basalis* was significantly oriented toward the footprints of gravid host females. Both parasitoids preferentially oriented towards young eggs rather than footprints. The parasitism rate of *T. japonicus* was not significantly different between young and old eggs unlike *T. basalis* which preferred parasitising on young eggs. We identified γ -butyrolactone and β -funebrene in the headspace of *N. viridula* eggs and we discussed the putative role of these secondary metabolites on *T. basalis* locating their host. Behavioural, performance and VOCs collection of this study contribute to a nuanced understanding of host–parasitoid dynamics along with implications for developing effective pest management strategies.

Compounds in larval oral secretions of *Sesamia nonagrioides* determine host recognition and acceptance behaviour by its parasitoid *Cotesia typhae*

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Abstract

The Mediterranean corn borer, *Sesamia nonagrioides* (Lepidoptera: Noctuidae), native to sub-Saharan Africa, is an important corn pest in France. In Africa, the caterpillars of *S. nonagrioides*, are naturally parasitized by the specialist parasitoid *Cotesia typhae* (Hymenoptera: Braconidae). This hymenopteran is a promising candidate as a biological control agent against *S. nonagrioides* in Europe, thanks to its specificity, its reproductive success on European corn borer populations, and its low environmental impact. The Biocosma project aims to develop a biocontrol solution against this corn borer using annual field releases. To optimize parasitoid mass production is important to understand the mechanisms underlying host recognition and acceptance in *C. typhae*. The compounds present in the insects' oral secretions may constitute chemical signals recognized by these insects to discriminate between host and non-host species. Previous studies have highlighted the role of alpha-amylase digestive enzymes in these behaviours in parasitoids of *C. flavipes* complex, to which *C. typhae* belongs. The synthesis of *S. nonagrioides* alpha-amylases in the laboratory was realised by selecting the most productive clones from recombinant *Pichia pastoris* yeast. Then, behavioural tests confirmed the involvement of these enzymes, even at low concentrations, in host recognition and acceptance in *C. typhae*. A metabolomic analysis of *S. nonagrioides* oral secretions has allowed to identify other candidate compounds. Behavioural tests showed that one these compounds, like vanillin, is also involved in host recognition and acceptance in *C. typhae*. Although the functioning of sensory system of this hymenopteran parasitoid remains poorly understood, these compounds could be used to stimulate the parasitoid's oviposition behaviour and help to regulate *S. nonagrioides* populations in the field.

Clove-derived eugenol induces strong avoidance behaviour in the invasive fruit fly, *Drosophila suzukii*

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Abstract

The success of invasive species often relies on sensory adaptations that allow them to exploit new environments. Unlike most of its relatives, the spotted-wing drosophila (*Drosophila suzukii*) lays eggs in ripening fruit, making it a serious and rapidly spreading agricultural pest worldwide. Spice plants produce volatiles that repel many insects, presenting potential sources of behavioural modulators for *D. suzukii*. Here, we examined whether volatiles from clove (*Syzygium aromaticum*) affect adult behaviour and offspring performance in *D. suzukii*. Behavioural assays revealed strong aversion: adults avoided grapes treated with clove extract, and gravid females laid significantly fewer eggs on treated fruit in both no-choice and choice assays. Clove exposure also reduced fitness, resulting in slower larval growth, lower adult weight, decreased emergence rate, and shortened lifespan. Gas chromatography–mass spectrometry analyses identified eugenol as the predominant volatile. Synthetic eugenol elicited strong avoidance across multiple host fruits, including apple, banana, blueberry, guava, mango, orange, papaya, raspberry, strawberry, and tomato. Molecular docking and single-sensillum recordings indicated that eugenol binds most strongly to DsuzOR88a and DsuzOR69aA odorant receptors. Cheminformatic screening of 1,000 eugenol analogues revealed several structural variants predicted to interact strongly with OR88a, providing additional candidate repellents. By integrating behavioural, analytical chemistry, electrophysiology, and cheminformatics, our study shows that clove, through its major volatile eugenol, modulates host choice and reduces offspring performance in *D. suzukii*. These results highlight the ecological role of plant-derived volatiles in insect–plant interactions and support eugenol as a promising natural compound for sustainable fruit pest management.

Did ecology overrides phylogeny: multilevel convergence of olfactory traits in in host-parasitoid fig wasps

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Abstract

Host–parasitoid interactions impose strong selection on sensory traits involved in resource location, making olfactory systems key targets of ecological adaptation. In the tritrophic fig–wasp system, the pollinating mutualist *Blastophaga psene* and the non-pollinating parasitoid *Philotrypesis caricae* are deeply divergent phylogenetically, yet both rely on volatile organic compounds (VOCs) emitted by the fig tree to access their only reproductive resource.

Here, we test the hypothesis that shared ecological constraints can override evolutionary history and drive multi-level convergence of olfactory traits. We predict that *Blastophaga* and *Philotrypesis* show convergent functional responses to fig VOCs, together with molecular signatures of convergence in genes involved in the detection of these key signals.

To test these predictions, we use an integrative approach combining behavioral assays, electroantennographic recordings, and comparative analyses of olfactory gene repertoires, gene phylogenies, and expression profiles. Our goal is to determine how specialization on the same plant resource can shape convergent evolution of sensory systems and reveal how ecology can outweigh phylogeny in the evolution of insect olfaction.

Protective Symbiosis in Insect Systems

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Abstract

Integrating organismal interaction studies with advanced genomic and metabolomic approaches holds great promise for elucidating the chemical ecology of symbiotic systems, yet this integrative strategy remains relatively underexplored. We have recently demonstrated its potential by investigating the farming symbiosis between fungus-growing termites and their cultivated fungi—a system that has long fascinated researchers due to its ecological importance as well as its evolutionary history and stability, as well as complex chemical interactions. Termites of the subfamily Macrotermitinae (Termitidae: Blattodea) cultivate mutualistic basidiomycete fungi of the genus *Termitomyces* as their primary food source, supported by a diverse and metabolically active bacterial microbiome within subterranean fungal gardens that facilitates the conversion of recalcitrant lignocellulosic plant material into nutrient-rich fungal biomass. Such nutrient-rich symbiotic environments inevitably attract parasitic or opportunistic species. In termite colonies, *Xylaria* species are frequently associated with decaying fungal combs, where a sit-and-wait strategy enables these coevolved fungi to colonize combs and outcompete both the fungal cultivar and protective Actinomycetota when conditions are favourable.

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How pheromone detection evolves: lessons from weevil odorant receptors

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Abstract

Insects have long served as key models for studying chemical communication, both among conspecifics via pheromones and between insects and their environment, especially host plants. In insects, the detection of volatile compounds by the olfactory system relies on neuronal membrane proteins called odorant receptors (ORs). While some OR lineages in model insects such as moths are known to have specialized in pheromone detection roughly 100 million years ago, the evolutionary origins of these receptors remain incompletely understood. By contrast, in weevils—one of the most diverse animal families worldwide—ORs tuned to aggregation pheromones appear to have evolved independently multiple times within the last few million years, offering a unique opportunity to examine how pheromone detection capacities arise.

Here, we investigated the pheromone receptor repertoires of two major pest species, the Asian palm weevil *Rhynchophorus ferrugineus* and the American palm weevil *Rhynchophorus palmarum*. These species use distinct aggregation pheromones to attract conspecifics to their palm hosts. Using a combination of functional assays and comparative genomics, we identified multiple ORs in each species that respond to their own aggregation pheromone, as well as ORs capable of cross-detecting the pheromone produced by the other species. In silico structural analyses further revealed molecular features associated with pheromone recognition and specificity.

Moreover, comparative analyses of recently duplicated OR genes in *R. ferrugineus* revealed receptors responsive not only to pheromones but also to host plant volatiles. This pattern supports an evolutionary scenario in which ORs initially involved in host plant discrimination later acquired sensitivity to insect-produced volatiles, paving the way for the evolution of aggregation pheromones.

Hidden Chemists: How Stenammini Ants Synthetize Nicotinic Alkaloids?

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Abstract

Ants produce a wide range of chemical compounds with diverse functions, including nestmate recognition, trail following, and defence against competitors or predators. In this context, certain ants of the subfamily Myrmicinae have evolved an alkaloid-based venom, composed of molecules well described in plants and often used for therapeutic purposes, but largely unexplored in ants. Therefore, characterizing the alkaloid diversity present in ant venoms, particularly within the tribe Stenammini, through metabolomic analyses of venom glands using LC-MS/MS is of great interest, as it is essential for deciphering both their biosynthetic origins and their functional roles for the ants.

Stenammini are unique in producing nicotine-related alkaloids, such as anabasine and anabaseine, in their venom glands [1]. As these nicotinic alkaloids, known from tobacco plants, are not the result of environmental sequestration, their biosynthesis may be intrinsic to the ant, derived from an ancient horizontal gene transfer, or associated with the gut microbiota [2]. Ants collected through a citizen-science program were dissected to identify these alkaloids using LC-MS/MS. Among the 13 Stenammini species analysed, we found that species of the genus *Stenamma* still produce peptide-based venoms, corresponding to the ancestral state, whereas *Aphaenogaster*, *Messor* and *Goniomma* produce alkaloid-based venoms containing various nicotine-related molecules in species-specific proportions. Furthermore, transcriptomic data from *Aphaenogaster senilis*, combined with gene-function molecular approaches, have already allowed the identification of two genes encoding enzymes involved in the biosynthesis of these compounds. A deeper understanding of these metabolic pathways may shed light on the ecology and evolution of these ants and open the door to discovering new bioactive molecules of pharmacological interest.

References:

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Gasterophilus intestinalis Chemical Ecology

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Abstract

*Equal contribution of these authors

Gasterophilus intestinalis is a bot fly and an equine endoparasite distributed around farms worldwide. Despite its high prevalence, infected horses typically exhibit no specific clinical signs, resulting in frequent underdiagnosis or concurrent treatment with other gastrointestinal parasites such as nematodes. Adult flies have a short lifespan outside the host, during which they do not feed but engage in multiple mating events and oviposit several hundred eggs on the host. We hypothesize that the brief adult stage, coupled with the urgent need to locate a mate and a suitable host for oviposition, highlights the central role of chemical ecology in optimizing time use and reproductive success. This study is the first to investigate the olfactory detection abilities of male and female *G. intestinalis*. Electroantennography (EAG) was used to assess antennal responses to host and conspecific extracts, while adult and pupal extracts of both sexes were analyzed by GC–MS. The chemical profiles of host and non-host fecal materials are discussed in relation to the EAG response patterns observed in both sexes.

Molecular basis of aggregation pheromone biosynthesis in spruce bark beetle *Ips typographus* as a target for gene-level manipulation of pest behavior

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Abstract

The Eurasian spruce bark beetle, *Ips typographus* (Coleoptera: Scolytinae), is a major pest of spruce forests throughout Eurasia, causing extensive damage through mass attacks coordinated by a male-produced aggregation pheromone. This pheromone consists of minor components, including cis-verbenol, and the main component 2-methyl-3-buten-2-ol (MBO).

In this study, we investigated the biosynthesis of the monoterpene MBO at both the metabolite and gene levels. To date, monoterpene alcohol biosynthesis has not been described in insects. Our long-term goal is to identify molecular targets for disrupting aggregation behavior in this economically important pest. Using an integrated metabolomic, proteomic, and primarily transcriptomic approach, we demonstrated that MBO is synthesized *de novo* via the mevalonate pathway and we identified the key genes involved in this pathway. Special attention was given to a species-specific isoprenyl diphosphate synthase (IPDS), which catalyzes the terminal step of MBO production. Two IPDS gene orthologs were identified. Both resulting enzymes use dimethylallyl diphosphate as a substrate and are capable of producing monoterpene geranyl diphosphate; however, only ortholog 1 was able to catalyze the formation of MBO. Both orthologs were heterologously expressed in bacteria and functionally characterized using a series of enzymatic assays.

Subsequently, RNA interference (RNAi) was used to silence the IPDS orthologs *in vivo* with the aim of reducing pheromonal MBO production in male beetles. Laboratory behavioral assays revealed that MBO-RNAi-treated males exhibited significantly reduced aggregation behavior. These results confirm that pheromone production and host-attack coordination in *I. typographus* can be influenced at the gene level, highlighting a potential molecular target for bark beetle control strategies.

Electrophysiological and Behavioural Responses of *Ips typographus* to Fungal Volatiles from *Beauveria bassiana*

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Anna JIROŠOVÁ

Abstract

As critical carbon sinks, forests protect the fragile ecosystems that are under attack by multiple stressors. A significant biotic concern, the Eurasian spruce bark beetle (*Ips typographus*) represents a major biotic threat and a driver of the general decline of coniferous forests across Europe. Although beetle-host and beetle-microbe interactions have been the subject of earlier chemical ecology research, the potential of volatile organic compounds (VOCs) produced by entomopathogenic fungi in pest management remains uninvestigated. This study investigates the potential of *Beauveria bassiana*-derived VOCs in altering the behaviour of *I. typographus*. Using headspace sampling in conjunction with gas chromatography–mass spectrometry (GC–MS) and electroantennographic detection (GC–EAD), we characterise the volatile organic compound (VOC) profile of *B. bassiana* in order to discover chemicals that elicit olfactory and behavioural responses in the beetle. We identified a few fungal VOCs that trigger olfactory and behavioural responses in the beetle. Preliminary behavioural assays demonstrate that these compounds exhibit repellent effects on beetle orientation and interfere with aggregation cues. Future research will focus on dose–response studies and field-level validation to assess the practical applicability of this approach in forest protection systems.

Uncovering the chemosensory repertoire of *Ips typographus* Larvae: annotation and gene expression profiling

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Martin N ANDERSSON

Abstract

The Eurasian spruce bark beetle (*Ips typographus*) is both a keystone species and a major forest pest, driving extensive spruce mortality across Europe and Asia during epidemic outbreaks. Despite the central role of chemical cues in bark beetle ecology, research on insect chemosensation has been overwhelmingly adult-focused, leaving larval sensory biology largely unexplored. This gap is notable, as larvae, together with their symbiotic fungi, are directly responsible for phloem degradation and host tree death.

Here, we investigate larval chemosensation in *I. typographus* through gene expression profiling of chemosensory genes across two larval instars and tissue types. We identify larval-specific candidate genes from key chemosensory gene families, including odorant receptors, providing targets for subsequent functional characterization.

To link molecular patterns with ecological function, we assessed larval behavioral responses in two-choice arena assays using ecologically relevant bark beetle pheromones. Here, we found that the larvae were significantly attracted to several adult-produced pheromones, suggesting cross-generational chemical communication in this species. In parallel, we conducted single-sensillum electrophysiological recordings to examine neural responsiveness to these compounds.

Together, this integrative approach advances our understanding of larval chemosensation in *I. typographus* and highlights previously overlooked sensory mechanisms that may influence bark beetle development and behavior.

E-NICHE: a European Network In CHemical Ecology: translating the language of life into sustainability

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Core Group of E-NICHE

Abstract

The main aim and objective of this EU COST Action network is to unify European players in chemical ecology, enhancing cooperation, promoting visibility and sharing knowledge, tools, and platforms. It addresses major societal issues for environmental and sustainable development goals by describing chemodiversity, evolutionary forces, and global changes that will impact biodiversity and ecological interactions. E-NICHE is bringing together researchers and companies who study natural compounds that can act as semiochemicals (i.e., communication signals) across a diversity of organisms and ecological systems, including insects. This work will be nourished by a deeper understanding of the living world through the lens of chemical mediation, the main system of biological communication. It will also aim to prevent the loss of the chemical biodiversity found in nature, under threat because of global changes. Within this collaborative scientific effort, the participation of Young Researchers plays a key role in fostering innovation, ensuring continuity, and promoting inclusiveness within the European chemical ecology community.

Consequently, E-NICHE's overarching objective is to establish a strong, extended European CE network that catalyses international, interdisciplinary, and cross-sectoral exchanges with a view to building knowledge and intergenerational sustainable development solutions. Ultimately, the Action aims to build a European Association in Chemical Ecology as it exists already in Asia-Pacific (APACE) and the Latino Americas (ALAEQ) linked to the international one (ISCE).

#11266

GLOBAL CHANGE: Thermal ecology and climate change 1

29/06/2026 at 11:00, Descartes

Thermal performance revisited

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Abstract

The physiological performance of insects is intrinsically linked to environmental temperature. For decades, thermal biologists, ecologists, and evolutionary biologists have been leveraging the ‘predictable’ physiological response to temperature to explain past, present, and future characteristics of insects. For everything from phenotypic distribution to the potential for invasion to global insect decline, thermal performance in response to environmental temperature has been leveraged. It is becoming increasingly clear that looking at temperature in a vacuum has the potential to be misleading. Here, I will describe some of the complexities of both environmental temperature as well as measures of physiological performance. By examining some of the details and considering more than the number on the thermometer, we may be able to make more informative predictions about how insects will respond to global change at different spatial and temporal scales.

Uncovering the thermal niche of the *Collembola Folsomia candida*: Insights into niche breadth, genetic variation, and plasticity

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Abstract

Understanding how temperature shapes insect responses across physiological, ecological, and evolutionary scales is critical amid climate change. This study dissects the thermal niche - its breadth, plasticity and genetic variability - of *Folsomia candida*, a cosmopolitan parthenogenetic Collembola, focusing mainly on survival as a key life-history trait.

We quantified thermal responses over multiple timescales on different clonal lineages. Short-term experiments exposed adults to temperatures from -20°C to 37°C for 2–24 hours, revealing nonlinear mortality escalation near critical limits. Long-term assays tracked cohorts at 6–31°C for up to 490 days, mapping survival curves across the thermal niche.

Survival curves demonstrated broad thermal tolerance (viable 6–31°C), with lifespan declining asymmetrically: gradual at low temperatures, steeply above 26°C. Short-term assays refined reaction norms, showing mortality rising faster at upper (34–37°C) than lower bounds, with 24-hour exposures amplifying rates beyond linear expectation.

Comparing genetically distinct clonal lineages revealed significant lineage × temperature interactions, particularly above 30°C and below 0°C, with some lines exhibiting superior heat or cold resilience. Critically, thermal niche evolvability displayed asymmetry: genetic variability was markedly higher on the cold side than near the upper critical thermal limit.

This approach illuminates the organism's capacity to modify niche width and shape under changing thermal regimes, probing symmetry in thermal reaction norms from subcritical to extreme limits. The study exemplifies short-term assessment of thermal niche adaptability in springtails, highlighting genetic reservoirs for plasticity and asymmetric evolutionary potential in response to climate-driven thermal shifts.

Can native bees keep pace with climate change?

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Abstract

Species vulnerability to climate change depends in part on their capacity to evolve in response to increasing heat. Within terrestrial ectotherms, heat tolerance generally corresponds weakly to current climates, which has led many to conclude that this trait is evolutionarily constrained and implies that many species will not have the capacity to evolve with climate change. However, most studies have not accounted for differences in species behaviour and the corresponding microclimates they use, potentially obscuring signals of local adaptation. We examined heat tolerance in 95 species of wild bees that varied in nesting behaviour across the latitudinal extent of Australia (ground, cavity and stem). We show that nest microclimate temperature drives heat tolerance evolution, and species vulnerability to further warming. Incorporating nesting behaviour into species risk predictions changed the rank order of species vulnerability. Thus, underscoring the importance of incorporating species behaviour and relevant microclimates into vulnerability models.

While heat tolerance can indeed tell us about the rank order of species vulnerability to warming and how species might evolve in response to further climate change, it does not tell us how warming climates are already impacting animal performance. To understand sub-lethal impacts of climate warming on wild bees, we tested how flight performance (key trait for escaping predators, finding floral resources, dispersing etc) is impacted by temperature. Here I show how climate is already impacting key ecological traits in Australian wild bees.

Adaptive evolution can mitigate the negative effects of temperature stress on plant–pollinator interactions

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Quint RUSMAN, Florian SCHIESTL

Abstract

Increasing temperatures may impose strong fitness costs on plants, partly by affecting plant–pollinator interactions, but whether plants can overcome these adverse effects through adaptive evolution is largely unknown.

To test that, we carried out a six-generation evolution experiment, in which we kept fast-cycling *Brassica rapa* plants at ambient and elevated temperatures, with bumblebee pollination. At the end of the experiment, we re-grew the evolved lines at ambient and elevated temperatures, phenotyped them, and conducted pollinator bioassays. We assessed phenotypic evolutionary divergence, the evolution of temperature-mediated phenotypic plasticity, and local adaptation.

Plants that evolved with bumblebee pollination in both temperature regimes produced more seeds than control plants, which had reduced seed set when evolved under elevated temperatures. We also found that flower number, an important trait for plant attractiveness to bumblebees and for seed production, was increased in bumblebee-pollinated plants, as was heat-induced plasticity in flower number. Plants evolved at high temperature showed higher UV reflection, an increased association between flower size and nectar content (honest signaling), and reduced flower scent emission.

Our results indicate that plants evolving under pollinator-mediated selection may mitigate at least some of the negative impacts of temperature stress through adaptive evolution.

Do rising nest temperatures influence pollen provisioning in the solitary bee *Osmia bicornis*?

ELISA GOMES (University of Hull, UK, E.gomes@hull.ac.uk)

Elizabeth MILLER, Jamie SMITH, Evelyn OWEN, Milissa SLIPEC-DALY, Jamie DODD, Jeremy, E. NIVEN, Elizabeth NICHOLLS, James, D. GILBERT

Abstract

Wild bees provide the ecologically and economically crucial ecosystem service of pollination - but are impacted by human-induced environmental changes such as rising temperatures. Temperature affects insect behaviour and physiology, but the interplay between temperature and nutrition has rarely been studied despite its potentially severe consequences for bee fitness. Solitary mason bee larvae (*Osmia bicornis*) develop on finite pollen loads collected by adults and provisioned prior to hatching. Pilot data showed that larval nutritional requirements change with temperature, but whether adults adjust their foraging rules to anticipate and meet these requirements is still unknown. We therefore investigated the effects of nest temperature on parental pollen provisioning in *O. bicornis* in field conditions. We analysed the plant species and nutritional composition (macronutrients: proteins, lipids, carbohydrates) of pollen loads gathered by females provisioning nest boxes which were either at ambient temperature or heated to two temperature offsets (ambient +4°C or +8°C) based on future climate projections (UK RCP8.5). Pollen provisioning was observed for all three nest temperatures but females showed a preference for heated nests, which were occupied by more females and occupied significantly faster than nests at ambient temperature. Multivariate analyses revealed that plant species composition differed between pollen loads in heated and non-heated nests. The protein :lipid:carbohydrate ratio in pollen loads also varied between heated and non-heated nests. Our study therefore suggests that climate warming can change pollen foraging behaviour of solitary bees and hence has the potential to modify the pollination services they provide, with wider consequences for wild but also agricultural ecosystems.

Facing the right direction: how topography and microclimate predict bee nesting in quarry habitats.

William FIORDALISO (Interaction Ecology and Global Change, University of Mons, William.FIORDALISO@umons.ac.be)

Victoria FRAGAPANE, Florian COSA, Alice MARIN, Clément TOURBEZ, Denis MICHEZ, Kévin TOUGERON, Guillaume GHISBAIN

Abstract

To mitigate the decline of wild pollinators, it is crucial to deepen our understanding of their ecological requirements so that effective actions might be planned. This is particularly true for ground-nesting bees, whose nest-site selection remains insufficiently documented. This study examines active quarries, an often overlooked refuge within anthropized landscapes, in order to identify the physical and microclimatic drivers of nest presence, abundance, and species richness. We sampled nesting bees across 38 plots in nine Belgian quarries covering gradients in slope, aspect, vegetation cover, and soil texture. Soil temperature was recorded for one month on each plot, and mixed models were used to predict soil temperature from physical variables and then quantify bee responses with and without the mediating effect of temperature.

The sampled communities were dominated by a few Halictidae species, which shaped the observed patterns. Microclimatic modeling showed that slope aspect was the main driver of soil temperature, with maximum heating on south-facing slopes. However, bee presence, abundance, and richness all peaked on south-southeast aspects, a shift that may reflect an advantage for sites warming earlier in the morning. Although maximum soil temperatures occurred on moderately sloped terrain, bee responses increased linearly with slope angle, indicating a clear preference for the steepest slopes. This pattern suggests that factors beyond thermal maxima, such as reduced waterlogging due to runoff, play an important role in nest-site preferences. Soil texture and vegetation cover influenced temperature but had no direct effect on bees once temperature was accounted for.

Overall, thermoregulation contributes substantially to nest-site selection, but interacts with other physical constraints. The combination of early-day warming and the potentially improved drainage offered by steep south-southeast slopes appears particularly favorable, at least for the dominant species in our study, suggesting that these features may constitute relevant targets for habitat management.

Predatory mites, leaf surfaces and microhabitats

Sophie LE HESRAN (Wageningen University & Research, Sophielehesran@gmail.com)

Suzanne OTTER, Marcel HEIJKOOP, Kyra VERVOORN, Denise SEWKARANSING, Nathan KOEDIJK, Ada LEMAN

Abstract

Arthropods living on plants are in close interaction with leaf surfaces, notably through the leaf topography and microclimate. Predatory mites of the family Phytoseiidae, used worldwide for biological pest control, are highly dependent on the presence of leaf hairs and high humidity conditions at the leaf surface for the survival of their offspring. Plants with glabrous leaves and thick wax layer therefore represent a challenging environment for these predators. In this study, we investigated the possibility to support the establishment of *Amblyseius swirskii* populations on challenging leaf surfaces by providing them with artificial hairs and a water source. We used microhabitats with different types of fibers to mimic leaf hairs and placed a water source at different distances from the microhabitats. We also developed microsensors to measure the temperature and humidity at the leaf surface, inside and outside the microhabitats, with and without water source. Our results indicate that microhabitats with fibers and water availability have a significant effect on the establishment of *A. swirskii* populations. We also observed that *Amblyseius swirskii* females prefer specific fiber materials for oviposition. The temperature and humidity measurements are in progress and will give us more information on the impact of microhabitats on the microclimate at the leaf surface. These results provide new insights into the interactions between arthropods and leaf surfaces and enhance our understanding of the effects of microclimate on arthropod behaviour. This knowledge will be relevant for future research on biological control strategies in adverse climatic conditions.

Is Geographic Variation in upper Critical Thermal Limits Related to Temperature or Precipitation?

Cameron GHALAMBOR (Norwegian University of Science and Technology (NTNU), Cameron.ghalambor@ntnu.no)

Alfredo ESCANCIANO-GOMEZ

Abstract

Understanding the drivers of geographic variation in thermal tolerance plays a fundamental role in our ability to predict responses to global climate change. Most research to date has focused on the role of latitude as the primary predictor of thermal limits under the climate variability hypothesis, which posits that the range of temperatures historically experienced shapes thermal limits. However, critical thermal limits may be constrained by hydration state, suggesting that geographic variation in precipitation could also impact thermal tolerance. In this study we measured critical thermal maximum (CT_{max}) and rates of water loss across in a diversity of insect species at study sites that varied in temperature and precipitation: Madrid, Spain (warm and dry), Lyon, France (warm and wet), Trondheim, Norway (cool and wet), and Kirkenes, Norway (cool and dry). We measured over 1,000 individuals from over 70 species across all four sites. After controlling for phylogeny and body size, we found a negative relationship between CT_{max} and water loss rates; species with higher CT_{max} lost less water compared to species with lower CT_{max}. Surprisingly, mean CT_{max} and rates of water loss were highest in dry locations (Madrid and Kirkenes), while CT_{max} and rates of water loss were lower in the wet locations (Lyon and Trondheim). Such results suggest that variation in CT_{max} across species and geographic locations may be related to water balance, leading to new perspectives on the mechanisms that underlie upper thermal limits.

Thermal adaptation and seasonal dynamics amplify projected effects of climate warming on crop losses to insect pests

Loke VON SCHMALENSEE (Uppsala University, Department of Ecology and Genetics, Loke.von.schmalensee@ebc.uu.se)

David BERGER

Abstract

Climate warming is expected to increase crop losses from insects through plastic changes in physiology and demography, but evolutionary adaptation may further amplify these effects. To investigate this, we conducted 10 years of experimental evolution in *Callosobruchus maculatus*, a major beetle pest, evolving replicate lines from three geographic origins at 23°C, 29°C, and 35°C. We measured evolved thermal reaction norms for fecundity, viability, growth, and development. Additionally, we developed a simulation algorithm for generating diverse hourly thermal regimes under various warming scenarios. Integrating these regimes with our empirical data, we estimate heat-adapted beetles to cause ~64% higher crop losses than their ancestors, due to trait-specific evolution enhancing growth and fitness in warm conditions. In contrast, plastic responses alone predicted a ~20% increase in losses per °C of warming. Thus, the effects of evolutionary adaptation were on par with plastic responses to >3 °C of climate warming, suggesting that past projections may significantly underestimate future crop losses by ignoring the evolutionary potential of pest insects.

From First to Second: Environmental temperature and reproductive investment trajectories

Jakob WIIL (University of St Andrews, Jw414@st-andrews.ac.uk)

Solène MORELLE, Natalie PILAKOUTA

Abstract

Rising global temperatures are expected to impose increasing thermal stress on ectothermic organisms, with consequences for reproduction. While the direct physiological effects of thermal stress on fertility are increasingly well documented, far less is known about how adverse temperatures indirectly influence reproductive outcomes through behavioural pathways such as parental investment. In species with parental care, reproductive success reflects a balance between investment in current offspring and self-maintenance to preserve future reproductive opportunities. We investigated how constant warm conditions influence this balance via reproductive investment across breeding bouts in the burying beetle *Nicrophorus vespilloides*, a species exhibiting extensive biparental care. Breeding pairs were exposed to either a benign (20 °C) or chronically warm (23 °C) thermal environment and allowed to breed twice with the same partner. We quantified pre- and post-hatching parental care, reproductive output, offspring performance, and parental mass change as a proxy for somatic investment. We found no evidence that thermal stress altered reproductive investment trajectories across breeding bouts. Instead, breeding bout and temperature exerted independent effects. Across both thermal treatments, the first breeding bout was characterised by smaller broods and greater parental mass gain, consistent with higher residual reproductive investment. In contrast, the second bout showed increased allocation to current reproduction, with larger broods and reduced parental mass gain. Chronic warming significantly reduced brood size and brood mass and decreased female mass gain, irrespective of breeding bout. Notably, parental care duration and carcass preparation did not differ between treatments or bouts. Together, these results indicate that moderate chronic warming constrains reproductive performance and female condition without fundamentally altering parental care strategies. Importantly, pronounced differences between breeding bouts highlight that reproductive investment is dynamic across an individual's lifetime, emphasising the need to incorporate lifetime reproductive allocation when predicting the effects of climate warming on fitness and population persistence.

Feeling the urban heat - From the limits of thermoregulation to the consequences for larval development in bumble bee colonies

Jade ZANUTTO (Centre d'Ecologie Fonctionnelle et Evolutive (CEFE) UMR 5175, CNRS, Jade.zanutto@cefe.cnrs.fr)

Alexia LAFORGE--MAHÉ, Marie-Amélie PUSSACQ--CAILLET, Pierrick AURY, Maryse VANDERPLANCK

Abstract

Urbanization is posing important threats to pollinator populations via increasing stressors, such as the urban heat island (UHI) effect. The UHI can alter local thermal environments by increasing temperatures by 2–4 °C compared to surrounding rural areas. It can also generate distinct diurnal thermal patterns and is often associated to more intense heat events, which can significantly affect bee biology, making UHI a potential threat to their development and survival. For instance, bumble bee colony success depends on maintaining brood temperature within a narrow optimal range. Then, two main scenarios could arise within colonies exposed to local warming: (1) the sustained thermoregulatory behaviour of workers to compensate warming involves substantial energetic costs at the expense of other brood cares, reducing offspring production (allocation hypothesis); (2) the thermoregulatory behaviour can no longer maintain optimal brood conditions, which directly affects larval development, reducing offspring success (tolerance hypothesis). To disentangle these hypotheses, we performed two different experiments. First, we exposed bumble bee colonies to field realistic thermal scenarios, mimicking either rural or urban temperatures during 35 days, including or not a 5-day heatwave events. We assessed the thermal limits of colony thermoregulation and evaluated effects on colony success. Second, we exposed bumble bee larvae to brood realistic scenarios until emergence, mimicking optimal brood temperature, including or not a 5-day UHI heatwave. Larvae were exposed at UHI heatwave either at larval, prepupal or pupal stage; and manually fed when needed. We monitored mortality and recorded the mass of emerged individuals. Our results showed that UHI impact on bumble bee colonies may arise from both indirect (allocation hypothesis) and direct (tolerance hypothesis) effects, with different contributions according to the occurrence of heatwave and the brood developmental stage.

Impact of heat waves on colony foundation in ants

Alice ROUX (IRBI - Université de Tours, Alice.roux@univ-tours.fr)

Abstract

Climate change increases the frequency and intensity of extreme heat events, which have the potential to affect the survival and reproduction of organisms. These effects have broader impact when they target ecosystem engineers, such as ants. Ant colonies may appear relatively protected against thermal perturbations by the nest architecture and their collective behavior, but founding queens that start their colonies alone are more exposed to heat events. We recently demonstrated that a short, acute heat stress reduced the success of colony foundation in the black garden ant *Lasius niger*. Here, we tested whether 4-day long exposures to constant temperatures (35°C or 38°C) had a different effect on colony foundation compared to fluctuating temperatures (35°C or 38°C during the day; 25°C during the night). In addition, we investigated whether these heat treatments had different impacts depending on whether queens founded their colony alone (haplometrosis) or in cooperation with another queen (pleometrosis). Preliminary analyses suggested that fluctuating temperatures reduced the negative impacts of heat treatment on queen mortality, worker production and/or brood development. However, there appeared to be limited evidence that cooperative founding provided protection against the negative effects of heat stress on the success of colony foundation. Further analyses will confirm or complement these findings to provide a better understanding of the impact of climate change-driven thermal perturbations on the foundation of ant colonies, and thus potentially on the density of their populations and the ecosystemic services they provide.

Does heat stress induce transgenerational effect on worker behaviour in the ant *Lasius niger*?

Sophie VAN MEYEL (Insect Biology Research Institute (IRBI, UMR 7261) CNRS - University of Tours, Sophie.vanmeyel@univ-tours.fr)

Alice ROUX, Irene VILLALTA, Marlene GOUBAULT, Romain LIBBRECHT

Abstract

Climate change is increasing the frequency and intensity of heatwaves defined as periods of unusually high day and night temperatures. Because insects have limited thermoregulatory capacity, these extreme events strongly affect their life-history traits and behaviour. In addition to their direct effects, heatwaves may also produce transgenerational effects: parents exposed to heat stress may produce offspring with altered developmental time, body mass, reproduction and survival. However, transgenerational effects of heatwaves on offspring behaviour in insects remain poorly studied. In this study, we used the black garden ant *Lasius niger* to test whether the experimental exposure of founding queens to a temporary heat treatment affected the behavior of workers that were subsequently produced. In this species, founding queens establish their colonies in early summer and are thus likely to experience intense heatwaves. We exposed 72 *L. niger* founding queens for four days to one of three temperature treatments: constant 25°C, constant 35°C or fluctuating 35°C/25°C (12h/12h). The queens were then returned to standard laboratory conditions to let them establish their colonies. Once colonies were large enough, we investigated the behaviour of the workers produced by the treated queens. We conducted group-level measurements of their general activity, exploratory behaviour, intraspecific aggression, brood care, and foraging. We are currently in the process of performing the behavioural analyses to determine whether the heat treatments experienced by the queens induced transgenerational effects on worker behaviour. This study will inform on potential consequences of climate change-driven thermal perturbations for ant colony efficiency and performance.

Can bumble bees take advantage of dietary antioxidants to face thermal stress?

Maryse VANDERPLANCK (CEFE, Univ Montpellier, CNRS, EPHE, IRD, Montpellier, France, Maryse.vanderplanck@cefe.cnrs.fr)

Pierrick AURY, Jade ZANUTTO

Abstract

To face environmental stressors, animals including bees may display behavioral plasticity to improve their physiological status through ingestion of specific food items. However, the significance of medicating resources may be limited by the ability of bees to exploit them. Until now, studies have mainly focused on the medicinal effects of floral resources on parasite infection after forced-feeding experiments, but overlooked spontaneous food intake, social context and abiotic stressors. Among abiotic stressors, elevated temperatures are posing important threats to pollinators. Beside the global warming of the annual average temperature, bees also face stressful thermal patterns either locally, such as urban heat island (UHI) effect, and/or temporally, such as seasonal heat waves. These stressors are likely to impact the physiology of wild bees as they can affect their oxidative status, giving rise to structural and functional damage, potentially causing death (i.e. oxidative stress). In this context, the ingestion of dietary antioxidants should allow for attenuating the damaging effects of elevated temperatures. Here, we present an experiment to determine whether bumble bees favored antioxidant resources when exposed to UHI heat waves, taking into account social context (i.e. brood occurrence). We exposed bumble bee micro-colonies, with or without brood, to field realistic thermal scenarios mimicking either rural temperatures or urban heatwave events during eight days. All micro-colonies were given the choice between food resources with and without antioxidant effects. We measured the daily consumption of each solution and assessed the reproductive success for micro-colonies with brood. This experiment aims to demonstrate potential self-medicative behavior in bees, which could be one of the key mechanisms determining their capacity to cope with living in a changing world. A better understanding of such behavior could greatly improve pollinator conservation programs by proposing nature-based solutions, such as promoting a medicative flora.

The value of purposeful Citizen Science for insect monitoring, action and engagement

Michael POCOCK (UK Centre for Ecology & Hydrology, Michael.pocock@ceh.ac.uk)

Abstract

Getting involved with citizen science provides great benefits for participants – breaking down barriers for volunteers to contribute to evidence-based decision-making, while boosting their connection with nature, people and places. It benefits science and monitoring through the cost-effective collection of data at unprecedented scales – on common, rare or invasive insect species. But how do we develop citizen science that is purposeful, so that it has even greater impact on action for nature and for people? National and global platforms for opportunistically collected insect species records are incredibly valuable – including, as we have shown, supporting early detection of invasive species. But I contend that in many instances we don't simply need more data points from citizen science, we need more informative data. In addition to structured citizen science, such as the highly successful butterfly monitoring schemes across Europe, we have explored 'targeted citizen science', using tools to motivate volunteers to collect records from where they are most needed. Technology has transformed what is possible in citizen science, such as using AI for image recognition which, combined with our new, validated design for low-cost LED moth traps, has opened up moth recording to farmers. It can also transform feedback, enabling us to personalise the feedback given to volunteers, thus boosting their motivation and sustained participation in projects. But simple methods are great too. Simple methodologies, such as those we have developed for school children to monitor pollinators or rear parasitoids from micromoths (revealing the hidden side of insect ecology), give more people the opportunity to contribute to science and monitoring and boost their skills, connection to nature and hence their wellbeing. While biodiversity is in crisis across the world, insect citizen science is valuable - let's ensure it continues to make a difference for people and for nature.

Insect Investigators: a school based citizen science project transforming insect education, Australian (wasp) taxonomy and biodiversity data

Andy HOWE (University of the Sunshine Coast, Australia, Ahowe@usc.edu.au)

Abstract

Citizen science is a powerful approach to advance entomological research; embedding it in schools also enriches opportunities for STE(A)M education. In Australia, the Insect Investigators project demonstrates how school based biodiversity surveys can simultaneously foster meaningful learning outcomes for students and build teachers' confidence, while also mapping and describing Australia's arthropods. From 2021–2023, 50 schools across Australia operated Malaise traps to document local arthropod diversity, contributing thousands of specimens and 10,147 BINs (54.7 % new to BOLD) to BOLD and national databases, while empowering students to participate directly in entomological research.

Evaluation of the project's educational impact showed that participation significantly increased students' intentions to engage in insect–nature–science activities including 'acting to' and 'encouraging others to protect nature; students highlighted hands-on discovery, interacting with scientists, and the excitement of uncovering undescribed species as valued experiences. Teachers reported heightened motivation to incorporate entomology, taxonomy, biodiversity and sustainability into their teaching.

Student collected specimens made tangible research contributions including the description of 15 previously undescribed parasitoid wasps (to-date) with students participating in the naming process through structured collaborative workshops. Student collections expanded insect distribution records, helped document native wasps exploiting the invasive Fall armyworm (*Spodoptera frugiperda*), and provided critical DNA barcodes for ongoing biocontrol and biodiversity research, and biosecurity monitoring.

This talk will explore examples from Insect Investigators which integrate real entomological research into real schools, providing STE(A)M opportunities, enhancing biodiversity datasets, and accelerating parasitoid taxonomy while demonstrating that school students can meaningfully contribute to (and do give a damn about) entomology.

#12057

INSECTS & SOCIETY: Entomological education and citizen science in entomology

29/06/2026 at 11:45, Bourgueil

The Spipoll citizen-science programme: ecological and social findings from more than 15 years of experience monitoring plant-visitor interactions in France.

Nicolas DEGUINES (Université de Poitiers, Laboratoire EBI, Nicolas.deguines@univ-poitiers.fr)

Mathieu DE FLORES, Baptiste BEDESSEM, Ana-Cristina TORRES, Grégoire LOIS, Romain JULLIARD, Colin FONTAINE

Abstract

Understanding threats to flower visitors – beyond bees – amid global environmental changes is crucial for ecosystem function and human well-being.

The Photographic Survey of Flower Visitors (Spipoll) was launched in 2010 in France, engaging citizen scientists to document plant-visitor interactions using a standardized protocol. Volunteers photograph all organisms visiting a plant species' flowers for 20 minutes. Identifications are verified by experts and/or peer volunteers. Over 650,000 interactions across 75,000 locations have been recorded. This unique dataset informs research on flower visitors' responses to environmental gradients.

Based on the 16 years and counting of experience of the Spipoll programme, the talk will i) highlight its main ecological and social findings, ii) discuss methodological development, and iii) envision scientific perspectives.

#12256

INSECTS & SOCIETY: Entomological education and citizen science in entomology

29/06/2026 at 12:00, Bourgueil

A citizen science program as an educational tool for understanding the relationships between pollinating insects and plants

Simon BÉNATEAU (CESCO - Museum national d'Histoire naturelle, Simon.benateau@mnhn.fr)

Vincent CHASSANY

Abstract

SPIPOLL is a citizen science program that involves photographically monitoring pollinating insects according to a specific protocol. It is available to the general public and schools (Vigie-Nature École). For 20 minutes, students participating in “Vigie-Nature Ecole” can photograph all the insects present on a given species of flowering plant. Once sorted, cropped, and identified, the photos are uploaded to a dedicated interface and added to a database for research purposes. Vigie-Nature Ecole has developed an interactive analysis tool that allows this database to be used for educational purposes. It is thus possible to represent pollinating insect/plant networks in order to answer simple scientific questions, leaving a large part of the initiative to the students while developing their critical thinking skills.

BOB: a citizen science initiative for studying eto-ecological traits of stag beetles

Alice LENZI (CREA, Council for Agricultural Research and Economics, Italy, Alice.lenzi@crea.gov.it)

Alessandro CAMPANARO, Silvia GISONDI, Fiorenza SPOTTI, Matteo BISANTI, Cristina CASTRACANI

Abstract

Lucanus cervus is an obligate saproxylic beetle protected under the EU Habitats Directive whose distribution is linked to dead wood availability in mature and unmanaged forests. Nevertheless, the species also occurs in urban parks or agricultural areas with isolated old trees. While numerous studies have addressed its biology, ecology, population dynamics and monitoring methods, few have leveraged citizen science for systematic investigations of its ethological traits.

The project “Behavioural Observation in Beetles” (BOB) represents the first Italian citizen science initiative specifically aimed at recording observations on *L. cervus* eto-ecological traits. BOB started in 2024 building on experience gained from two previous projects (i.e., LIFE11 NAT/IT/000252 “MIPP” and the national initiative “InNat”), which focused on the collection of distributional data on protected insects, including the stag beetle. The analysis of photographic records from these projects allowed the identification of behavioural traits that can be easily detectable by volunteers and highlighted potential challenges in data interpretation. These insights informed the design of the sampling protocol implemented in BOB, the development of a dedicated smartphone application and the definition of volunteers engagement strategies.

Following a pilot phase conducted in summer 2024 in the Boschi di Carrega Regional Park (Northern Italy) with a group of trained volunteers, the protocol and the app were refined for broader application. In summer 2025, the first national data collection campaign was carried out. To date, the BOB platform includes 557 validated records (~90% of the total), collected by 105 contributors from more than 130 municipalities and 13 regions.

This contribution presents the preliminary results of the project, describes the app structure and the sampling protocol and discusses lessons learned during the initial implementation phase. Moreover, this conference session will represent a valuable opportunity to promote BOB at international level and to engage new participants for future field seasons.

Beyond distribution maps: what citizen science reveals about protected insect species

Alessandro CAMPANARO (CREA, Council for Agricultural Research and Economics, Italy, Alessandro.campanaro@crea.gov.it)

Alice LENZI, Silvia GISONDI

Abstract

Citizen science initiatives are increasingly recognized as effective tools for collecting large-scale biodiversity data, for a wide range of organisms, including insects. The MIPP/InNat project, active in Italy between 2014 and 2024, engaged citizens in recording occurrences of protected insects by uploading photographs of the encountered species via a dedicated smartphone application or the project website. Over ten years, 1,180 volunteers contributed 5,968 validated occurrence records, encompassing 6,292 specimens belonging to Coleoptera, Lepidoptera, Odonata, and Orthoptera. Analyses conducted on nine species revealed a significant increase in distributional knowledge, without no evidence of a spatial saturation. Such a result is observed both considering the growing numbers of newly occupied UTM 10x10 km cells, and the different shapes and densities of alpha-hulls polygons. Beyond the distributional data, we explored the potential of these opportunistic photographic records for eco-ethological investigations, using 2,090 images of the beetle *Lucanus cervus*. Despite the absence of a standardized protocol, approximately 39% of records were suitable for behavioural interpretation, revealing sex-specific patterns consistent with literature: e.g., males mostly associated with flight and, in case of resting, with trunks or branches of trees, females mostly ground-dwelling, and mating pairs associated with dead wood. Finally, to assess the educational and social dimensions of the project, a sociological survey covering 364 participants was conducted. Results identified two main volunteer profiles based on the number of records collected and the duration of participation. In addition, engagement resulted strongly linked to leisure, social interactions, and interest in science and conservation. Face-to-face communication emerged as a key entry point, while digital tools and social platform supported the long-term involvement. Overall, MIPP/InNat demonstrates how citizen science can simultaneously enhance scientific knowledge on protected insect species, support conservation planning, and foster public engagement and entomological education.

Arthropods on the world-wide web: generating social-ecological insight with internet search volume data to estimate abundances, distributions and public perceptions

Jordan CUFF (Newcastle University, Jordan.cuff@ncl.ac.uk)

Rafael BADELL-GRAU, Fredric WINDSOR, Kyle MILLER, Ben HAWTHORNE, Maximilian TERCEL

Abstract

As we move deeper into the Anthropocene, the interactions between people and arthropods become increasingly frequent, but also increasingly take place in digital spaces. The data linked to these digital interactions, particularly internet search volumes, present an unprecedented opportunity for social-ecological insight and ecological inference, yet remain scarcely explored.

Here, we demonstrate the utility of Google Trends as a tool for investigating interactions between people and arthropods using three exemplar applications. We first demonstrate the alignment of search volume data with insect phenologies to assess the utility of Google Trends for generating a continuous proxy for traditional biomonitoring data. Second, we show that search volume data can reveal the adoption and use of both common and scientific names, with implications for communicating science to both public and scientific communities. Third, we show how search volume data can be used to assess public awareness of invasive species, which may be key for tracking and mitigating invasive establishment and other animal distribution shifts. Integration of search volume data into these and broader ecological contexts, which we refer to as 'ecological inforeveillance', could provide valuable data related to our evolving interactions with arthropods. By facilitating wider adoption of this approach, we hope to stimulate further development and extension of these ideas for enhanced social-ecological insight.

#10438

INSECTS AS SOLUTIONS: Biomimetism - From biological to bio-inspired photonic materials

29/06/2026 at 14:30, Bourgueil

Insect Inspired Structural Colour

Ulrich STEINER (Adolphe Merkle Institute, Univeristy of Fribourg, Ulrich.steiner@unifr.ch)

Abstract

Although photonic colouration derived from 100-nm morphologies is widespread in the animal kingdom, it is rarely employed in synthetic colourants. This is largely because of the high level of precision required to produce photonic materials. My group's research therefore begins by studying the natural world. Using 3D tomography, we examine the internal structure of coloured insect scales. This enables us to identify the underlying structure of the scales and relate it to their colour. The aim of these studies is to develop a physical model that explains the origin of colour, enabling us to replicate insect colouration synthetically. Our ultimate goal is to formulate inexpensive 'photonic paints'. This presentation summarises the progress we have made towards achieving this goal.

#11910

INSECTS AS SOLUTIONS: Biomimetism - From biological to bio-inspired photonic materials

29/06/2026 at 15:00, Bourgueil

The arthropod cuticle: Materials toolbox for functional diversity

Yael POLITI (TUD Dresden University of Technology, Yael.politi@tu-dresden.de)

Abstract

Nature has evolved materials that are used for a wide range of functional challenges with minimal compositional changes. The exoskeletal cuticle of arthropods is such as example -made of a combination of chitin, protein, water and small amounts of organic cross-linkers or minerals. The cuticle serves mechanical, optical and sensory functions with minimal compositional modification, achieving a wide range of materials properties based on its hierarchical structure. How the 'design space' of a single type of is capable to serve a remarkable diversity of functions, when engineered systems are typically based on a large variety of materials? In this talk I will focus on our recent work in the context of cuticle optical performace.

Under the Surface: A Novel 2.5-Dimensional Photonic Structure in Fiddler Beetles

Laura Bibiana OSPINA ROZO (School of Biosciences - University of Melbourne - Parkville Victoria 3010 – Australia, Laura.ospinarozo@unimelb.edu.au)

Zezheng ZHU, Nicola Serenity KUBZDELA, James A. HUTCHISON, Mia WANSBROUGH, Nanfang YU, Devi STUART-FOX

Abstract

Despite decades of study, beetle photonic architectures continue to reveal new ways of manipulating light. While beetles exhibit a wide range of one-, two-, and three-dimensional photonic structures with varying degrees of order and disorder, 2.5-dimensional architectures are rare in this group. Here we report the discovery of a novel 2.5-dimensional photonic structure in the green stripes of the fiddler beetle, *Eupoecila australasiae*. Unusually for a scarab, the colour arises from a continuous sheet of fin-like elements located beneath the endocuticle, while the characteristic chiral exocuticle contributes little to the overall reflectance. Electron microscopy shows that each flat fin is covered on both sides by complementary arrays: a triangular lattice of spheres and a matching lattice of holes, each controlling different regions of the reflected spectrum. The fins are tightly packed but vary in orientation, a form of disorder that produces an intense opaline appearance at the microscopic scale and enhances broadband diffuse reflectance at the macroscopic scale. The fins are perpendicular to the endocuticle, so light enters the structure and travels along the patterned faces rather than interacting perpendicularly with a two-dimensional surface. At the same time, the lattices do not repeat through a large volume like a three-dimensional crystal, placing the structure in the 2.5-dimensional category. In line with this, computational models show that the structure supports leaky optical modes, a desirable feature for creating strong, broadband, and angle-robust light–matter interactions. Our work expands the known diversity of biological photonic materials and offers new inspiration for developing scalable 2.5D biomimetic photonic systems.

UV reflectance and scale ultrastructure in *Eriogaster catax* (Lepidoptera: Lasiocampidae)

Lorenzo GIULIVI (University of Perugia, Lorenzo.giulivi@dottorandi.unipg.it)

Matteo PALLOTTINI, Enzo GORETTI, Gianandrea SALERNO, Silvana PIERSANTI, Manuela REBORA

Abstract

Ultraviolet wing patterns are widespread in Lepidoptera, playing important roles as visual cues in intra- and interspecific communication. Within Lepidoptera, crepuscular species appear to display UV patterns more frequently, potentially due to the reduced pressure from UV-sensitive predators like birds. Here we investigate the UV optical properties and scale ultrastructure of *Eriogaster catax* (Lepidoptera: Lasiocampidae), a species of high conservation priority under the EU Habitats Directive (Council Directive 92/43/EEC) and the Bern Convention. Reflectance measurements revealed a high contrast between wing regions. The characteristic white spot on the forewings of both sexes showed strong UV reflectance, whereas the surrounding brown areas reflected almost no UV. Hindwings also reflected UV light, although at noticeably lower levels. Preliminary observations of the white and brown scales under stereomicroscopy showed that white colour has a structural origin (scattering due to ribs and microribs and interference due to overlapping scales), whereas brown colour is due to pigmentation. At scanning electron microscopy (SEM), both white and brown scales appeared palmate and are anchored to the surface by peduncles. The upper surface shows well developed ridges with overlapping lamellae. The space between the ridges is closed by a lamina with microribs. Large windows are absent: instead, an irregular row of small pores is present in the central area between two ridges. The ultrastructural organization of the white and brown scales was compared using transmission electron microscopy (TEM). This study expands our knowledge of a poorly studied species of high conservation interest, revealing complex optical features in its wings and setting the groundwork for future research on the ecological and behavioural function of UV reflectance in *E. catax* and related taxa.

Reverse engineering the Christmas beetle (*Anaplognathus aureus*) – towards creation of structural gold colouration

Mia WANSBROUGH (University of Melbourne / University of Manchester, Mia.wansbrough@student.unimelb.edu.au)

Laura OSPINA-ROSO, Ahu GUMRAH-PARRY, Devi STUART-FOX

Abstract

Across beetle species, a striking diversity of structural arrangements produces intense golden colouration - natural designs that could guide the creation of synthetic materials. Although human-fabricated materials can be engineered to produce tuneable hues, they seldom achieve the saturation and brightness of beetle structural colour without complex fabrication. As such we compared the ways in which two unrelated beetle species, *Paropsisterna hectica* and *Anaplognathus aureus*, produce gold, with the goal of identifying and replicating the most efficient way to maximise the broadband reflectance of cellulose nanocrystals (CNCs). We found that *P. hectica* uses over 100 alternating layers of two different materials to produce gold, where each layer is roughly 100nm in thickness. Conversely, *A. aureus* generates gold using only a single chiral material, arranged in a sandwich-like structure where layers of larger pitch bookend layers of smaller pitch. Drawing on this natural architecture, we designed a 'sandwich' arrangement of self-assembled CNC layers that mimics the organisation of *A. aureus*. This approach eliminates the need for complex layer by layer deposition required to fabricate *P. hectica*-like multilayers. To realise this design, we assembled CNC layers of larger (red-shifted) and smaller (blue-shifted) pitch, separated by a thin layer of shellac and stabilised with glutaraldehyde as a crosslinker. The resultant stack possessed similar broadband and intense gold reflectance as has been observed in beetles. Further work will focus on the optical characterisation of these films to quantify how this design provides a more efficient route to enhancing broadband reflectance and intensity in CNC-based thin films. This will expand our ability to tune not only colour but also brightness and amount of light reflected in self-assembled, human-fabricated materials.

When is a simple chitin multilayer not a simple chitin multilayer?

Jeton KOXHA (University of Bath, Jk2488@bath.ac.uk)

Rox MIDDLETON, Sepideh KHODAPARAST

Abstract

Damselfly (*Neurobasis chinensis*, *N. kaupi*) wings are a classic example of an optical multilayer system. The wing membrane consists of six bilayers of chitin and melanised chitin atop a thick, melanin-rich base, a structure that is well established and has been successfully modelled using transfer matrix methods as a simple multilayer stack [1]. Here, we extend this model by incorporating a disordered nanopillar surface layer, which accounts for a substantial visible shift in the reflected colour relative to the bare multilayer. Although moth-eye-like nanostructures are widespread on biological surfaces, their contribution to the spectral position of reflected light has been treated only sporadically [2]. The wax-based nanopillars, unlike chitin-based moth-eye structures, undergo a melting phase transition when exposed to conductive or radiative heating, collapsing into a flat interfacial wax layer. The wax layer can also be selectively removed by chemical or mechanical delamination, enabling access to multilayer structures with a nanopillar-covered surface, a flat wax interface, or no wax layer. Using these controlled structural states, we investigate the coupled heat- and moisture-responsive behavior of the damselfly wing as a composite multilayer-nanopillar system.

[1] Remarkable iridescence in the hindwings of the damselfly *Neurobasis chinensis chinensis* (Linnaeus) (Zygoptera: Calopterygidae) Vukusic, Wootton & Sambles, Proc Biol Sci (2004)

[2] Antireflective Multilayer Surface with Self-Cleaning Subwavelength Structures, Rombaut et al. ACS Photonics (2021)

A genetic dive into how UV-iridescent butterfly wings make multilayered interference filters

Arnaud MARTIN (The George Washington University, Arnaud@gwu.edu)

Joseph HANLY, Ling Sheng LOH

Abstract

Butterfly wing scales are derived from single cells and can develop extraordinary 3D ultrastructures. For example, males of the sulphur butterfly *Colias eurytheme* develop bright UV-iridescent color scales used in courtship displays, characterized by highly organized stacks of ~80-nm-thick air/cuticle layers that act as a quarter-wavelength Bragg's reflector. Using genetic mapping in crosses with a sister species that lacks this male-specific signal, CRISPR and RNAi perturbations, and analysis of gene expression during pupal development, we previously showed that alleles of the transcription factor Bric-a-brac repress UV scale identity, and that the sexual differentiation gene Doublesex is required to prevent the formation of UV iridescence in females. In other words, Bric-a-brac and Doublesex act as master regulators of UV-trait differences between species and sexes, respectively. This knowledge provides a wedge into the deeper molecular basis of scale differentiation, particularly the formation of the chitinous ridges involved in UV iridescence. Using bulk and single-cell transcriptomics, we are describing the gene expression profiles that demarcate this specialized scale type, providing new insights into the molecular control of cytoskeletal patterning, cuticle secretion, and chitin modification. We believe that integrating functional genomics, cell biology, and biophysics in the study of butterfly scale development will enable breakthroughs in our understanding of how cells construct nanoscale 3D morphologies with extraordinary precision.

Biomimetics of hierarchical mesoscopic structuration in insect scales

Vinod Kumar SARANATHAN (IRBI (UMR 7261), CNRS/Université de Tours, Saranathan@univ-tours.fr)

Abstract

Insects are the most numerous and the most successful animals on Earth. Among organisms, not surprisingly, insects display a remarkable and possibly unrivalled array of multi-functional nanostructures especially within specialised setae or scale cells. These nanostructures are sculpted hierarchically (layer by layer) by membranous precursors that are back-filled with cuticle, and later the cytoplasm is replaced by air when the cell dies. These intracellular processes pre-empt contemporary engineering ones and offer considerable biomimetic interest to physicists and engineers interested in sustainable manufacturing. Many of these features are self-assembled at the hard to achieve mesoscopic length scales (100-500 nm), i.e., in the visible regime, but also function to simultaneously impart thermoregulatory, aerodynamic and hydrophobic properties in addition to photonic. Insect scale nanostructures can also be patterned mechanically by buckling producing sub-micron features that rival our most complex designs for flexible electronics and soft robotics. Synthetic self-assembly (colloidal, lyotropic, surfactant or block-copolymers) cannot easily produce nanostructures with large dimensions. Currently, lithographic techniques are restricted to near IR regimes, and while nanostructures with smaller lattice parameters can be fabricated via 3D-printing (stereolithography) followed by heat shrinkage, they are defect-ridden, not scalable or sustainable. Current nano-imprint lithographic techniques are also not defect tolerant and the toxic photoresists used are similarly not sustainable. In this talk, I will summarize the current understanding of how biology patterns multi-functional nanostructures and conclude with some biomimetic lessons for engineering given our dire need for sustainable manufacturing approaches for next-generation functional devices and technology.

#10116

WORKSHOP: Long-term perspectives on biomimetics

29/06/2026 at 17:30, Bourgueil

Amorphous photonic networks in insect cuticles

Bodo WILTS (University of Salzburg, Bodo.wilts@plus.ac.at)

Abstract

Complex nanostructures grant butterflies, beetles, birds, and spiders their stunning visual displays. These photonic nanostructures exhibit varying degrees of local order, and their interactions with light determine the final appearance of these creatures. With diverse chemical compositions, these structures blend structural and pigmentary colors in unique ways. Insects, with their vast array of colorful displays, serve as particularly fascinating subjects. We present recent findings on insect species that showcase vivid colors by combining (dis)order and pigments. Employing light microscopy, FIB-SEM tomography, and FDTD simulations, we present and investigate into the mechanisms behind angle-independent color patterns and emphasize the significance of disorder in the creatures' final appearance. Our work demonstrates the intricate interplay between structural and pigmentary color, and thereby offers insight into the development of innovative optical materials. Indeed, there is much to learn from nature's mastery of color and light, particularly by imaging the metamorphosis of insects in vivo.

Field entomological research towards implementation of gene-drive based malaria control

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Abstract

The University of California Malaria Initiative (UCMI) is a not-for-profit collaborative program developing innovative malaria control strategies based on genetically engineered mosquitoes (GEM) with gene drive. We aim at modifying wild *Anopheles* populations with a *Plasmodium*-refractory GEM, unable to transmit malaria parasites.

Since 2019, UCMI has conducted research on the islands of São Tomé and Príncipe (STP), in partnership with the Ministry of Health and the University of São Tomé and Príncipe, with the purpose of generating baseline data on malaria transmission and vector biology to support evidence-based decisions on GEM deployment. The objectives are: i) determine mosquito population structure, essential for GEM field trial design; ii) assess bio-ecological and phenotypical impacts of colony establishment, to predict GEM fitness; iii) study potential environmental impacts, to inform risk analysis and mitigation plans.

In STP, malaria is transmitted by a single vector, *Anopheles coluzzii*. Genetic studies reveal strong isolation, with negligible gene flow between islands and with the continent. Conversely, there is considerable inter-island mosquito movement, especially in the dry season. Compared to mainland populations, these mosquitoes show unusual behaviors, namely strong zoophilic feeding and propensity for outdoors biting and resting. These traits likely reflect selective pressures from indoor insecticide use and adaptation to the predominant local housing type. High levels of pyrethroid resistance agree with this interpretation. Aquatic macroinvertebrate surveys identified Odonata dragonflies as key ecological indicators for monitoring GEM impacts.

These findings led UCMI to propose a first experimental release on the island of Principe, pending STP government approval. Challenges and prospects of the program will be discussed.

Metabolic resistance of the tiger mosquito to pyrethroid insecticides in La Réunion Island likely results from local adaptation

Jean-Philippe DAVID (Centre National de la Recherche Scientifique, Grenoble, Jean-philippe.david@univ-grenoble-alpes.fr)

Tiphaine BACOT, Jean-Marc BONNEVILLE, Vincent LACROIX, Pascal OBERBACH, Thierry GAUDE, Louis NADALIN, Frederic LAPORTE, Nausicaa HABCHI-HANRIOT, Guillaume DUPUY, Cyrille CZEHER, Michael FONTAINE, Frederic BOYER

Abstract

The resistance of mosquitoes to insecticides is a valuable model system for studying the genetic bases of xenobiotic adaptation in insects. The spread of the Asian tiger mosquito *Aedes albopictus* combined to the massive use of pyrethroid insecticides to limit arbovirus transmission resulted in the rise of resistance in various continents. Here, we investigated the genetic mechanisms underlying the recent adaptation of this mosquito to deltamethrin in La Réunion island. Bioassays confirmed the presence of resistance alleles in field populations. The resistance phenotype was further enhanced in the laboratory following a few generations of controlled selection. Combining whole genome Pool-seq and RNA-seq revealed no evidence of target-site resistance mutations but the over-expression and variant selection of detoxification enzymes associated with pyrethroid metabolism including cytochrome P450s, transferases and ABC-transporters. Among over-expressed detoxification genes, only one was linked to a gene duplication while polymorphism data suggest most of them being trans-regulated. Genome-wide selection signatures also revealed a 9 Mb inversion acting as a superlocus likely under insecticide selection. Altogether, this study indicates that the multigenic metabolic resistance phenotype observed in this insular territory mainly results from local adaptation. From an applied perspective, this study provides a set of markers to track pyrethroid resistance in the tiger mosquito in the South-West Indian Ocean. As this region is subjected to recurrent arbovirus outbreaks, the additive resistance phenotype that may arise from the introduction of Kdr mutations from other territories also calls for improving resistance surveillance at the regional scale.

The Snapshot Mosquito Survey: a stratified approach to sampling mosquito biodiversity and arbovirus risk across England's wetlands.

Bathsheba GARDNER (UK Health and Security Agency , Bathsheba.Gardner@ukhsa.gov.uk)

Robert BRUCE, Alexander VAUX, Anthony ABBOTT, Arran FOLLY, Jolyon MEDLOCK

Abstract

As climate change reshapes local micro-climates and influences species dispersal, temperate regions such as England face heightened susceptibility to arbovirus expansion, presenting challenges for public and veterinary health agencies. Usutu virus (USUV), first identified in a wild blackbird in London in 2020, is now thought to be endemic to the Southeast of England. Furthermore, for the first time, West Nile virus (WNV) has been detected in native *Aedes* mosquitoes in 2023.

To improve mosquito surveillance coverage, the Snapshot Mosquito Survey was initiated in 2024. This project aimed to provide a stratified approach to wetland sampling across England, provide data on native mosquito distributions and arbovirus presence, and develop collaboration and public engagement to support vector surveillance.

Volunteers from across the country were recruited to run a BG Pro mosquito trap at a wetland habitat in every 50km² grid square in England. Traps were deployed for three-night trapping sessions, and run two to three times, during the season of peak vector activity and peak USUV virus transmission (July – September). All mosquitoes captured were morphologically identified using dichotomous keys and screened for USUV and WNV.

The project successfully expanded mosquito surveillance in 2024 and 2025, covering a total of 73 of the 82 major grid squares in England, and engaging 87 separate sites, some of which had never been surveyed for mosquito populations before.

Across years, the project caught 2,298 mosquitoes, representing 14 of the UK's native species. Most were ornithophilic wetland-associated species, demonstrating that stratified sampling can successfully target probable USUV and WNV vectors. The project also identified areas of local USUV transmission, providing evidence that transmission events were more widely distributed than previously confirmed.

Results demonstrate that a citizen-science-driven snapshot survey is an effective approach for identifying local arbovirus transmission and vectors in previously unstudied habitats.

#11045

INSECT VECTORS: Medical entomology 1

29/06/2026 at 15:30, Chinon

UK Nationwide Wetland Mosquito Programme

Anthony ABBOTT (UK Health Security Agency, ANTHONY.ABBOTT@UKHSA.GOV.UK)

Harrison HARDY, Bathsheba GARDNER, Roksana WILSON, Amy EDWARDS, Colin JOHNSTON, Alexander VAUX, Jolyon MEDLOCK

Abstract

The Nationwide Wetland Mosquito Programme has been run since 2010, at over 70 Wetlands across the UK. The project aims to better understand the seasonality and distribution of native mosquitoes and detect new and novel mosquito species. Native mosquito populations can pose a public health risk, with some UK species known to be competent bridge vectors for Usutu virus, which has recently been detected in mosquito and bird populations in the UK, and West Nile Virus, Notably *Culex modestus*. In addition, some native mosquitoes, such as *Aedes vexans* and *Aedes caspius* are prolific human biters, leading to nuisance biting complaints where they occur.

This is an update on the results 2023, 2024 and 2025 Nationwide Wetland Mosquito Programme, and how the distribution and abundance of mosquitoes at key sites has changed over these years. Over the three years, mosquito traps were run by volunteers at 46 sites across England and Wales. The traps were run from June to October, on a fortnightly basis. During these years the programme focused primarily on wetland habitats, reflecting the diverse ecological niches these environments offer for mosquito populations. A small number of nature reserves in urban areas were also included, this allows us to study the seasonal and distribution of mosquito species in areas where they are most often interacting with the human population, and therefore most likely to pose a public health risk.

By better understanding the seasonality and distribution of native mosquitoes, we can better advice local authorities and wetlands where nuisance biting does occur, and be better prepared should Usutu and WNV.

Advancing Sustainable Solutions for Genetic Vector and Pest Control

Alessandra BOITI (Biocentis, Alessandra.boiti@biocentis.com)

Kyros KYROU, Gerard TERRADAS, Dario MEACCI, Philippos KONDYLIOU, Andrea DE ANTONI, Anna STRAMPELLI, Daniela MAYORGA, Giulia MONACCHIA, Giulia MORSELLI, Ariane CLEMENT, Alice SANTI, Martina CARLINI, Riccardo MORACCI, Alessandra GATTI, Eugenia PIGNATARO, Matteo RUCCO, Andrew M HAMMOND

Abstract

Advancing sustainable solutions for genetic pest and vector control

Invasive pests are a growing concern for public health as well as agricultural production worldwide. Disease-transmitting vectors such as *Aedes aegypti* greatly contribute to the spread of pathogens affecting millions of people, while agricultural pests such as *Drosophila suzukii* cause significant crop damage and economic losses. Current chemical and genetic control methods are limited by the development of resistant strains, mass-rearing limitations, deployment capabilities and costs, and environmental footprint, highlighting the need for more sustainable and adaptable alternatives.

Our technology enables the suppression of invasive pest populations in a localized and temporally restricted manner, while avoiding long-term persistence of the trait in the environment. Even though this approach is species-specific, it is adaptable to most arthropods, thus offering a scalable and flexible framework that aids the control of a wide range of insect vectors and agricultural pests, all while minimizing environmental impact.

Suppressive gene drives and genetic methods to limit them

Chrysanthi TAXIARCHI (Polo d'Innovazione di Genomica Genetica e Biologia (Polo GGB), C.taxiarchi@pologgb.com)

Abstract

CRISPR-Cas9 gene drives hold great promise for sustainable vector control of malaria. The highly suppressive gene drive targeting the doublesex gene in *Anopheles gambiae* has been able to collapse caged populations, in various laboratory settings. Following WHO guidance for a phased approach to testing genetically modified mosquitoes, we conducted long-term studies of *Anopheles gambiae* transgenic lines in large population cages, complex ecological settings that better simulate natural conditions and reveal fitness effects not observable in small-scale experiments.

We engineered an anti-drive system based on the AcrIIA4 protein that effectively suppresses the activity of the suppressive gene drives in *Anopheles* mosquitoes. Cage trials confirmed that the anti-drive strain efficiently contains the spread of the doublesex-targeting gene drive, preventing population collapse. Critically, the complex ecological conditions of large cages uncovered transgene-associated fitness effects that validate the robustness of both constructs under conditions approximating field scenarios.

We present enhanced anti-drive variants and complementary genetic strategies designed to limit gene drive activity and provide control over population dynamics. These approaches expand the toolbox for population-level vector control, enabling dynamic modulation of drives and operational flexibility. Large-cage settings will be used for validation to bridge small-scale laboratory studies and potential field releases.

Spread of Invasive Aedes Species on the Northern Black Sea Coast

Kseniia SYCHEVA (Department of Entomology, Biological Faculty, Lomonosov Moscow State University, Moscow, Russia, K.sycheva2019@gmail.com)

Yuliya LOPATINA, Irina KOVALENKO, Evgeny MOROZKIN

Abstract

The spread of insects beyond their endemic ranges has long attracted scientific attention due to their capacity to survive and adapt. This issue is of particular importance when invasive species are effective vectors of hazardous infectious diseases. Therefore, the study of the spatial dynamics of invasive mosquito species remains highly relevant for Europe.

We investigated the spread of *Aedes albopictus* and *Aedes koreicus* in the southwestern North Caucasus and Crimea between 2019 and 2025 and their potential distribution until 2050 using MaxEnt and dynamAedes predictive models.

The current range of *Ae. albopictus* in the Caucasus (43,384 km²) has remained unchanged since 2021, when its northern distribution limit was first identified. In Crimea, the species' range expanded from a single recorded location in 2019 to 30 km in 2021 and exceeded 258 km along the coastline by 2025.

Aedes koreicus exhibits a mosaic pattern of spread. In the Caucasus, its distribution increased slightly from 23 to 73 km² over the study period. In Crimea, occurrences are concentrated in three clusters located along the E-105 highway.

Prediction for 2050 suggest that *Ae. albopictus* will not expand its range in the Caucasus due to precipitation deficits and low winter temperatures, whereas in Crimea it may spread within forested areas on mountain slopes. *Ae. koreicus* is expected to continue dispersing in the foothill zones of both regions, being constrained by the same climatic factors.

Overall, our results indicate continued expansion of invasive mosquito vectors in Crimea and stabilization of their ranges in the Caucasus, where precipitation appears to be the primary limiting factor. These findings are significant for epidemiological risk assessment and forecasting.

Our results confirm significant population spatio-temporal heterogeneity at the national level and significant phenological changes. It suggests that climate-driven surges in vector populations create favorable conditions for isolated viral introductions to escalate into major outbreaks. Anticipating such conditions that would inform current vector control and surveillance strategies to take into account evolving epidemiological risks. Geographic expansion of high-risk areas highlights the urgent need to integrate fine-scale entomological modelling into early warning systems and disease preparedness strategies.

“It is warm. Stay alive, stay active, and bite as much as you can” – New insights into *Culicoides imicola* activity, host preference and biting rates in the Mediterranean basin.

Adi BEHAR (Kimron Veterinary Institute, Adibehar@gmail.com)

Nina NINYO, Dor SAHAR, Omri URIEL

Abstract

Culicoides imicola (Diptera: Ceratopogonidae) is a successful biting midge, infamous for its role as a vector of numerous pathogens of veterinary significance, particularly arboviruses. These viruses are responsible for outbreaks of congenitally deformed ruminant neonates (the arthrogryposis-hydranencephaly syndrome (AH-S)) as well as abortions, dystocia, neurological symptoms and causing significant losses to the dairy and meat industries in the Mediterranean basin. The ecology of *C. imicola* is poorly understood. Our work shows that climate change is likely to play a central role in the density and composition of vector populations, their activity, and the transmission dynamics of the arboviruses they transmit.

From 2020 to 2024, we conducted a comprehensive multivariate analysis of the environmental drivers of *C. imicola* activity in the Mediterranean basin. We showed that *C. imicola* is active year-round and identified six months of high activity, along with the climatic factors that determine its duration. During this season, we demonstrated that *C. imicola* remains active throughout the night, not only at dusk and dawn. Our results indicate that, due to the effects of climate change, the impact of *Culicoides*-transmitted viruses on livestock production will continue to increase. Additionally, we conducted a host-preference experiment to identify the dynamics of *Culicoides* biting activity and quantify biting rates. This experiment was conducted throughout the high-activity season, both during the day and at night. The results of this experiment shed new light on the epidemiology of *Culicoides*-transmitted viruses and explain why these viruses pose such a serious challenge to animal health and welfare.

Genetic structure of *Culicoides imicola* (Diptera: Ceratopogonidae), the main afrotropical vector species of veterinary viruses, in the Indian Ocean

Lorn RIBON-CHAUDAT (UMR ASTRE - CIRAD, Lorn.ribon_chaudat@cirad.fr)

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Abstract

Culicoides imicola (Diptera: Ceratopogonidae) is the main historical vector of livestock viruses, such as bluetongue virus (BTV), Epizootic Haemorrhagic Disease virus (EHDV) and African Horse Sickness virus (AHSV), in the Afrotropical region. Understanding the demographic history and genetic structure is crucial for inferring the colonization pathways. The aim of this study is to explore the genetic structure of this species over the Great Indian ocean with a special interest for the South-Western Indian Ocean (SWIO) island territories. We investigated how passive wind-driven dispersal and recent animal movements associated with human colonization may have shaped the genetic structure of this vector.

We used two mitochondrial markers (Cytochrome Oxidase 1 and 2) to genotype 345 *C. imicola* individuals from four SWIO territories (South Africa, Madagascar, Mauritius and Reunion Island). We compared genetic indices and haplotypic composition between these territories. In addition, phylogenetic analyses have been conducted with 177 COI sequences from 11 territories bordering the Indian Ocean retrieved from Genbank database.

Phylogenetic analyses on *COI* sequences suggest no clear lineage or genetic grouping among the 11 territories. In the SWIO, concatenated *COI* and *COII* genes analyses show significant genetic differentiation between the four territories, especially between Mauritius and Reunion Island where populations exhibit signs of demographic expansion. Haplotypes network suggests multiple events or potential pathways of colonisation, supporting the hypothesis that animal trade is the primary means of introduction from the continent or Madagascar to Mauritius and Reunion Island.

This work serves as a basis for understanding the risk of introduction of viruses transmitted by *Culicoides* into the island territories of the SWIO and highlights the need to strengthen practices in animal trade in the region.

Exploring phlebotomine sand flies' communities in residential areas of Southern Europe through a citizen science approach.

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E PÉREZ-MARTÍNEZ, M LÓPEZ-DE-FELIPE, E ESTÉVEZ-SÁNCHEZ, JP BARRERA, C GÓMEZ VELASCO, C COLLIGNON, A BECK, R GÁLVEZ, G MIRÓ

Abstract

Canine leishmaniosis (CanL) is an important zoonotic disease, endemic in countries within the Mediterranean basin caused by the parasite *Leishmania infantum*, with phlebotomine sand flies being the sole known vector and dogs the main peridomestic reservoir. Whilst leishmaniosis has traditionally been considered a rural disease, the importance of peri-urban environments remains undetermined. The Phlebex project ("Phlebotomine sand flies' exposure") aimed to characterize the phlebotomine sand flies' communities in residential areas of Spain, Southern France, Italy and Greece through a citizen science approach. As such, trained enrolled pet owner participants from 49 selected households across the four selected countries operated two light traps (commercial Bg-Pro and homemade Flebocollect model traps) over night, from dusk to dawn, every two weeks between June and December 2024. Collection nets were brought to participating veterinary clinics in each study site, and samples were shipped to the research laboratory in Madrid (UCM), for taxonomical identification and *Leishmania*-DNA detection through molecular diagnosis. A total of 3,035 specimens were captured and identified, with a mean of 1.44 female collected per household and night. Whilst *Phlebotomus perniciosus* was the main detected vector in residential areas of Spain and Italy, *Ph. ariasi* was more abundant in France. Greek phlebotomine communities diverged from the rest of the studied countries, being *Ph. perfiliewi* the main detected vector species, whilst *Ph. simici*, a suspected vector of *L. infantum*, was also detected in high abundances. Our preliminary analysis of the results points to the importance of residential areas across Southern Europe, which may represent important settings for canine leishmaniosis transmission. As such, the implementation of ectoparasiticides with proven efficacy against sand flies, is considered an essential preventative measure even within residential environments across the Mediterranean basin.

One Health Approach to Crimean-Congo Hemorrhagic Fever Virus Detection in Livestock and Ticks in 2020 and 2025 in Tanzania

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Jalika JOYNER, Woutrina SMITH, Macdonald FARNHAM, Cheryl MEEHAN, Sonja MONTANUS, Phoebe LAWTON, Grace MWANGOKA, Mwanzalilla MWOKOZI, Maxmillian MPINA, Robert SUMAYE, Silas TEMU, Alexandre TREMEAU-BRAVARD, Tracy DRAZENOVICH, Rebecca RADISIC, William SWAIN, George MAKINGI, Robinson MDEGELA, Zikankuba SIJALI, Ahmed AMASHA, Abdallah Kinyogori AMINA, Yumba YEKONIA, Brian H. BIRD

Abstract

Crimean-Congo hemorrhagic fever virus (CCHFV) is a lethal zoonotic *Nairovirus*, with an expanding geographic range likely influenced by climate factors affecting tick vector distribution and animal host movement. The virus causes fatal hemorrhagic disease in up to 50% of infected humans but is often asymptomatic in animal species. Ticks of the genus *Hyalomma* are the predominant known vector for CCHFV; however, other potential vector species include ticks in the genera *Amblyomma* and *Rhipicephalus*. In the current study, we assessed risk factors associated with CCHFV antibody seroprevalence detected by enzyme-linked immunosorbent assay (ELISA) in livestock in Central Tanzania in 2020 (n=385) and 2025 (n=2576). We also performed reverse transcription quantitative PCR (RT-qPCR) assays to detect CCHFV RNA in ticks of multiple genera found on sampled cattle. Our results indicate that animal location, age, breed, and burden of attached ticks are associated with CCHFV antibody detection. Furthermore, although we did not detect CCHFV RNA in *Hyalomma* ticks collected from cattle, we did detect viral RNA in ticks of other genera, including *Rhipicephalus microplus*, *Rhipicephalus evertsi evertsi*, and *Amblyomma variegatum*, as confirmed by DNA barcoding. The study contributes to our understanding of CCHFV prevalence in Tanzanian livestock and supports the need to further investigate the factors driving disease spread in the country. The report is part of a longitudinal study of CCHFV in humans, animals, and ticks in the region. Understanding the distribution of virus in competent hosts, as well as the interplay between host, vector, and pathogen across time, will improve surveillance and prevention of future CCHFV outbreaks.

Using équine VOCs to diagnose endoparasite infestations

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Milla MENOUILLEARD, Marielle ZAYANA, Fabrice REIGNER, Elfie* PERDEREAU

Abstract

*Equal contribution of these authors

Diagnosing diseases or endoparasitic infestations is particularly challenging when the infested host exhibits no specific clinical signs. Among the most prevalent endoparasites affecting horses worldwide are *Gasterophilus* spp. and gastrointestinal nematodes. Because of their recurrent presence and the difficulty of achieving reliable diagnosis, broad-spectrum antiparasitic treatments are commonly administered once or twice a year to target both groups simultaneously. However, the growing problem of antiparasitic resistance, especially among nematodes, has become a major concern in equine health management.

In this study, we investigate the chemical interactions between horses and their endoparasites to determine whether parasitic infestation alters the equine volatilome. Specifically, we aim to assess whether volatile organic compounds (VOCs) can serve as reliable diagnostic biomarkers to distinguish infested from non-infested horses. This approach could enable more targeted treatment strategies and help slow the emergence of antiparasitic resistance.

Coordinating a One Health framework for plant health, crop protection and vector management

Archie MURCHIE (Agri-Food and Biosciences Institute, Archie.murchie@afbini.gov.uk)

Florentine SPAANS, Lesley HADDOCK, Daniel LEYBOURNE, Neil WARNOCK

Abstract

One Health is a popular conceptual framework that refers to a holistic approach to dealing with issues affecting human health, animal health, plant health and the wider environment. As an umbrella concept, One Health makes good sense but how does it function at the field and laboratory level, i.e. what does it mean in practice? What are the synergies and what are the barriers between the differing approaches to plant, animal and ecosystem health from an insect management perspective and how can we make best use of this framework to provide effective protection to both our primary industries and the environment? Plant health is concerned with preventing the establishment of harmful plant pests in a region. Crop protection is about preventing economic losses to our food supply. Whilst vector management is necessary to prevent the spread and impact of human and livestock diseases. For example, within the EU there are well developed legislative frameworks under 'Plant Health Law' that govern the definition of pests, a listing of the most damaging and the required surveillance for them. Can we take the approaches developed under plant health and apply these to animal health (e.g. for vectors of livestock pathogens) and invasive species, or vice-versa? What then about integrated pest management (IPM), and the use of pesticides: we have the need to control economic pests or even eradicate invasive species which may damage the ecosystem, whilst at the same time limiting harmful effects on the wider environment. This presentation will explore how One Health approaches can be coordinated using emergent issues in animal health (a vector-borne disease), bee health, plant health and integrated pest management, on the island of Ireland.

Imaging of malaria parasites inside the mosquito and their neutralization after skin inoculation

Rogério AMINO (Institut Pasteur, Rogério.amino@pasteur.fr)

Abstract

Malaria still remains the world's deadliest vector-borne disease. The disease is caused by *Plasmodium* spp, unicellular parasites that develop inside mosquitos and are inoculated into the vertebrate skin during the bite of an infected insect.

Our group is interested in understanding how parasites develop inside mosquitos - with special emphasis in the acquisition of insect and mammalian host infectivity - and how the immune system effectively eliminates parasites transmitted with the saliva. Our ultimate goal is to develop monoclonal antibodies and multi-antigen vaccines to block infection, disease, and parasite transmission. By offering state-of-the-art BSL3 facilities dedicated to arthropod production and infection of both hosts, as well as, to ultrastructural cryo-electron and dynamic light microscopy, the Vector-Borne Disease Center (Centre des Maladies à Transmission Vectorielle, CMTV) will foster synergy based on the nucleation of multidisciplinary expertise. This innovative and original combination will greatly support the training of students and staff, the mechanistic studies of host-pathogen interactions and the diseases they cause, and the development of new strategies to combat vector-borne diseases.

The Sand Fly Midgut as the Natural Site for *Leishmania* Sexual Hybridization: Insights from In Vitro and In Vivo Models

Isabelle LOURADOUR (Institut Pasteur, Isabelle.louradour@pasteur.fr)

Abstract

Phlebotomine sand flies are responsible for the transmission of *Leishmania* parasites, the causative agent of Leishmaniasis, a neglected tropical disease with important human mortality and morbidity. Although intrinsic insect parameters such as immune response are known to impact vectorial capacity, the vector/pathogen interaction remains poorly understood.

Leishmania parasites typically reproduce by simple clonal division, but they can also occasionally engage in a cryptic sexual cycle resulting in the production of hybrids. This process occurring inside the sand fly midgut is a major source of *Leishmania* genetic diversity, which drives changes in tissue tropism, pathology and drug resistance. Experimental generation of hybrids has long been confined to parasites growing in the sand fly gut, which is associated with an inherent difficulty to identify and observe the process of hybridization and its underlying molecular mechanisms. We developed a protocol enabling the reproducible production of *Leishmania* hybrids in vitro, independently of the use of their sand fly hosts. However, despite the successful generation of hybrids in axenic cultures, the frequency of hybrids generated in vivo is much higher than in vitro, showing that the vector gut environment is particularly favorable to *Leishmania* sexual mating. The mechanisms of *Leishmania* hybrid production and the parameters rendering the vector gut favorable to this process are currently undeciphered and are the focus of our research.

We previously reported that culture conditions inducing genotoxic stress, such as exposure to X-irradiation or to Reactive Oxygen species (ROS) lead to a drastic increase in *Leishmania* hybrid production in vitro, suggesting a link between DNA damage repair and hybridization. We are currently investigating the role of *Leishmania* genes of interest, such as the nuclear fusogen Gex1, in hybrid formation, as well as the complex links between the sand fly gut environment, DNA damage repair and hybridization.

Institut Pasteur Symposium: From Lab to Field—A New Center for Vector-Borne Diseases- Why study ticks and tick-borne pathogen transmission ?

Sarah BONNET (Institut Pasteur, Sarah.bonnet@pasteur.fr)

Abstract

Institut Pasteur Symposium: From Lab to Field—A New Center for Vector-Borne Diseases- Why study ticks and tick-borne pathogen transmission ?

Sarah Bonnet

Ecology and Emergence of Arthropod-borne pathogens unit, Institut Pasteur, Université Paris Cité, CNRS UMR 2000, INRAE USC 1510, Paris, France.

Ticks are the primary vectors of pathogens affecting humans and animals in the Northern Hemisphere. Globally, they rank as the leading vectors in veterinary health and second only to mosquitoes in human health. Ticks are strictly hematophagous acarids capable of feeding on all terrestrial vertebrates, and all the pathogens they transmit have animal reservoirs. Due to ongoing global changes, the geographical distribution and seasonal activity of ticks are rapidly evolving. There are approximately 900 tick species worldwide, each capable of transmitting a specific range of pathogens. This highlights the importance of accurately identifying tick species, understanding their biology and ecology, and determining the pathogens they may carry in order to develop effective and environmentally responsible surveillance and control strategies. To achieve this, both field epidemiological studies and experimental laboratory research are essential and complementary. Our work aims to assess tick-related risks in various environments, including urban areas, through field sampling and laboratory analysis of the pathogens they harbor. The establishment of laboratory colonies also enables us to develop surveillance tools, with the validation of biomarkers of exposure to tick bites. Finally, these colonies provide a means to study the vector competence of ticks for various pathogens and to develop experimental models of different tick-borne infections, such as tick-borne encephalitis virus.

#14805

WORKSHOP Institut Pasteur: From Lab to Field

29/06/2026 at 17:45, Chinon

poster/category insect vectors/other contributions

Sarah MERKLING (Institut Pasteur & CNRS, Sarah.merkling@pasteur.fr)

Abstract

poster/category insect vectors/other contributions

Through the dark continent: African trypanosome development in the tsetse fly

Brice ROTUREAU (Institut Pasteur, Rotureau@pasteur.fr)

Abstract

Trypanosoma brucei is the extracellular parasite causing human and animal African trypanosomiasis in Sub-Saharan Africa. The parasite undergoes a complex life cycle from the glucose-rich blood and tissues of a mammalian host to the proline-rich alimentary tract and salivary glands of its blood-feeding insect vector, the tsetse fly. The cyclical development of the parasites in the tsetse involves successive steps of proliferation, migration and differentiation highly organized in space and time. The accomplishment of this complex development is necessary for the parasites to ensure their transmission to the next host. Yet, a drastic population bottleneck is observed during the parasite cycle due to diverse natural barriers imposing a selective metabolic pressure on the parasite populations, some of which remaining unexplored. How do trypanosomes sense their environment and adapt their central carbon metabolism to initiate midgut infection and colonize the salivary glands, to eventually ensure their transmission? In the new research centre on vector-borne diseases (CMTV) at Institut Pasteur, we will unravel the last key steps of African trypanosome development directly in vivo. Using state-of-the-art technologies, i.e. marker-free CRISPR-Cas9 multi-editing, metabolic analyses including NMR and mass spectrometry metabolomics, electron microscopy-based ultrastructural approaches, experimental infection and in vivo imaging of tsetse flies, we will unravel some of the last unknown steps of the parasite cycle, enhancing our understanding of the trypanosome biology, and providing new potential targets for controlling the parasite transmission by future para-transgenesis approaches.

Automated insect monitoring with camera traps is transforming ecological understanding

Toke T. HØYE (Aarhus University, Tth@ecos.au.dk)

Mark Andrew Kusk GILLESPIE, Jamie ALISON, Guillaume MOUGEOT, Asger SVENNING, Kim BJERGE

Abstract

With computer vision and deep learning, insect camera traps have become important tools to improve our understanding of insect responses to environmental change. Through computer eyes, it is possible to effectively, continuously, and non-invasively observe insects throughout diurnal and seasonal cycles and deep learning models combined with statistics can provide estimates of their abundance, biomass, and diversity. We highlight four key areas of ecological understanding: phenology, abundance, richness, and community dynamics, and show how automated data can correct phenological estimates by weeks and improve biodiversity assessments. Data from insect camera traps offer unprecedented resolution and scalability, making them powerful tools for tracking insect communities and in forming conservation strategies. I will also highlight outstanding challenges and future research avenues to facilitate the broad scale implementation of insect camera traps for day active and nocturnal insects.

#10768

BIODIVERSITY: Insect monitoring 1

29/06/2026 at 11:30, Courteline

Automated Insect Identification Machine for spruce bark beetles

Viki WEBSTER (Forest Research, Viki.webster@forestresearch.gov.uk)

Ruth CARTER, Barley Rose COLLIER HARRIS, Tim LUKINS, Ainoa PRAVIA, Jason SUMNER-KALKUN, Patrycja LACKOWSKA, Alice WALKER, Owen VAUGHAN, Alicia THEISSEN, Cerian WEBB, Helen SANDISON, Rachael WAKEFIELD, Steven BREMNER, John WHELAN, Max BLAKE, Steven BEMNER

Abstract

The eight-toothed spruce bark beetle *Ips typographus* has decimated European forests and is one of the largest current threats to British forestry. *Ips typographus* was found in England in 2018 and is now known to naturally blow across the English Channel from continental Europe. An extensive trapping network and eradication programme has since been set up to monitor *Ips typographus* populations and prevent its establishment in Britain. Samples are collected from cross-vane traps every 2 weeks across Britain and every *Ips* is individually identified and counted by hand which is a highly labour and resource intensive process. We therefore developed the Automated Insect Identification Machine (AIIM) to automate the processing of these samples and reduce the costs associated with the monitoring network.

A trap-mounted automated imaging system

Markus KRAMER (Karlsruhe Institute of Technology , Markus.kramer@kit.edu)

Felix DEHON, Christian PYLATIUK

Abstract

Timely detection and monitoring of invasive and economically relevant pest insects remain major challenges for entomological surveillance programs. Traditional trapping approaches rely on periodic manual inspections, resulting in low temporal resolution and considerable labor demands. In addition, image material generated from field traps is often inconsistent due to variable lighting, motion blur, and background clutter, limiting the effectiveness of automated identification tools.

To address these challenges, we developed a trap-mountable automated imaging system designed to integrate directly into standard interception traps. The system captures insects as they fall through the trap and employs a custom laser-line light barrier to ensure rapid and reliable event detection across the full passage area. Upon detection, a global-shutter camera records a short burst of high-resolution images under controlled, diffused LED illumination, producing sharp, distortion-free images suitable for morphological assessment and machine-learning-based classification.

Laboratory validation with multiple Coleoptera species demonstrated high detection accuracy, no false positives, and consistently high image quality. The system's low idle power consumption and short, event-based energy peaks support future deployment in battery- or solar-powered field settings. Its modular design allows its use with non-lethal release, dry collection, or wet-preserved collection, ensuring compatibility with diverse monitoring objectives.

By generating standardized, high-fidelity images without altering trap performance or field protocols, this trap-mountable automated imaging system provides a practical method to overcome the current data limitations in automated insect identification. It represents a promising tool for advancing next-generation entomological surveillance, particularly for the early detection and monitoring of invasive and other pest insect species.

Imaging Dried and Wet Invertebrates from Multiple Perspectives and 3D Modeling

Christian PYLATIUK (Karlsruher Institut für Technologie (KIT), Pylatiuk@kit.edu)

Nathalie KLUG, Rudolf MEIER, Markus KRAMER

Abstract

Accurate taxonomic identification of invertebrates based on morphology remains challenging, particularly for small and delicate specimens. Multi-perspective imaging can substantially improve morphological assessment, yet existing photogrammetric approaches typically rely on insect pins, which can irreversibly damage specimens and require extensive preparation time. This limitation is especially problematic for very small or rare insects, including many undescribed species.

Here, we present two complementary, non-destructive methods for handling and imaging insects that enable high-quality, multi-view image acquisition without physical contact or permanent alteration of the specimen. The first method employs acoustic levitation for dried, unpinned insects. Using standing ultrasonic waves generated by 87 individually controlled transducers arranged hemispherically, lightweight insects are suspended in mid-air. Precise, timed control of the transducers via a field-programmable gate array (FPGA) enables automated rotation of the specimen in 5° increments, allowing multi-perspective imaging with a stationary camera. Unlike previous acoustic levitation systems, this approach does not require prior knowledge of the specimen's geometry, making it suitable for small, winged insects with unknown morphologies. Using this setup, automated digitization, extended depth-of-field imaging, and multi-view datasets can be acquired for insects up to 8 mm in size. We demonstrate the suitability of the resulting images for 3D reconstruction by generating a neural radiance field (NeRF) model from 72 perspectives captured in under ten minutes.

The second method enables non-destructive wet imaging within a glass capillary, preserving the specimen for downstream DNA sequencing. In this setup, the specimen remains stationary while the camera rotates around the capillary, and the imaging chamber is filled with glycerine to minimize optical refraction. Together, these methods provide efficient, non-invasive alternatives for high-resolution morphological imaging, supporting integrative taxonomy and large-scale digitization of entomological collections.

From Trap to Cloud: Autonomous Vision-Based Monitoring of the Olive Fruit Fly (*Bactrocera oleae*)

Flora MORENO ALCAIDE (University of Cordoba, Flora95ma@gmail.com)

Abstract

The olive fruit fly (*Bactrocera oleae*) is the key pest of olive orchards, and its accurate monitoring is essential for informed decision-making within Integrated Pest Management (IPM) programs. In this context, as an initial step, the trapping system was optimized through the evaluation of trap type, color, size, and density. This process identified double-sided yellow chromotropic traps (10×25cm) as the most effective configuration, achieving the highest captures of *B. oleae* adults while significantly reducing the incidental capture of natural enemies. These results provided the foundation for the development of technologies aimed at automating population monitoring, leading to the design of an intelligent electronic trap. This device, equipped with an 8-megapixel camera, a Raspberry Pi processing unit, and an autonomous power system, enables the periodic acquisition of images. Furthermore, through the integration of trained detection models, the system performs on-device inference using the previously developed algorithm and transmits the processed data via LoRaWAN communication to a digital platform, where population dynamics can be visualized with high temporal resolution.

To provide the trap with autonomous recognition capabilities, a heterogeneous dataset of 2.420 images from both field and laboratory conditions was developed and expanded through data augmentation. This dataset enabled the training of multiple YOLOv5 configurations, demonstrating that the YOLOv5s-300 model offered the best balance between accuracy (≈ 0.99), robustness, and computational efficiency, making it suitable for deployment on low-power embedded devices.

The integration of this model into the electronic trap enables a continuous, automated, and scalable monitoring system, representing a significant advance toward precise and sustainable automated surveillance solutions for the control of *B. oleae*. Moreover, the combination of trap optimization, computer vision, and IoT technologies within a single operational architecture reduces the need for field inspections and establishes reliable early-warning systems, thereby supporting more informed and effective decision-making.

Loud and clear! Towards wild bee acoustic monitoring

Fernanda HERRERA-MESÍAS (Fondation faune-flore (FFF), Fhmesias@gmail.com)

Antonio CRUZ, Freddy SARATHCHANDRA

Abstract

Bioacoustics is a discipline that records, stores, and analyses animal sounds to capture species-specific signals that enable non-invasive wildlife monitoring. Acoustic techniques are widely used in ornithology, herpetology, chiropterology, and marine biology. Insects can also be studied acoustically, but this has most often been confined to laboratory settings. Studies on wild insects that lack specialised sound-producing organs are rarer, largely due to the challenges in obtaining high-quality, repeatable field recordings.

Wild bees are a particularly compelling target for field bioacoustics because they are ecologically important, widely distributed, and difficult to monitor at scale with conventional survey methods.

Bee “buzzing” (wingbeat sound) is an airborne by-product of flight that is produced by all bees. This offers a potentially universal acoustic feature that can be recorded and monitored as an “acoustic fingerprint”.

Here, we present preliminary results from a pilot experiment conducted in Luxembourg using customised anechoic insect bioacoustic chambers, aiming to test whether species-specific wingbeat “fingerprints” can be captured from wild bees and used for automated identification of Central European species.

Over the past three years, we have conducted in-field, in-vivo acoustic characterisation of multiple wild bee taxa and progressively refined our methods across different soundscapes. We have also carried out more focused investigations on selected target species, evaluating how intertegular span (ITS), body mass, and wing damage influence acoustic profiles.

Overall, these early findings indicate that acoustic identification of wild bees is feasible and promising, supporting the development of new automated monitoring approaches and non-lethal identification tools for pollinator research and conservation.

Remote laser assessment of micro- and nano features for insect diversity

Meng LI (Lund Univeristy, Meng.li@fysik.lu.se)

Mikkel BRYDEGAARD

Abstract

The alarming decline in global insect populations and diversity calls for improved monitoring methods with species-specific capabilities. While conventional trapping techniques are widely used, they are labor-intensive and fail to provide real-time, in-situ data on species composition. In response, novel remote and automated monitoring methods have emerged, offering the potential for high-resolution, efficient data collection. However, existing remote sensing techniques, which primarily rely on wingbeat frequencies or direct imaging, have inherent limitations. These include overlapping wingbeat frequencies between species and the difficulty of focusing on small, rapidly moving insects in flight.

To address these challenges, our research group has developed an entomological lidar that uses the Scheimpflug principle to capture detailed spectroscopic and dynamic features from insects at various distances. Lidar presents a promising photonic solution for monitoring insect populations and diversity. Our research focuses on enhancing in-situ identification by leveraging the unique optical properties of insects, characterized using infrared hyperspectral imaging. Specifically, We are exploring how features like wing reflectance, interference patterns, surface roughness, and polarimetry can improve species differentiation. Our work aims to develop advanced methodologies, such as dual-band and hyperspectral lidar, capable of identifying insects in flight by their micro- and nanoscopic characteristics.

Megabarcoding for Insect Monitoring: Linking Specimens, Images, and Sequences to Build Biodiversity Baselines

Vivian FENG (Museum für Naturkunde Berlin, Vivian.feng@mfn.berlin)

Amrita SRIVATHSAN, Rudolf MEIER

Abstract

Megabarcoding leverages portable sequencing technologies to generate DNA barcodes for thousands of individually processed insects. By coupling high-throughput sequencing with rapid, field-deployable workflows, it enables large-scale biodiversity assessments while retaining the crucial link to physical vouchers. This provides accurate abundance data, preserves genomic resources, and supports monitoring systems that are sustainable and globally accessible. A defining strength of megabarcoding is its ability to link each DNA sequence to the photographed specimen from which it originated. This connection can be established automatically through devices such as the DiversityScanner or manually through imaging workflows like the Entomoscope. The resulting specimen–image–barcode datasets provide reliable reference material needed to train and validate automated image recognition systems, which in turn accelerate and scale biomonitoring by enabling rapid, consistent, and cost-effective insect identification. By uniting molecular and imaging pipelines, megabarcoding contributes to the construction of reliable, scalable biodiversity baselines.

Enhancing wood-boring beetle surveillance through innovative traps and AI-driven image identification

Davide RASSATI (University of Padova, Davide.rassati@unipd.it)

Abstract

The continuous increase in global trade in recent decades, together with past intentional plant introductions, has led to a growing number of non-native insects being moved outside their native ranges. This trend is particularly evident for wood-boring insects, especially bark and ambrosia beetles (Coleoptera: Scolytinae), longhorn beetles (Cerambycidae), and jewel beetles (Buprestidae), which can be inadvertently transported in wood packaging materials, logs, processed wood, and live nursery plants. Among the various tools developed for the surveillance of wood-boring beetles, traps baited with attractive lures represent a key component of biosecurity systems in several countries worldwide. In addition to being low-cost and easy to deploy, baited traps benefit from recent advances in longhorn beetle chemical ecology and from improved understanding of the factors influencing trapping success. However, trap-based surveillance still faces two major limitations: (i) the need to implement multiple trapping protocols for different target species, and (ii) the taxonomic expertise required for sorting and identifying trapped specimens. The first limitation can be mitigated through the use of traps capable of attracting multiple species, even across different beetle families, simultaneously. The second can be addressed through AI-based technologies enabling automatic identification of trapped specimens. Recently developed multi-lure, multi-colored baited traps, together with automated image-based identification systems such as the Entomoscope, offer promising solutions to these challenges.

Combining Computer Vision AI and DNA Barcoding for High-Throughput Invertebrate Specimen Processing

Jarrett BLAIR (Aarhus University, Department of Ecoscience, Jarrett@ecos.au.dk)

Toke Thomas HØYE

Abstract

Identifying and sorting specimens is a major logistical challenge for many ecological entomology studies. DNA barcoding and, more recently, computer vision classification have emerged as efficient alternatives to classic manual specimen sorting. Both approaches have clear strengths, but also substantial limitations. Computer vision excels at high-throughput specimen processing but requires large amounts of training data and can struggle at separating morphologically similar taxa. In contrast, DNA barcoding is morphology-agnostic and is supported by large, public DNA sequence databases, but is slower and more expensive than computer vision. In this presentation, we introduce an integrated specimen-processing pipeline that combines computer vision with DNA barcoding to leverage the strengths of both methods while reducing their individual weaknesses. Our pipeline uses the BIODISCOVER robotic imaging system to automatically process bulk invertebrate samples, while nanopore DNA barcoding provides training labels for the classifier and resolves cryptic taxa. As a proof of concept, we used our pipeline to sort pitfall trap specimens from a long-term invertebrate community monitoring project in southern Greenland. Overall, our combined approach enables faster, scalable, and more accurate invertebrate specimen processing.

Molecular monitoring of terrestrial biodiversity: towards a national long-term monitoring system

Lucas SIRE (International Barcode of Life, Lucas.sire.17@gmail.com)

Johandre VAN ROOYEN, Brianne SAINT-JACQUES, Kate PEREZ, Michelle VAN DER BANK, Paul D. N. HEBERT

Abstract

Biodiversity monitoring has never been more important given the scale of the current biodiversity crisis. However, this monitoring presents a major challenge for long-term and/or large-scale geographical tracking, particularly when dealing with highly diverse and poorly understood taxa such as insects, or territories with taxonomic deficits and limited resources. In that sense, DNA metabarcoding offers an attractive alternative to morphological identification, with the potential for efficient processing of all taxa via numerous multiplexable samples, thus accelerating inventories.

This presentation outlines the political context and national needs in terms of biodiversity monitoring and data, and also presents the pilot deployment of a long-term monitoring program using non-destructive metabarcoding focused on terrestrial biodiversity in France (metropolitan France and overseas territories). Initiated around Malaise traps and flying insects to align with current international standards, a total of 25 traps were deployed in various ecosystems over more than a year, yielding over 700 samples, including 360 metabarcoded samples to date. This molecular monitoring highlights variations in biomass and species richness over time and lays the logistical groundwork for a national insect monitoring program in France. Beyond the initial results, the logistical challenges encountered during this pilot study are also discussed—challenges that must be overcome before establishing a long-term monitoring program involving hundreds of operational traps, which is currently under discussion for the coming years.

Toward repurposing global passive air sampling networks for insect monitoring: promises and pitfalls of airborne eDNA

Jordi VILANOVA (Concordia University, Jordi.vilanovaibroto@mail.concordia.ca)

Luis Rodrigo ARCE-VALDÉS, Xianming ZHANG, Julia J. MLYNAREK, Rassim KHELIFA

Abstract

Over the past decades, insect biodiversity has shifted rapidly, with biomass declines and extinctions reported worldwide. To understand and counter these shifts, environmental DNA (eDNA) techniques have been at the forefront of innovation to accelerate sampling processes and allow for faster assessments. One of the methods currently being developed is airborne eDNA, where DNA is extracted from air suspended particles and then sequenced to assess local species composition. While this method has many promises, its taxonomic coverage and biases have not been explored, which is crucial knowledge to track and monitor biodiversity effectively. Therefore, the goal of this study is to analyze the taxonomic coverage and bias of an airborne eDNA sampling method, by comparing the output of polyurethane passive air samplers (PUF-PAS) to the output of a traditional sampling method of flying insects, malaise traps.

From May to October 2024, we installed malaise traps and PUF-PAS in 5 different locations around Montreal, Canada. Every 2 weeks, we collected the malaise traps and the polyurethane disks from the PUF-PAS to compare the insect diversity at the order level. We separated and weighed the contents of the malaise traps, and successfully extracted and sequenced the DNA from the air particles sampled by the disks.

Preliminary results show a bias in sampling of the different insect orders, with the relative abundance of insect orders in the malaise traps not being a strong predictor of their presence in the PUF-PAS. This bias might be explained by differences in the morphological and anatomical features of the orders that affect their likelihood to release airborne eDNA-associated particles. While this is a useful first step into understanding the taxonomic coverage in airborne eDNA, future studies should focus on alternative airborne eDNA sampling techniques taxonomic coverage, and what other factors can bias these sampling methods.

Advancing Entomological Biomonitoring with Metabarcoding: a Case for Assessing Agri-Environment Schemes (AES)

Ben HAWTHORNE (Newcastle University, B.hawthorne2@newcastle.ac.uk)

Jordan CUFF, Larissa COLLINS, Ian ADAMS, Darren EVANS

Abstract

Invertebrate biomonitoring in agroecosystems is increasingly crucial given the need to understand the impact of environmental change and land management on insects, in line with sustainable development and global conservation targets. Agri-Environment Schemes (AES), such as those under the EU Common Agricultural Policy and England's Environmental Land Management Schemes, partly aim to benefit nature. With their uptake, it is important to assess actions continuously and provide feedback. Traditional morphological identification, whilst an important component of the biomonitoring toolbox, can be laborious, introduces latency, and limits scalability. Molecular techniques such as DNA metabarcoding provide a demonstrably effective alternative for identification, yet adoption for widescale biomonitoring is relatively scarce.

Here I will discuss evidence to support utilising DNA metabarcoding for invertebrate biomonitoring schemes. First, the added benefits and limitations of integrating traditional entomological sampling techniques with metabarcoding will be outlined. Evidence will be presented from a replicated field experiment in which eight entomological sampling methods were integrated with metabarcoding for the assessment of biodiversity in an agroecosystem. Through these findings, the practicality of combining these methods with metabarcoding and one another will be discussed, as well as the future prospects of utilising these methods to inform policy and targets on biodiversity and food security. I will also discuss incorporating metabarcoding data into ecological networks, and the benefits of doing so for developing our understanding of changing invertebrate assemblages and their evolving contributions to people.

A world on every plant - Plant-derived eDNA reveals fine-scale arthropod community structure in grasslands

Lisa MAHLA (Trier University, Mahla@uni-trier.de)

Abstract

The loss of plant diversity in grasslands is implicated as one of the main causes of arthropod decline. The loss or exchange of a single plant species can have a cascading effect on specialized arthropod species. It is thus critical to expand our understanding of plant–arthropod interactions. Detecting plant–arthropod interactions, however, has been difficult, as it requires the observation of individual plant visits. A possible solution to this problem is offered by environmental DNA (eDNA) analysis.

We test the utility of eDNA to detect fine-scaled community differentiation in grassland arthropods in Germany. Based on eDNA from different plant species, we explore community differentiation between plant species, and between flower and green parts of individual plants. We show that eDNA successfully recovers extremely fine-scaled community differentiation. Plant species, as well as plant compartment, emerge as major drivers of arthropod community composition in grasslands, with the differentiation being particularly pronounced in herbivorous arthropods.

Terrestrial eDNA on plants thus appears to be deposited in a very localized fashion, making this tool ideally suited to detect very fine-scaled community differentiation. Considering the high specificity we observe in our analysis, our results highlight the necessity of integrating vegetation surveys into future monitoring of arthropod communities.

#12532

EVOLUTIONARY GENETICS: Symbionts and insects as holobionts 1

29/06/2026 at 11:00, Loches

Microbial bases of folivory in beetles

Hassan SALEM (John Innes Centre, Hassan.salem@jic.ac.uk)

Abstract

Symbiosis binds organisms from all domains of life. These interactions evolved frequently in insects and exhibit remarkable functional diversity. Where numerous traits are encoded by beneficial microbes, as a research group, we study the role of symbiosis in facilitating adaptation in folivorous beetles. Using tortoise beetles as an experimental study system, I will outline (i) the molecular, developmental, and behavioural features ensuring symbiont maintenance, (ii) the beneficial roles microbes fulfill towards host nutrition and defense, (iii) the context dependency governing these interactions, and, finally, (iv) the molecules that underpin the propagation of the symbiosis following 60 million years of co-dependence. Throughout this talk, I will highlight how timing the acquisition of a beneficial symbiont relative to the evolutionary history of its host can shed light on the adaptive impact of a partnership. This theme is further contextualized relative to our work on mutualism loss.

The influence of *Wolbachia* infection on transcriptional and epigenomic variation in *Chorthippus parallelus*

Patricia JIMÉNEZ-FLORIDO (Departamento de Biología (Genética), Facultad de Ciencias, Universidad Autónoma de Madrid, E28049, Madrid, Spain, Patricia.jimenez@uam.es)

José L. BELLA, David BUCKLEY, Rosario PLANELLÓ

Abstract

Wolbachia pipientis is an obligate intracellular alphaproteobacterium widely distributed among arthropods, in which it exerts diverse reproductive and physiological effects with potential implications for the host evolutionary trajectories. In the grasshopper *Chorthippus parallelus* (*Pseudochorthippus parallelus* for other authors), a well-established model for studying early stages of speciation, the two subspecies—*C. p. parallelus* and the Iberian endemic *C. p. erythropus*—harbour distinct *Wolbachia* strains. These strains contribute to the maintenance of a reproductive barrier through cytoplasmic incompatibility. The contact zone between both subspecies forms a natural hybrid zone in the Pyrenees; it constitutes an excellent framework for investigating how *Wolbachia*–host interactions may influence genomic divergence and the preservation of lineage boundaries.

The analysis of gene expression and global DNA methylation level has recently been incorporated into the study of this model to improve our understanding of *Wolbachia*'s influence. Infected individuals display pronounced changes in the expression of genes related to essential key pathways: development, reproduction, energy metabolism, immunity and epigenetic molecular mechanisms. Concurrently, *Wolbachia* induces modifications in genome methylation level, revealing a potential mechanism through which *Wolbachia* may fine-tune host physiology. Several of these responses are also influenced by sex, underscoring the complexity of host regulation in the presence of this endosymbiont.

The next phase of this research will extend these analyses to both subspecies and their natural hybrid forms to elucidate the combined contributions of host genetic background, sex, and *Wolbachia* strain identity. By integrating molecular, epigenomic, and evolutionary data, this work aims to refine our understanding of how *Wolbachia* influences the biology of its host, and regarding this case-model its role in the divergence processes shown by these grasshopper's subspecies and the maintenance of their hybrid zone.

Invasion dynamics of horizontally acquired *Wolbachia* on invasive cherry fruit fly populations

Hannes SCHULER (Competence Centre for Plant Health, Free University of Bozen-Bolzano, Hannes.schuler@unibz.it)

Erika CORRETTO, Lapo RAGIONIERI, Thomas M WOLFE, Daniel BRUZZESE, Lisa KLASSON, Christian STAUFFER, Jeffrey L FEDER

Abstract

Wolbachia is a widespread endosymbiont that has spread throughout arthropod species. Key factor of its successful lifestyle is the ability to manipulate the reproduction of its host and promote vertical transmission. However, *Wolbachia* does not only cause reproductive parasitism but can also benefit its host, particularly infected females which inherit the symbiont. Such positive fitness effects are now believed to help *Wolbachia*'s spread through new host populations after horizontal acquisition. However, examples of the occurrence of horizontal transmission in field populations and particularly the early stages of *Wolbachia* spread in new hosts are still poorly understood. Here we study the dynamics of a recent horizontally acquired *Wolbachia* strain in the invasive American cherry fruit fly *Rhagoletis cingulata* using a combination of spatial and temporal population screening, genomics, and lab crosses. Although genomics confirmed that the newly acquired strain originated from the European congener *Rhagoletis cerasi*, and that all the necessary components for cytoplasmic incompatibility are present in this strain, lab crosses showed conditional positive effects on the host egg hatch rate, but no cytoplasmic incompatibility caused by the new strain. Our extensive screening of European populations show that infection frequency variation of the new strain forms a north-south cline, and that fixation has yet to occur in distant populations. Our results demonstrate a unique example of a recent intraspecifically acquired *Wolbachia* and its invasion dynamics in natural field populations.

Co-speciation and genomic instability in the Whitefly *Portiera* symbiosis.

Théo MANFÉ (INRAE - ANSES, Theo.manfe@inrae.fr)

Guénaëlle GENSON, Jean-Claude STREITO, David OUVARD, Emmanuelle JOUSSELIN, Diego SANTOS-GARCIA

Abstract

Numerous cases of endosymbiotic interactions have been described in insect hosts, yet the evolutionary trajectories and impacts of these associations remain poorly understood. In this study, we focus on the co-speciation phenomenon between whiteflies (Hemiptera: Sternorrhyncha: Aleyrodidae), a family of sap-feeding insects, and *Candidatus Portiera aleyrodidarum*, the bacterium with which they maintain an obligate mutualistic symbiosis. We sequenced eight samples representing seven whitefly species and incorporated additional reference genomes from the NCBI database. We used these datasets to extract proteomes and reconstructed phylogenetic trees of *Portiera*, whitefly and mitochondrial. Results suggest a general pattern of co-speciation, but we observe phylogenetic incongruences between the nuclear and mitochondrial genomes in a specific group of whiteflies. Interestingly, within the same group, *Portiera* exhibits unstable and larger genomes. These findings, which deviate from the typical evolutionary patterns of genome stability in obligate symbionts, highlight the need for further analyses of additional specimens from this and closely related groups to better elucidate the mechanisms driving this phenomenon.

Could co-evolution explain Wolbachia-driven loss of pesticide resistance in spider mite populations?

Flore ZÉLÉ (Institut des Sciences de l'évolution de Montpellier, CNRS UMR 5554, Flore.zele@umontpellier.fr)

Camila VELASTEGUI, Gabin FOURNIER, Pierrick LABBÉ, Sara MAGALHÃES

Abstract

The ability of Wolbachia to manipulate host reproduction have attracted considerable attention for its use as a gene drive vehicle to control pest populations. Such strategies are generally based on genes carried by Wolbachia itself, but their success also hinges on the potential effect of this symbiont on the dynamics of host genes, including those involved in other control strategies. We addressed this issue with a combination of approaches.

We first showed theoretically that, given the range of fitness effects that Wolbachia can have on their hosts, even transient association between different host genotypes and this endosymbiont may lead to the fixation or elimination of host alleles. Then, we used experimental evolution of spider mite populations sharing the same genetic background but carrying or not a SNP conferring resistance to the pesticide etoxazole, and infected or not with Wolbachia. We found that the host genotype alone did not affect the spread of Wolbachia, nor did Wolbachia infection alone affect the dynamic of the resistance allele. However, the frequency of the resistance allele dropped when Wolbachia infection originated from resistant hosts and simultaneously invaded the host populations. Finally, we measured life history traits and levels of Wolbachia-induced cytoplasmic incompatibility (CI) in host carrying or not the etoxazole resistance allele. Preliminary results show that Wolbachia infection increases the growth rate of hosts carrying the resistance allele in compatible crosses, and that Wolbachia-infected resistant males induce lower CI levels than susceptible ones in incompatible crosses.

One possibility to explain such genotype-specific fitness effects of infection, and observed dynamics, hinges upon the long co-evolutionary history between this allele and Wolbachia in the laboratory. Although they call for further investigations to determine whether and how co-evolution would explain this outcome, these results undoubtedly show that Wolbachia can play an important role in host evolutionary trajectories.

Genome assembly of *Diadegma fenestrale* (Hymenoptera: Ichneumonidae), and genome integration of its symbiotic virus, DfIV

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Abstract

Diadegma fenestrale is a parasitic wasp of ecological and agricultural significance that regulates pest populations. However, limited genomic resources have hindered a deeper understanding of its biology and symbiotic interactions. This study presents a chromosome-level genome assembly of *D. fenestrale* using Nanopore and Illumina sequencing. The assembled 221.1 Mb genome comprises 68 scaffolds, including 11 at the chromosomal level, and exhibits high completeness with a BUSCO completeness score of 99.6%. A total of 13,544 protein-coding genes were predicted, with BUSCO assessment of the gene set indicating 97.5% completeness (single-copy: 96.8%, duplicated: 0.7%), 0.7% fragmented, and 1.8% missing genes. Comparative genomic analysis of closely related hymenopteran species provides new insights into genome evolution, including gene family expansions and contractions, as well as chromosomal rearrangements. Additionally, this study examines DfIV, a symbiotic virus associated with *D. fenestrale*, identifying 62 genome segments integrated into the host genome. Most segments are present in one or two copies, while four segments exhibit three copies, suggesting a dynamic interaction between the virus and the host genome that may influence gene regulation and chromosomal stability. This study provides a comprehensive genomic resource for *D. fenestrale*, enhancing our understanding of its genomic architecture, evolutionary dynamics, and functional adaptations. The findings contribute to broader research on parasitoid wasps and symbiotic virus-host interactions, with implications for biological pest control and evolutionary biology.

Distinct *Wolbachia*-induced male-killing mechanisms in *Hypolimnas bolina*

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Abstract

Male-killing bacterial symbionts distort host sex ratios by selectively eliminating male progeny, profoundly shaping host ecology and evolution. A recurrent host response is the evolution of suppressors that restore male survival, yet how such suppression interacts with male-killing mechanisms remains poorly understood. Here, we demonstrate that *Wolbachia* endosymbionts have evolved mechanistically distinct routes to male killing within a host species that possesses a male-killing suppressor. Genome analyses and crossing experiments revealed that the butterfly *Hypolimnas bolina* harbours two closely related male-killing *Wolbachia* variants, wBol1J and wBol1Y, which differ in their sensitivity to a host-evolved nuclear suppressor. wBol1J failed to kill males carrying the suppressor but restores male killing in a suppressor-deficient background. By contrast, wBol1Y killed males irrespective of suppressor status by inducing female-type sex determination through production of female doublesex (dsx) isoforms and by disrupting dosage compensation through upregulation of Z-linked genes. Such effects were absent in wBol1J-infected dying males, which instead exhibited elevated male-type dsx expression and reduced expression of Z-linked genes. Together, these results suggest that closely related *Wolbachia* variants induce male killing by acting on different components of the sex-determination pathway within a single host species.

Extreme genome reduction and evolutionary dynamics of planthopper symbionts

Anna MICHALIK (Jagiellonian University, Faculty of Biology, A.michalik@uj.edu.pl)

Diego C. FRANCO, Junchen DENG, Adam STROIŃSKI, Piotr LUKASIK

Abstract

Ancient maternally transmitted nutritional symbionts of sap-sucking hemipterans are known for extreme genome reduction, yet the limits and dynamics of this process remain poorly understood. To address this problem, we investigated ancient symbionts' genome evolution across the taxonomic diversity of planthoppers (Auchenorrhyncha: Fulgoromorpha), which have maintained associations with two bacteria - *Candidatus Sulcia muelleri* and *Candidatus Vidania fulgoroidea* - for >263 million years.

Our comparative analyses of >150 symbiont genomes revealed substantial diversity in genome organization and gene content, ranging from impressive long-term stability to dramatic changes. Most strains retained the ancestral genome organization and conserved set of nutritional functions. No gene gains were detected, whereas gene loss was frequent - especially in *Vidania* - and primarily affected genetic information processing and metabolic functions. However, some of the surveyed *Vidania* strains have undergone extensive genomic reduction, resulting in convergent evolution of genomes of barely 50-52 kb that retained core rRNAs, ribosomal proteins, and polymerase subunits, while losing most aminoacyl-tRNA synthetases and amino acid biosynthesis pathways except phenylalanine. Patterns of gene loss correlated with host dietary shifts and the presence of additional symbionts. In other planthopper lineages, *Sulcia* genome reduction coincided with extreme reorganization, resulting in genomes composed of multiple circular contigs encoding single genes, or else, in complexes of multiple interdependent symbiont lineages that together function as the single ancestral symbiont.

Overall, these findings reveal the remarkable genomic diversity and ongoing evolution of ancient hemipteran symbionts. They provide key insights into the mechanisms of genome reduction, functional retention, and co-evolution, showing that even long-established symbioses can remain evolutionarily dynamic and approach the lower functional limits of cellular life.

Molecular and cellular basis of whitefly-bacteria symbiosis

Jun-Bo LUAN (Shenyang Agricultural University, Jbluan@syau.edu.cn)

Abstract

The whitefly *Bemisia tabaci* is a globally important agricultural pest. The invasive whitefly *B. tabaci* MEAM1 and MED harbors ‘*Candidatus Portiera aleyrodidarum*’ (hereafter *Portiera*) and ‘*Candidatus Hamiltonella defensa*’ (hereafter *Hamiltonella*) in the same bacteriocyte and *Rickettsia* spp. (hereafter) in the whole body cavity. The symbiosis between the whitefly and its bacterial symbionts underlies whitefly biology. I focused on the role of symbionts in whitefly reproduction, the mechanisms by which whiteflies control symbiont abundance and transmission, and the function of horizontally transferred genes in whitefly-microbe symbiosis. We revealed that *Hamiltonella* induces a female-biased sex ratio in *B. tabaci* by facilitating fertilization and supplying five B vitamins; *Hamiltonella*-derived B vitamins regulates host histone methylation modifications, which influences ovary mitochondrial function and determines the host sex ratio. We elucidated that whiteflies can mediate the vertical transmission by bacteriocyte maternal inheritance and control abundance and metabolism of symbionts by autophagy and vitellogenin. We demonstrated that horizontal gene transfer facilitates the persistence of whitefly-microbe symbiosis. These studies reveal the key role of whitefly-symbiont interactions in the survival and reproduction of *B. tabaci*. Our findings provide new insight into the basis of the insect-symbiont interactions. Furthermore, our studies also provide the new avenue for whitefly control via interfering in the whitefly-symbiont interactions.

The role of gut microbiota in insecticide resistance of *Spodoptera frugiperda*

Julie SÉNÉCAL (IRD, Marion.javal@gmail.com)

Enric FRAGO, Peter MALUSI, Fathiya KHAMIS, Sophie GAUDRIAULT, Marion JAVAL, Jean-Claude OGIER

Abstract

Symbiotic interactions play a crucial role in insect biology, influencing nutrition, development, and adaptation to environmental stressors, including pesticides. In agricultural systems, the ability of insect pests to metabolize toxic compounds is particularly concerning, as it can drive the evolution of insecticide resistance and challenge pest management strategies. Understanding these mechanisms is particularly critical in invasive species, such as the fall armyworm (*Spodoptera frugiperda*). Since 2016, this Lepidoptera, native to the Americas, has rapidly spread in Africa, in Asia and recently some European countries, causing severe damage to maize crops. Recent studies highlight the relationship between resistance mechanisms and microbiota dynamics, emphasizing the need for a deeper understanding of these interactions.

We hypothesize that insecticide pressure alters insect microbiota and contributes to the development of resistance in this species. To test this, we first assessed variation in insecticide resistance toward two insecticides across wild Kenyan *S. frugiperda* populations. We fed larvae with maize leaves treated with different insecticide concentrations and examined relationships with different life-history traits such as survival, development time, and growth rate. Our results showed marked differences in resistance levels both between insecticides and across populations. We then assessed if pesticide treatment led to shifts in gut bacterial community diversity and abundance by using both metabarcoding and culturomics. This last approach allowed obtaining a bacterial collection that may subsequently be used for functional analyses and to explore potential associations between bacterial taxa and pesticide resistance. As a research perspective, we plan microbiota transplantation experiments to test whether specific microbiota compositions contribute to insecticide resistance whether by direct microbial degradation of insecticides and/or from changes in the expression of detoxification genes. This study will provide valuable insights into the microbiota-mediated mechanisms underlying insecticide resistance and the invasion success of *S. frugiperda*.

Bacterial endosymbionts and the evolution of sex determination in the isopod *Armadillidium vulgare*

Richard CORDAUX (CNRS UMR 9191 EGCE, Richard.cordaux@universite-paris-saclay.fr)

Abstract

In animals, sex is generally determined by genetic factors carried by sex chromosomes. Sex chromosomes are remarkably variable in origin and they can differ even between closely related species, indicating that transitions occur frequently and independently in different groups of organisms. However, the evolutionary causes underlying sex chromosome turnovers are poorly known. I will present results supporting that selfish genetic elements distorting host sex ratio can be powerful agents of transitions between sex determination mechanisms, as exemplified by feminizing *Wolbachia* bacterial endosymbionts in terrestrial isopods.

In the common pillbug *Armadillidium vulgare* (Crustacea, Isopoda), chromosomal sex determination follows female heterogamety (ZZ males and ZW females). In addition, many *A. vulgare* populations harbor maternally-inherited *Wolbachia* bacterial endosymbionts which can convert genetic males into phenotypic females, leading to populations with female-biased sex ratios. This bias selects against the W sex chromosome in lines infected by *Wolbachia*, such that all individuals are ZZ genetic males. Therefore, sex is only determined by the inheritance of *Wolbachia* by the *A. vulgare* individual, thereby leading to a shift from chromosomal to cytoplasmic sex determination. Surprisingly, some *A. vulgare* lines exhibit biased sex ratios despite the lack of *Wolbachia*. This bias is induced by the *f*-element, which we identified as a large piece of the *Wolbachia* genome recently transferred to the *A. vulgare* nuclear genome. The *f*-element is another sex-determining locus and the chromosome carrying the insert is a new feminizing chromosome. Furthermore, a dominant masculinizing allele also segregates in some populations. It is thought to have evolved to restore balanced sex ratios in response to female excesses. The locus bearing this allele, termed the *M* gene, is equivalent to an XY system of sex chromosomes.

Overall, our results indicate that bacterial endosymbionts can be powerful sources of evolutionary novelty for fundamental biological processes in animals, such as sex determination.

Drivers of “*Candidatus Symbiodolus*” infection in leaf beetles of *Cryptocephalus flavipes* species group

Giulia MAGOGA (Department of Insect Symbiosis, Max Planck Institute for Chemical Ecology, 07745 Jena, Germany, Gmagoga@ice.mpg.de)

Marilù CARDINALE, Matteo BRUNETTI, Paola COSTAGLIOLA, Roy KIRSCH, Martin KALTENPOTH, Matteo MONTAGNA

Abstract

“*Candidatus Symbiodolus*” (Enterobacterales) is a recently identified intracellular bacterial endosymbiont detected in insects from six orders. The bacterium infects multiple host tissues, including the adult germline, and is vertically transmitted, but its prevalence varies among host species and their populations. Although it represents one of the few known generalist insect symbionts, the nature of its association with hosts remains unclear. Here, the factors influencing *Symbiodolus* infection were investigated using species of the *Cryptocephalus flavipes* group (Coleoptera, Chrysomelidae) as a model system, which includes both infected and uninfected species. Specifically, the following aspects were examined: (i) *Symbiodolus* infection prevalence within species; (ii) the relationship between infection status and host geographic location, altitude, sex, and diet composition; (iii) co-presence or co-absence of *Symbiodolus* with other bacterial taxa within the same host; and (iv) genomic differentiation of *Symbiodolus* and other dominant bacterial symbionts across host populations. A total of 161 individuals of six species from the *C. flavipes* group were screened for *Symbiodolus* infection using PCR targeting *Symbiodolus* 16S rRNA gene. Bacterial community composition and host diet were characterized in 62 individuals using DNA metabarcoding targeting bacterial 16S rRNA and plant ITS genes, and metagenomes from three infected populations per species were sequenced. *Symbiodolus* was detected in three of the six species, confirming that the infection is not fixed within species or populations. No significant association was observed between *Symbiodolus* infection and host sex, diet composition, or collection altitude. In contrast, infection presence was related with geographic localization, with infected individuals occurring in specific regions of the host species range. Additionally, *Symbiodolus* infection was strongly associated with a bacterium of the genus *Rickettsia*, detected in approximately 90% of *Symbiodolus*-infected individuals. Together, these findings support the view that *Symbiodolus* infection is shaped primarily by population-level dynamics and symbiont-symbiont interactions than by host ecology.

Imperfect vertical transmission of the highly diverse gut microbiota of termites: causes and consequences

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Simon DUPONT, Lucas MARIE-ORLÉACH

Abstract

Many insects are associated with beneficial microbial symbionts that live inside their hosts. Co-adaptation between the hosts and their symbionts often relies on vertical transmission, whereby the symbionts are passed from parents to offspring. In simple symbioses, where hosts harbour a single symbiont species, vertical transmission rates tend to be high, ensuring the symbiont remains prevalent in host populations. However, in complex systems where each host harbours a diverse community of microbes made of many species, vertical transmission rates can be low. The causes and consequences of such imperfect vertical transmissions remain poorly understood.

In this talk, I will present our recent findings on the subterranean termite species *Reticulitermes grassei* and its diverse gut microbiota made of bacteria, archaea and protists. Overall, our results revealed that vertical transmission rates for many gut symbiont taxa are imperfect. Our estimates were so low that they called into question the mechanisms by which gut microbial diversity is maintained from one termite generation to the next. Using simulation models, we investigated how various factors could explain the maintenance of gut microbial diversity in termite populations despite low vertical transmission rates. We specifically studied the following three factors: (i) the mating systems occurring in termite populations, such as panmixia and disassortative mating; (ii) the potential for horizontal transmission of symbionts between termite colonies; and (iii) natural selection at the colony level in relation to the composition of the gut community. Our results indicate that mating systems and horizontal transmission are insufficient to explain the observed data, and that a remarkably high strength of natural selection at the colony level is necessary. Hence, our analyses suggest that an imperfect transmission of gut symbionts may significantly reduce the average fitness of colonies within populations, playing a major role on host population dynamics and evolution.

Sequestration of a pro-viral protein from *Aedes aegypti* by the *Wolbachia* surface protein may contribute to dengue virus-blocking

Sassan ASGARI (The University of Queensland, S.asgari@uq.edu.au)

Mazhar HUSSAIN, Zhi QI

Abstract

Aedes aegypti transmits a variety of viruses to humans, including dengue, Zika, Yellow fever, and chikungunya viruses. *Wolbachia pipientis*, when artificially transinfected into the mosquito, blocks the replication of these viruses, although the mechanism(s) of this blocking are relatively unknown. In this project, we explored *Ae. aegypti* host proteins that interact with *Wolbachia* surface protein (wsp) secreted into the host cytoplasm using immunoprecipitation and mass spectrometry. A serine/threonine kinase (STK) was identified and found to be induced following dengue virus infection of mosquito cells lacking *Wolbachia*. However, in the presence of *Wolbachia*, STK expression was significantly attenuated. Our results showed that STK is proviral, as its knockdown or overexpression in mosquito cells reduced or increased virus replication, respectively. Further, we found that wsp by itself is antiviral. Overall, in the presence of *Wolbachia*, STK, which is proviral, is suppressed by downregulation of its expression and through sequestration of the protein by binding to wsp. These mechanisms may contribute to the virus blocking observed in the presence of *Wolbachia*.

Variation in variation: the benefits (and costs) of genetic diversity in insect populations

Kelley LEUNG (Wageningen University and Research, Kelleyleung@gmail.com)

Abstract

An intuitive assumption is that more genetic variation results in better population health. For insects, their massive diversity in life history and ecological niches translates to many nuanced responses to this “rule”. Insects naturally have drastic fluctuations in seasonal population size, making it difficult to establish a baseline for a “healthy” population size. Inbreeding is also often inherent to their reproductive biology. Complicating things further, many insect populations undergo major changes to genetic diversity in their relationship to humans. They can be introduced as invasive pests; produced in captive genetic isolation as e.g. pollinators, biological control agents, or food and feed; and undergo rapid decline as the biodiversity loss crisis continues. Across these scenarios, genetic bottlenecks are common, but the empirical evidence for relative gains versus costs of retaining or reintroducing more genetic diversity is mixed. Underappreciated for example are the drawbacks of outbreeding depression, and losing selection for commercial insects optimized production and performance. In this talk, I explore insect-specific concepts of inbreeding and outbreeding depression and the complex implications for the genetic diversity management for captive and wild populations. An illustrative case is the paradoxical scenario of hymenopterans (sawflies, bees, ants, wasps), which variously represent some of the world’s most prominent human-managed pollinators and biological control agents, but also some of the most endangered and most invasive insect taxa. In particular, many phylogenetically distant species have complementary sex determination, in which inbreeding at a single locus results in sterile males, an extreme form of inbreeding depression. With work from ants, bees, and parasitoids, I explore the delineation and differentiation of explanatory mechanisms that result in contrasting cases of inbred CSD hymenopteran population expansions (invasive species) and severe declines (endangered species).

Note: this is for an invited talk, apologies for late submission.

#10668

EVOLUTIONARY GENETICS: Genetic variation and selection in insect population

29/06/2026 at 11:30, Montlouis

Assessing human impacts on the genomic diversity of honey bees

Thibault LEROY (GenPhySE, Université de Toulouse, INRAE, ENVT, 31326, Castanet Tolosan, France, Thibault.leroy@inrae.fr)

Alain VIGNAL, Sonia EYNARD, David WRAGG, Benjamin BASSO, Pierre FAUX

Abstract

For the Western honey bee (*Apis mellifera*), as for any species, maintaining enough genetic diversity is essential for adaptation and thereby for long-term survival. This is why goal A of the UN CBD 15 (2022 Kunming-Montreal conference) highlights the importance of maintaining genetic diversity, one of the three fundamental units of biodiversity, in both wild and domesticated species to safeguard species' adaptive potential. In practice, tracking genetic diversity over time is complicated, but demographic modeling approaches, combined with large genomic datasets, can give insights into human impacts.

In 2014, our lab (BeeGEES, UMR GenPhySE) sampled 600+ honey bees across three main lineages (M, C and O) and breeds in Europe (Buckfast as well as bees selected for the production of royal jelly) and performed whole-genome sequencing. In this talk, I will review the main insights from a decade of research. Specifically, inferences of effective population sizes based on patterns of linkage disequilibrium revealed moderate to strong bottlenecks over the past 25 generations. Coupled with analysis of their genetic diversity, our results suggest that modern beekeeping practices (e.g. queen rearing) have substantially reduced the diversity of honey bees. We also report bottlenecks in black honey bee (*A. m. mellifera*) populations from two conservatories, but only with a limited increase in deleterious mutation load. For some populations, the analysis of diversity took advantage of a new sampling, a decade later (2024).

Our study gives insights about the determinants of present-day genetic diversity in honeybees. Given the key role of *A. mellifera* for crop pollination worldwide, this loss of diversity raises concerns about the long-term sustainability of the current trajectory. From a conservation perspective, we highlight the need for increased public funding for black honey bee conservatories to protect these genetic resources.

#10822

EVOLUTIONARY GENETICS: Genetic variation and selection in insect population

29/06/2026 at 11:45, Montlouis

Host-plant specialization and adaptation to agricultural practices in the *Ostrinia* corn borers

Vincent CACLAGNO (Institut Sophia Agrobiotech, Vincent.calcagno@inrae.fr)

Abstract

A fundamental question in evolutionary biology is how repeatable evolutionary trajectories are when species adapt to new environments: will similar evolutionary solutions be found, or will alternative routes be followed? Does evolution repeatability depend on the scale considered (phenotype, molecular determinants, genetic changes) and on the trait considered? I'll address these questions using *Ostrinia* pests as a model system: following maize introduction from America 500 years ago in Europe and in Asia, two maize-specialized species have independently emerged on each side of the continent. I will discuss the key evolutionary changes that occurred in these pests, and the strategies they developed to thrive on maize crops, comparing the European and the Asian species.

Phylogeny of Coelopidae seaweed flies and evolution of wing polymorphism

Dominique HICKS (ECOBIO, UMR 6553 CNRS, Université de Rennes, Dominique.hicks@univ-rennes.fr)

Maren WELLENREUTHER, Claire MÉROT

Abstract

Intra-specific polymorphisms, such as ecotypes or morphotypes, are often found to be encoded by specific genetic architectures carrying multiple co-adaptive genes, termed supergenes. How such discrete polymorphisms and supergenes originate and persist over long evolutionary timescales is a fascinating open question. Recent empirical studies suggest it involves different processes including balancing selection on ancestral polymorphism, parallel evolution, and introgression.

In the seaweed fly *Coelopa frigida*, an inversion-supergene polymorphism is associated with high polymorphism in male size and development time. One class of males exhibits traits similar to females, while two other classes of males have a larger size, associated with higher reproductive success. Interestingly, historical qualitative records of male size polymorphism similar to what is observed in *C. frigida* are reported in nine other species of Coelopidae across the globe, suggesting that the supergene polymorphism may be shared across species boundaries. To address this hypothesis, we have gathered whole-genome sequencing data from 17 species (spanning almost the whole Coelopidae clade), to build a robust phylogeny and incorporate genome synteny and gene trees associated with Cf-Inv(1) when possible. To quantify wing size polymorphism, we used machine learning-assisted high-throughput phenotyping on 13 species. In parallel, we collected development time and life-history traits from lab-bred specimens from 5 *Coelopa* species. Altogether, our results support the presence of phenotypic polymorphism comparable to *C. frigida* in some coelopid species – but not all. Our study provides valuable information about the biology, morphology, and phylogenetic relationships of Coelopidae species, while shedding light on the evolution of genetic and phenotypic evolution across the Coelopidae clade, as well as on multi-species supergene evolution.

Phylogenomic characterisation of insecticide detoxifying genes in parasitoid wasps

Chung Laam TSUI (University of Exeter, UK, Clt216@exeter.ac.uk)

Angela HAYWARD, Ralf NAUEN, Nicola NADEAU, Chris BASS

Abstract

Recent work has demonstrated that many bee species have specific cytochrome P450 enzymes that can detoxify certain insecticides. The presence of these P450s (the *CYP9Q*-related subfamily) is well conserved across the diversity of bees. However, some bee species, such as *Megachile rotundata*, lack these P450s and are more sensitive to insecticides.

Current risk assessments rely heavily on data collected from a handful of model species. However, given that different insects have different sensitivity to insecticides, the robustness of this approach is highly questionable. This project aims to develop a pesticide risk assessment framework that identifies risk to beneficial insects by exploiting genomic information to predict their sensitivity to pesticides. My main focus is on parasitoid wasps as the recent advances in understanding of insecticide detoxification by P450s in bees serves as an excellent entry point. The Hymenoptera diversified over 281 million years, and it is unknown whether *CYP9Q*-related P450s are found across the order.

Genome of pesticide risk assessment model species *Aphidius rhopalosiphii* was assembled and annotated. Exploiting the explosion in genomic data, CYP9 P450s from 139 species of parasitoid wasp were identified and extracted. Phylogenetic analyses were run to locate the CYP9Q-type P450s in parasitoid wasps. None of the CYP9s in parasitoid wasps' clade with CYP9Q-type P450s in bees. Rather, they clade within their own superfamily/family. Functional expression of recombinant CYP9s in the Ichneumonoidea indicates that these enzymes are likely to metabolise certain insecticides. This suggests that each superfamily/family could have xenobiotic metabolising P450s.

Functional Analysis of Genetic Variation in an HR96-Related Nuclear Receptor Highlights Its Role in Detoxification Gene Regulation in a Major Crop Pest

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Marilou VANDENHOLE, Sander DE ROUCK

Abstract

The cosmopolitan pest *Tetranychus urticae* (two-spotted spider mite) is an extremely polyphagous herbivore, feeding on over 1,100 plant species from 140 families. Resistant to over 95 active ingredients, and rapidly evolving resistance to nearly all acaricide classes, it stands as one of the most resistant arthropods globally.

A pioneering eQTL study laid the foundation to unravel the basis of extensive metabolic transcriptional reprogramming driving both broad host range and resistance. Genetic mapping in resistant and susceptible *T. urticae* populations linked a trans-eQTL hotspot, responsible for substantial transcriptional regulation of detoxification genes, to heritable variation in an HR96-LBD gene segregating in these populations. We confirmed, with novel CRISPR/Cas tools, the causal effect of allelic variation within this transcription factor on global gene expression patterns, revealing its profound impact on the transcriptome and ability to fuel adaptive phenotypes. Furthermore, we found that lineage-specific expansions of both HR96-LBD genes and HR96 canonical genes in *T. urticae* suggests modular control of subsets of xenobiotic response genes. Through RNAi-mediated silencing of eight potential interacting factors, we explored the architecture of this major pathway underpinning the extreme regulatory plasticity of spider mites.

Using museum genomics to guide conservation of the Apollo butterfly in Central Europe

Tomasz SUCHAN (Institute of Geography and Spatial Organization, Polish Academy of Sciences, Tomasz.suchan@gmail.com)

Abstract

The Apollo butterfly (*Parnassius apollo*) is a species of major conservation concern in Europe. As a montane specialist, strongly dependent on specific climatic conditions and habitats, it is highly vulnerable to environmental change and anthropogenic pressures. Consequently, *P. apollo* has experienced dramatic population declines and local extinctions across much of its historical range. Despite its iconic status, surprisingly little is known about the species' genetic structure. However, a comprehensive understanding of genetic diversity and population structure is critical for effective conservation planning, particularly to safeguard evolutionary potential and inform reintroduction strategies. Museum collections represent an invaluable resource for such studies: they allow genetic assessment without additional pressure on endangered populations, enable the inclusion of already extinct lineages, and provide the possibility to evaluate temporal changes in genetic diversity. In this study, we apply shallow whole-genome shotgun sequencing of degraded DNA from historical museum specimens to investigate patterns of genetic structure in Central European populations of *P. apollo*, which have persisted in Slovakia, Poland, and Austria. Our objectives are to delineate genetically informed conservation units and to identify suitable source populations to support reintroduction efforts in the Czech Republic. Furthermore, we examine the controversial case of the Pieniny Mountains population in Poland, where illegal releases are suspected to have introduced foreign genetic material. We estimate the extent of introgression in the nuclear genome and evaluate its implications for future management and reintroduction actions in the region.

Over the ocean and beyond – phylogeny and zoogeography of the genus *Euchromia* Hübner, 1819 revealed by museomics (Lepidoptera: Noctuoidea: Erebidae: Arctiinae)

Marcin WIOREK (Institute of Systematics and Evolution of Animals Polish Academy of Sciences, ul. Sławkowska 17, 31-016 Kraków, Poland, Wiorek@isez.pan.krakow.pl)

Łukasz PRZYBYŁOWICZ, Niklas WAHLBERG, Pável MATOS-MARAVÍ, Emma KÄRRNÄS, Mar REPULLÉS

Abstract

The genus *Euchromia* is the only member of the Neotropical subtribe *Euchromiina* occurring solely outside the New World, but deriving from the Neotropical radiation of tiger moths. There are around 40 valid species in the genus (although around 100 have been described); they occur from West Africa to Fiji in Melanesia, and many species are endemics of particular islands and archipelagos of Australasia. For these reasons, and as an evolutionary young group of winged insects, *Euchromia* is a suitable object for studies on transoceanic Long Distance Dispersal (LDD) and further colonisation and diversification. Given the wide distribution and endemism pattern of *Euchromia*, using museum material collected over around 150 years facilitates a comprehensive coverage of species in molecular phylogenies. This research leverages Illumina-based genome sequencing of old specimens, so-called museomics, to infer a dated phylogeny of *Euchromia*, including almost all valid species. The data suggest that the genus's ancestor dispersed to the Old World through the Pacific Ocean. The genus subsequently diversified and extended its range westwards, with the African group of around ten species being a young monophyletic group. The dispersal routes will be discussed in the context of the main paleogeographical events, like e.g. the Gomphoterium land bridge formation between Africa and Eurasia, and the complex geological history of the Indo-Pacific region. This study contributes to a better understanding of the factors shaping the evolution and distribution of the Neotropical faunistic elements in the Old World biodiversity – a rarely reported but interesting phenomenon.

The research was funded by the National Science Centre, Poland, grant no. UMO-2021/41/N/NZ8/03334 to M. Wiorek.

Integrating genetic data from contemporary and museum specimens to assess population vulnerability in an iconic mountain butterfly through an approach of hybridization-capture

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Delphine RIOUX, Laurence DESPRES

Abstract

Mountain species are particularly vulnerable to global changes. *Parnassius apollo* (Linnaeus, 1758; Papilionidae, Lepidoptera) is an emblematic subalpine butterfly restricted to open habitats of Eurasian mountain regions, including grasslands and rocky slopes. Our study focuses on French populations, for which non-lethal sampling has been conducted since 2018 across the species' distribution range in France. More than 300 contemporary samples were sequenced using ddRADseq, generating a large genetic dataset (>3,000 SNPs) used to assess population characteristics through analyses of genetic diversity metrics, genetic differentiation and population sizes estimates. Demographic inferences suggest a decline in all French populations. To validate these recent demographic trends, we applied a Hybridization Capture approach using ddRAD probes (HyRAD) to 192 historical specimens from the Grenoble Museum collection, spanning all decades from 1934 to 2010, and collected in the same localities as the contemporary samples. This museomic approach is used to generate genetic markers from historical specimens that are directly comparable to those obtained by ddRADseq from contemporary samples. The objectives of this study are (i) to compare the temporal genetic structure, population size and current genetic diversity of populations (contemporary samples) with past genetic diversity (historical samples), thereby testing and validating inferences of recent population declines, and (ii) to investigate temporal changes in potentially adaptive alleles within populations over the last century, providing insights into population responses to global changes.

Enhancing phylogenetic inferences with museum specimens using a new method of Genome Alignment-Based Bait Inference and its application to the largely understudied tribe of Ochyromerini weevils

Benjamin ZELVELDER (University of Montpellier, Benjamin.zelvelder@gmail.com)

Julien HARAN, Anne LOISEAU, Laure BENOIT, Rémi ALLIO

Abstract

Targeted enrichment approaches have allowed substantial advances in phylogenomics by enabling the recovery of genomic data from ultra diverse taxa, notably relying on museum specimens. However, the efficiency of target capture often suffers from important limitations, including high proportions of missing data in old specimens and reduced phylogenetic resolution due to targeted loci conservation and/or saturation. These challenges are particularly acute in hyperdiverse insect lineages for which genomic resources remain scarce whereas museum samples abound. To address these limitations, we introduce a novel method of bait inference based on genome alignments, termed Genome Alignment-Based Bait Inference (GABBI), and compared its performance to the commonly used PHYLUCE pipeline by designing new probe sets for weevils (Coleoptera, Curculionoidea). These probe sets were tested at two taxonomic scales, the superfamily scale using 60 available genomes of Curculionoidea, and the tribe scale using available Pachyrhynchini data. Results show that the genomic regions extracted from a genome alignment achieve higher levels of internal sequence variation, making the GABBI-derived probe set more phylogenetically resolute at both broad and narrow taxonomic scales. By targeting more loci (>4k) and increasing the number of probes to map their inner variability (>100k), GABBI-derived probe sets reduce reliance on flanking regions that are more difficult to align and to acquire in degraded DNA samples. In vitro target capture using the new GABBI weevil probe set on both recent and historical specimens yielded a high median of 85% recovered loci and provided reliable DNA information in samples with barely more than 5% recovered loci. Phylogenetic analyses conducted with these newly-generated data provide the first phylogenomic framework to study the evolution of the largely understudied tribe of Ochyromerini weevils. By releasing the GABBI pipeline, we aim to facilitate the development of tailored target capture designs for other taxonomic groups facing similar challenges.

Two evolutionary pathways to koinobiont ectoparasitoids of spiders in Darwin wasps (Hymenoptera: Ichneumonidae: Pimplinae)

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Bernardo SANTOS F., Karin URFER, Ilari SÄÄKSJARVI, Gavin BROAD R., Seàn BRADY G.

Abstract

A unique parasitoid strategy is exhibited by polysphinctine parasitoid wasps, a group of Darwin wasps (Hymenoptera: Ichneumonidae: Pimplinae) that exclusively exploits subadult and adult spiders as hosts. Larvae of many species not only attach to and feed on active spiders throughout their development (koinobiont ectoparasitoidism), but also manipulate the web-building behaviour of their hosts for their own benefit. This strategy has long been hypothesised to have evolved only once, originating from pseudoparasitoids of spider egg sacs; however, testing this hypothesis has been hampered by inadequately resolved phylogenetic relationships. Here, we reconstruct first comprehensive phylogeny of polysphinctine wasps using museum specimens and targeted capture of ultraconserved genomic elements (UCEs). Our dataset comprises more than 1,400 UCE loci from 147 species, including representatives of 23 of the 25 known polysphinctine genera, as well as relevant outgroup taxa. In addition, we perform an ancestral state reconstruction (ASR) of host use, explicitly testing the hypothesis of a single origin of the koinobiont ectoparasitoidism of spiders in Darwin wasps. Across all analyses, polysphinctines are rendered paraphyletic by the pseudoparasitoids of spider egg sacs. This result is robust to alternative outgroup choices, locus subsampling schemes, and analyses restricted to protein-coding UCEs. The results of the ASR further support two independent transitions from pseudoparasitoids of spider egg sacs to parasitoids of errant spiders. These findings challenge the long-standing hypothesis of a single origin of spider parasitoidism in Darwin wasps and provide a new framework for future phylogenetic and evolutionary studies of this remarkable group.

Chemical communication at the heart of family life: insights from burying beetles

Sandra STEIGER (University of Bayreuth, Sandra.steiger@uni-bayreuth.de)

Abstract

Social life is a highly diverse phenomenon and comes in many forms and facets. A fundamental social core unit of immense importance is the family, the association of one or two parents with their offspring. Temporary family living is widespread across the animal kingdom, occurring not only in vertebrates but also in a wide range of insects. Family life is a cooperative event but also full of conflict, and the evolution of communication processes has been considered essential for the integrity of the family unit and the coordination of interactions among family members. Despite chemical communication being prevalent among animals, our understanding of the evolution of social pheromones within a family context remains very limited. The contrast between the extensive research available in eusocial insects and the limited knowledge about chemical communication in “subsocial” species is remarkable. In my talk, I will present research on family interactions in subsocial species, focusing on burying beetles (*Nicrophorus* spp.) as a model system, and show the fascinating complexity of these interactions. I will demonstrate how chemical communication can stabilize family life from the perspectives of (1) the entire family, (2) the father, (3) the mother, and (4) the offspring. I will show that socially induced reproductive “control” is not only a core feature of eusocial societies but plays a fundamental role in simple families. Moreover, our data suggest that offspring chemical signals are of high importance in the regulation of family life.

How insect parents optimise provisioning in a changing world

James GILBERT (University of Hull, James.gilbert@hull.ac.uk)

Abstract

Parental care is widespread across insects, but the strategies parents use — and the constraints they face — are dynamic and diverse. Here, I bring together findings across my research to show how parental provisioning behaviour evolves across species, how it can be fine-tuned in real ecological contexts, and the implications of rapid environmental change.

On macroevolutionary timescales, we showed that parental provisioning fundamentally restructures insect life histories. In insects with provisioning, species that are larger tend also to have fewer offspring than smaller species (as with birds and mammals). This contrasts with non-provisioning insects, where larger species have more offspring than smaller species (as with fish and amphibians). Thus, parents appear to limit offspring numbers to the number they can provision.

Parents' provisioning is sensitive to offspring nutritional needs. In wild bees, we found adults select different plant species when foraging for pollen for offspring versus nectar for themselves. Provisioning also changes to accommodate changing offspring needs. Solitary mason bees mass-provision young with a single pollen ball with variable amounts of protein and carbohydrate. Overall, we found larvae eat just enough to get a target amount of carbohydrate regardless of how much protein they ingest. However, their eating rules change as they develop. Accordingly, pollen balls are structured, such that larvae encounter different pollen species as they eat through the provisions.

Finally, provisioning is tuned to the environment. When we maintained larvae at elevated temperatures, they reversed their eating rules: now, larvae ate enough to meet a fixed amount of protein regardless of how much carbohydrate they ate to meet their target. Accordingly, when we heated field nests to different temperatures, provisioning adults gathered different species of pollen in response, tailoring provisions to the environment.

Thus, environmental change such as global warming can alter parent–offspring nutritional negotiation and potentially bees' foraging habits.

Maternal care, brood effects, and novel application of the Hinde Index in the cockroach *Blaptica dubia*

Georgia CASH (University of Aberdeen, G.cash.23@abdn.ac.uk)

David FISHER, Lesley LANCASTER, Gareth ARNOTT

Abstract

Parental care is thought to be a key stepping stone for the evolution of sociality. Cockroaches are an ideal group to test this idea as they display the full spectrum of care behaviours, ranging from no care to long-term biparental care and complete reproductive division of labour. Here, we use controlled laboratory experiments to investigate maternal care in *Blaptica dubia*, a species commonly described as subsocial, and the impact of maternal presence on offspring growth, survival, movement, and social behaviour. To disentangle the effects of maternal identity from the mere presence of an adult, we employed a cross-fostering design in which nymphs either remained with their biological mother, were placed with an unrelated adult female, or were reared without any adult female present. Additionally, for the first time in an invertebrate, we apply the Hinde and Brown indices to quantify the dynamics of mother-offspring interactions, distinguishing who is primarily responsible for maintaining contact rather than simply how much contact occurs. Behavioural observations revealed that maternal care in *B. dubia* is minimal and transient, consisting of short-term brooding behaviour immediately following birth. Consistent with this, we detected no differences between maternal presence treatments in offspring growth, survival, or behaviour. However, analysis of interaction dynamics revealed a significant shift in contact maintenance: while overall levels of contact (Brown Index) did not differ, Hinde index values indicated that nymphs paired with unrelated adult females were more responsible for initiating and maintaining contact than those with their biological mother. This suggests that offspring adjust their behaviour to compensate for reduced maternal responsiveness, maintaining overall interaction frequency despite changes in parent identity. These findings highlight the diversity and subtlety of parental care strategies in cockroaches and demonstrate the potential for adapting analytical frameworks, such as the Hinde and Brown indices, for studying invertebrate social behaviour.

Lifelong effects of parental care on adult traits in the burying beetle

Sheena COTTER (University of Lincoln, Scotter@lincoln.ac.uk)

Ekhlas AL SHAREEFI

Abstract

Whilst parental care is obligatory in some social insects, in others, offspring can survive if abandoned, but may suffer fitness consequences. The burying beetle, *Nicrophorus vespilloides*, engages in biparental care, shaping and preparing an edible nest for their offspring from a small vertebrate carcass. Once hatched, parents feed larvae and keep the carcass fresh, typically until the larvae are ready to pupate. However, if the parents die or abandon larvae, some may survive, but are typically smaller as they feed much less efficiently without care. Here, we asked i) whether the quality of adult beetles was affected by the care they received as larvae, and ii) whether any negative effects on reproduction, survival or immunity could be ameliorated by the adult diet. We hypothesised that adult beetles reared without care could partially compensate for poor larval diet by increasing their consumption of protein during maturation feeding.

To test this, we reared larvae with or without post-hatching parental care. Eclosing adults were assigned to one of 5 diets varying in their protein: fat ratios and reproduction, immune responses and survival were measured. Our results demonstrate that beetles who were reared without parents had lower reproductive output generally, lower efficiency in immune responses and a shorter lifespan. Moreover, this reduction in adult quality could not be ameliorated by nutritional compensation. The implications of this work are that a poor-quality larval environment cannot be compensated for by nutrient specific foraging as adults, suggesting that larval survival in the absence of care equates to a 'best of a bad job' scenario rather than an alternative tactic.

GWAS of indirect genetic effects and parental care in *Nicrophorus orbicollis*

Kyle BENOWITZ (Arizona State University, Benowitz@asu.edu)

Abstract

Indirect genetic effects (IGE) occur when the genotype of one individual influences the phenotype of a social partner. For species that live in groups or that provide parental care, IGE are expected to represent a substantial proportion of the heritability for fitness-related traits. Additionally, the presence of positive or negative correlations between IGEs and direct genetic effects (DGE) for a trait can have dramatic effects on the evolutionary trajectory of that trait. Despite this, there have been few studies identifying alleles underlying IGE in evolutionary and ecological model systems. Here, we performed a genome-wide association study (GWAS) to find alleles associated with IGEs conferred from mothers to offspring in the burying beetle *Nicrophorus orbicollis*. This species, like all burying beetles, provides parental care via the preparation of small vertebrate carcasses. We bred ~1,500 genetically distinct F₁ females from a single population in Tennessee/Kentucky using a cross-fostering design, where each female reared unrelated offspring. We sequenced all F₁ females and two F₂ offspring (one male and one female) from each family. Primarily, we sought to determine how offspring and maternal genotypes influenced body size, a key fitness-related trait in *N. orbicollis*. However, we also measured a variety of other phenotypes in the F₁ and F₂ generations, including morphological characters, amount and duration of parental care (in uniparental and biparental contexts), family size (on multiple carcass sizes), competitive ability, and mating rate. From these additional phenotypes, we can answer critical questions about the alleles influencing phenomena like GxE, dominance, sexual selection, and IGE conferred between male and female parents. In this talk, I will present preliminary results on phenotypic data as well as heritabilities, correlations, and specific genetic associations.

Immune cost of maternal care towards eggs and juveniles in the European earwig

Simon DE WEVER (IRBI, Simon.dewever@univ-tours.fr)

Joel MEUNIER

Abstract

Parental care is widespread in nature and typically benefits offspring by protecting them from pathogens, predators, and starvation. However, caregiving is expected to come at a cost to parents, as resources invested in care may trade off with other physiological functions. The immunological costs of parental care remain poorly understood, especially in insects. Here, we investigate the immune costs of maternal care in the European earwig (*Forficula auricularia*), focusing on care directed toward both eggs and juveniles. In this species, mothers lay eggs in early winter, cease foraging, and provide continuous care until hatching in early spring. They then take care of their juveniles for about two weeks before family dispersal, providing nest protection, egg grooming, desiccation prevention, temperature regulation, and food provisioning.

To test whether this investment in care compromises maternal immunity, we experimentally manipulated maternal investment by varying the number of eggs (0, 55, 110) and juveniles (0, 40, 80) present in the nests of 1040 mothers. Measurements were taken at four stages: before oviposition, right after oviposition, 35 days post-oviposition, and 15 days post-hatching.

We used different groups of mothers for various measurements. Hemolymph was extracted from mothers to measure two immune parameters: lytic activity and phenol oxidase activity. Other mothers were used to measure encapsulation rate and respirometry. These four measurements were taken both under basal conditions and after immune activation via injection of heat-killed *S. marcescens*. Additionally, survival against the bacteria *Serratia marcescens* was assessed in a separate group of mothers.

We predict that increasing maternal investment in care will reduce maternal investment in immune function, revealing a trade-off between parental care and self-maintenance. Identifying the magnitude and nature of these costs will improve understanding of the physiological limits of family life and the evolutionary constraints shaping parental care strategies in insects.

Parental care in communal carrion beetles *Necrodes littoralis* (Staphylinidae: Silphinae)

Szymon MATUSZEWSKI (Adam Mickiewicz University, Szymmat@amu.edu.pl)

Abstract

Carrion beetles, recently included in Staphylinidae, are divided into: Nicrophorini and Silphini. Parental care has been extensively studied in Nicrophorini, whereas Silphini were not the focus of such studies. Here, I summarise recent findings regarding parental care in *Necrodes littoralis* Linnaeus 1758. The species breeds on carrion of large vertebrates (wild boar, roe deer, etc.). Adult beetles usually visit carrion, while it is bloated. Under favourable conditions hundreds of them may colonize carcass. They oviposit in soil and larvae start to feed on carrion, where they may form massive aggregations, consisting of thousands of larvae.

Only pre-hatching care is present in these beetles. After locating carrion, adult beetles search for fly larvae. They preferentially kill late L2 or early L3, which are the most destructive for carrion, thus providing more food for their offspring. Then, they start to prepare carrion for their larvae. By applying secretions and excretions, the beetles form a feeding matrix. The microbial diversity of the matrix, polyamine levels and trypsin activity decrease, while lipase activity increases with the time adult beetles spend on meat. Furthermore, heat is produced in the matrix. Therefore, the key functions of the matrix in this phase are to preserve and predigest carrion. Females are primarily responsible for these forms of care. Subsequently, first instar larvae are attracted to the matrix, staying there for most of their development. They alter the quality and function of the matrix, causing large increase in thermogenesis and significant changes in the matrix microbiome.

We were also interested in, why no post-hatching care is present in these beetles. Experimentally doubling the time adult beetles spend on meat revealed a clear negative effect on juvenile fitness, suggesting that parent-offspring competition for shared food limits the time adults stay on carrion and, therefore, constrains parental care in these beetles.

Evolution of parental care in harvestmen (Arachnida: Opiliones): lessons from an eight-legged world

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Abstract

Parental care encompasses a diverse set of behaviors that enhance offspring survival but also impose costs on caregivers. Although extensive theoretical and empirical work has elucidated the ecological and evolutionary forces shaping parental care in vertebrates, the broader patterns governing its origin and diversification across invertebrates remain poorly understood. Harvestmen represent an exceptional system for addressing these gaps because parental care—either maternal or paternal—has evolved repeatedly. This presentation synthesizes two complementary studies that seek to clarify the evolutionary pathways leading to maternal and paternal care in harvestmen. In the first study, we test two alternative macroevolutionary hypotheses concerning the relationship between parental care and habitat type. The first hypothesis, rooted in E.O. Wilson's classical drivers, proposes that parental care—particularly maternal care—evolves in response to ecological pressures typical of tropical forests, such as intense predation and high fungal infection. The second hypothesis reverses the direction of causality, proposing that parental care itself acts as a pre-adaptation enabling subsequent colonization of tropical habitats. Using modern comparative methods and explicitly distinguishing between maternal and paternal care, this study evaluates the sex-specific predictions of these contrasting scenarios. The second study investigates whether the evolution of parental care in harvestmen is facilitated by the presence of specific behavioral or morphological precursors. Focusing on four major precursors (i.e., contusive defenses, oviposition on exposed substrates, spatial and temporal egg distribution, and male defense of oviposition sites), we use a newly developed comparative framework that allows all traits to evolve independently. This approach enables a rigorous evaluation of whether precursors promote the transition from ancestral no-care states to maternal or paternal care. Together, these two studies aim to advance our understanding of how ecological context, ancestral traits, and sex-specific selective pressures interact to shape the evolution of parental care in arthropods.

Parenting under pressure: how resources and rivals shape biparental care in burying beetles

Tom RATZ (University of Zurich, Tom.ratz@uzh.ch)

Abstract

Biparental care relies on cooperation between the sexes despite sexual conflict over optimal parental investment. Changing ecological conditions can shift the balance of cooperation by changing the costs and benefits of providing care to each sex. However, it is unclear to what extent such changes alter the level of sex differences in parental care. In this talk, I will show how two key environmental factors—resource availability and threats from conspecific intruders—can shift the balance of cooperation and shape sex differences in parental care in the burying beetle *Nicrophorus vespilloides*. When breeding resources were experimentally limited, males reduced their care whereas females maintained consistently high levels of care, resulting in more pronounced sex differences and less cooperative biparental care. The presence of intruders did not increase biparental cooperation overall, but females increased certain care behaviours on large carcasses. Together, these findings show that ecological conditions can modulate sex differences in care without fundamentally shifting the cooperation–conflict balance in biparental families.

Can plasticity in provision of parental care help burying beetles sustainably manage competition for resources with microbes?

Nick ROYLE (University of Exeter, N.j.royle@exeter.ac.uk)

Sarah DUXBURY, Michael JARDINE, Ben RAYMOND, Price TOM, David STUDHOLME

Abstract

Competition among organisms is a key driver of (social) evolution, but the effects of interspecific competition may be mitigated by cooperation – both intra- and interspecific – especially in the context of parental care. Male and female burying beetles use the cadavers of small vertebrates, such as mice, to feed their offspring during parental care, which they typically prepare together using antimicrobial secretions to control the microbes that are competing with them for resources on the carcass. They also transmit symbiotic microbes among family members. Fossil evidence indicates burying beetles have been providing parental care for over 100 million years, so sustainable coexistence with communities of microbes has been under long-term selection but burying beetles have not suffered the consequences of resistance from competing microbes. Why? Previous research indicates resource specialization constraints – the requirement for cadavers of small vertebrates to breed – has driven the evolution of behavioural plasticity in parental care in burying beetles. Can such evolved plasticity be key to understanding how burying beetle parental care has managed bacterial competitors so effectively for millions of years? An important step is to address how burying beetles respond to variation in competition from microbes. We manipulated microbial load and diversity of beetle-tended carcasses using a combination of carcass ageing and broad-spectrum antibiotics and assessed the microbial management response of beetles and putative microbial symbionts through comparison with the microbiomes of untended carcasses. Beetle-tended carcasses showed a decrease in microbial competitors such as *Citrobacter*, *Lysinibacillus* and *Mucor* fungus and a corresponding increase in likely symbionts such as *Vagococcus*, with fresh carcasses treated with antibiotics that are dominated by such commensals producing the largest offspring. However, the sustained abundance of some taxa, especially when microbial load is high and reproductive output correspondingly low, indicates that there are limits to microbial management.

HotSecretions: Effect of heat stress on burying beetle secretions

Camila ZENOBI (University of Bayreuth, Camizenobi@hotmail.com)

Charlotte WALLIS, Jos KRAMER

Abstract

Increased exposure to thermal stress expected in a warming world can reduce fitness by disrupting physiological and behavioral processes required for successful reproduction, especially in species that rely on parental care for offspring survival. However, how the effects of heat stress on specific components of care translate into negative fitness effects remains unclear. Here, we investigate this question by examining how heat stress shapes the production of antimicrobial secretions and associated fitness consequences in the burying beetle *Nicrophorus vespilloides*. In this necrophagous insect, parent-produced secretions play a key role in preserving the carcass used for breeding, aiding in microbial control and preventing decomposition. Although the importance of these secretions for reproductive success is well established, the effects of heat stress on their quantity and quality remain poorly understood. To tackle this issue, we maintained female-male pairs at either control (20°C) or increased temperatures (25°C) and quantified the amount and antimicrobial (lytic) activity of their anal secretions at multiple timepoints before and during breeding. To be able to link variation in the secretions' quantity and quality to fitness outcomes, we quantified offspring weight change and survival during breeding. We hypothesize that heat stress reduces both the amount and the antimicrobial activity of parent-produced secretions. Given the secretions' key role in carcass maintenance, we furthermore expect that these negative effects will go hand in hand with a reduced offspring weight gain and survival. Finally, we anticipate that those breeding pairs able to produce high amounts – or highly antimicrobially active – secretions will produce more and heavier offspring even under heat stress. Our results will provide insights into the effects of heat stress on a key parental behavior of burying beetles, and thereby contribute to our understanding of the potential impacts of global warming on animal social behaviors and their fitness consequences.

#12521

SOCIAL INSECTS: Parental care 2

29/06/2026 at 15:45, Villandry

Effects of thermal stress on parental care in burying beetles

Natalie PILAKOUTA (University of St Andrews, Npila1@gmail.com)

Abstract

Parental care is thought to have evolved as a means by which parents can improve their offspring's fitness by neutralising the detrimental effects of environmental stresses in hostile or unpredictable environments. When considering the potential effects of climate change on parental care, we might thus expect that parents will work harder in an effort to neutralise any negative effects of thermal stress on their offspring. On the other hand, parents might reduce their effort if higher temperatures make parental care more costly, which could exacerbate the effects of thermal stress on the offspring. In this talk, I will discuss a number of recent studies we have conducted examining how exposure to thermal stress at different life stages influences parental care in adulthood. This work was done using the burying beetle *Nicrophorus vespilloides*, which has facultative biparental care.

Males make worse mothers: Parental care pattern shapes offspring immunity in burying beetles

Leon MÜLLER (University of Bayreuth, Leon.mueller@uni-bayreuth.de)

Patrick LIMBURG, Maximilian KÖRNER

Abstract

During biparental post-hatching care, parents take over energy consuming tasks for the offspring's benefit and further reduce their individual costs by specializing in different care aspects. But how is this pattern evolutionary stable when parental care is facultative, i.e. when offspring survive well in absence of care? We examine this phenomenon in carrion-breeding *Nicrophorus vespilloides* beetles whose biparental care involves microbiome control of the carcass nursery and shielding offspring from adverse environmental conditions through their extensive social immunity capabilities, enabling offspring to focus on their development rather than on pathogen defense. The adaptive benefits of biparental care for parents and offspring, especially in terms of social immunity, remain unclear in this genus. We presented *Nicrophorus* adults with a microbial challenge while manipulating parental care patterns (male & female uniparental or biparental care), investigating consequences in parental and offspring performance and immunity. We find that microbial environment and parental care pattern influence adult's energy expenditure but that these factors also influence larval performance and survival. Additionally, we also show first-time evidence that larval immune response is dependent on both factors, microbial environment and care pattern, as well, providing new insights into the role of social immunity during the evolution of biparental care.

Disentangling the microbial selective pressures on parental care in the burying beetle *Nicrophorus vespilloides*

Chung-Fan CHANG (University of Bayreuth, Germany, David42727@gmail.com)

Jos KRAMER

Abstract

Understanding how environmental drivers shape the evolution of parental care remains a central issue in evolutionary biology, particularly in organisms that have evolved care as a strategy to secure resources in competitive environments. Here, we tackle this issue by experimentally disentangling the selective pressures exerted by different microbial communities on parental care in the burying beetle *Nicrophorus vespilloides*. These beetles breed on small vertebrate carcasses and use parental behaviors – including carcass preparation and the secretion of antimicrobial compounds – to control harmful microbial competitors on their breeding resource. To test whether different types of microbes exert distinct selective pressures on parental care, we will manipulate the occurrence of (post-hatching) parental behaviors and then quantify offspring fitness under three distinct microbial conditions: (1) a microbe-reduced control, serving as a baseline; (2) a natural microbial community, representing ecologically realistic conditions; and (3) targeted bacterial inoculations (e.g., using strains isolated from untended carrion), testing distinct microbial effects. We predict that microbial effects will fall into distinct functional categories, depending on their positive or negative impacts on larval mass and survival. This study will advance our understanding of how microbial challenges shape parental care evolution, laying the groundwork for future mechanistic studies on the specific drivers of family life in insects.

Illumina sequencing combined with taxonomy to unravel the surprising complexity of pecan canopy arthropod communities

Jason SCHMIDT (Department of Entomology, University of Georgia, Jschmid2@uga.edu)

Pedro TOLEDO, Angelita ACEBES-DORIA, James W. CORNISH, Joseph MCHUCH, Tara GARIEPY

Abstract

In perennial tree agroecosystems, communities are likely to persist due to lower overall system disturbance as compared to annual production system, which could lead to diverse herbivore communities and their corresponding natural enemies. Yet, often we lack information on the taxonomic composition, spatiotemporal dynamics, and sensitivity of arthropod groups to perennial system management. In a pecan system (*Carya illinoensis*) over the last few years we have gathered data on a variety of the "players" in the system, and the intention of the presentation here is to provide an overview of aspects of our work where we utilized molecular techniques to uncover a surprising level of diversity of taxa utilizing the canopy space and their corresponding responses to current management, and discuss the use of eDNA for targeting indicator taxa for monitoring community dynamics.

A tiny omnivore with multitrophic impact: *Pronematus ubiquitus* activates plant-mediated resistance and directly suppresses a tomato pest and pathogen

Lore VERVAET (Ghent University, Lore.vervaet@ugent.be)

Dominiek VANGANSBEKE, Marcus DUARTE, Felix WÄCKERS, Patrick DE CLERCQ, Thomas VAN LEEUWEN

Abstract

Tomatoes interact with a diverse community of herbivores, beneficial arthropods and pathogens, creating a highly dynamic multitrophic system. While predatory mites are widely used for biological control, their capacity to modulate plant defenses and thereby influence organisms across trophic levels remains insufficiently explored. Recent research has shown that pollen supplementation allows *Pronematus ubiquitus* to establish persistent populations on tomato plants as a “standing army”, providing protection against both tomato russet mite (*Aculops lycopersici*) infestation and powdery mildew (*Oidium neolyopersici*) infection. The iolinid *P. ubiquitus* is a small, omnivorous, leaf-feeding mite that is also partly mycophagous. However, the significant suppression of *O. neolyopersici* observed across entire tomato plants suggests that induced plant defenses may also contribute to this control. Such plant-mediated defenses could potentially enhance resistance against tomato russet mite as well. To investigate these multitrophic effects, we examined how *P. ubiquitus* alters interactions between tomato plants, the herbivorous tomato russet mite, and the fungal pathogen *O. neolyopersici*. We aimed to disentangle the relative contributions of direct feeding versus plant-mediated resistance by combining targeted bio-assays with comparative transcriptome analysis.

A meta-analysis of the impact of predator cocktails on the suppression of herbivorous arthropods

Enric FRAGO (CIRAD/UMR CBGP, Enric.frago@cirad.fr)

Francisco MARTINEZ-MARTINEZ, MArguerite CHARTOIS, Maximilien ADAM, Dirk SANDERS

Abstract

Herbivore populations are typically attacked by multiple predator species. These "natural enemy cocktails" often suppress herbivores more effectively than single predators. Their impact, however, depends on whether predators have complementary ecological niches and whether they engage in antagonistic interactions like intraguild predation, in which predators attack one another. This question has been particularly studied in the context of biological control, where the use of single or multiple predators to control arthropod pests has been largely debated. Previous meta-analyses have partially explored this question, but an integrative and up-to-date synthesis is lacking. I will present a meta-analysis evaluating the relative importance of predator complementarity and intraguild predation for herbivore suppression by predator pairs. We quantified complementarity as differences in predator phylogeny and functional traits, and antagonism as differences in predator efficacy and the degree to which different predator species reduce each other's populations. Our results show that the impact of predator cocktails on herbivore suppression vary across ecosystem types and depend on complex interactions among predator phylogenetic distances, functional traits, relative efficacies, and intraguild predation potential. Differences in predator efficacy on the shared resource emerged as a key driver of suppression outcomes, with its effect modulated by functional trait divergence. In an era of big data, our work tests ecological theory but it will also be useful to biocontrol practitioners. We are developing a public database of predator traits and an on-line decision tool to select, for each crop and pest species, the most promising predator cocktails.

Close Encounters in the Azores Atlantic Islands: Arthropod–Invasive Plant Multitrophic Interactions

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Abstract

Island ecosystems present simplified ecological networks and strong habitat heterogeneity, rendering them hotspots of vulnerability to biological invasions and their ecological consequences. The Azores, a volcanic archipelago of nine islands in the Macaronesian region, host extensive human-modified and natural habitats dominated by invasive plant species. This study provides an exploratory assessment of multitrophic interactions involving phytophagous piercing-sucking mites and hemipterous insects associated with invasive host plants, together with their natural enemies, across six islands of the archipelago. Field sampling was conducted during three missions in 2024 (April-May and September) and 2025 (July-September). Arthropods were identified using an integrative taxonomy approach combining morphological examination and COI DNA barcoding to assess species diversity and host associations. Arthropod communities were surveyed on invasive plants from 16 families (21 taxa), based on approximately 100 samples, including dominant hosts such as *Pittosporum undulatum*, *Acacia melanoxylon* and *Hedychium gardnerianum*. At least 25 hemipterans were recorded, spanning Heteroptera, Auchenorrhyncha and Sternorrhyncha (e.g. aphids). The remaining taxa belonged to eight other insect orders. The highest number of insect taxa was observed on *Cyrtomium falcatum*, followed by *Solanum mauritianum*, whereas Aphids were mainly associated with *Rumex obtusifolius*, *Arundo donax*, *Paspalum dilatatum*, *Pittosporum undulatum* and Asteraceae hosts. Regarding mites, 11 taxa were recorded on 13 invasive plant species, with most phytophagous species representing first records for the Azores and likely corresponding to alien taxa. Assemblages included phytophagous mites in Tetranychidae (e.g. *Oligonychus yothersi*, *Tetranychus evansi* and *Tetranychus ludeni*), as well as Tenuipalpidae and Eriophyidae, together with predatory mites. Previously unreported associations were also detected, for example *Brevipalpus* mites (Tenuipalpidae) on *P. undulatum*. Although identifications and analyses are still ongoing, available results already highlight how invasive host plants differ in their capacity to support arthropod communities and multitrophic interactions in island systems.

Amplicon sequencing reveals Diptera, parasitoids, and microbial associations inside mushroom sporocarps

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Abstract

Fungal sporocarps are known to host diverse communities of organisms, including animals, bacteria, and other fungi. Many insects specialise in feeding on mushrooms, with Diptera representing a significant group. Fungal tissues can be nutritionally challenging because they may lack key nutrients, contain toxins, or be structurally resilient. We therefore hypothesise that mycophagous insects may rely on microbial symbionts in substrate utilisation.

To investigate multilayered interactions between fungi, insects and bacteria, we used a molecular approach and sequenced bacterial (16S V4), fungal (ITS2), and animal (COI) amplicons. We compared two sampling strategies: (1) sequencing sporocarp homogenates and (2) sequencing individual Diptera larvae, which we applied to halves of 36 fruiting bodies of *Russula*.

Dipteran species were detected using both approaches, with homogenate sequencing revealing 10 species and sequencing of individual larvae revealing 9 species, mainly Mycetophilidae and Phoridae. Importantly, the single larva approach enabled the detection of 9 species of hymenopteran parasitoids that were not identifiable in the homogenates. We also found that most fly larvae lacked specialised bacterial symbionts, and their microbiome largely reflected that of the mushroom substrate; however, facultative endosymbionts *Wolbachia* and *Rickettsia* were detected in some individual larvae.

Our results show that amplicon sequencing of mushroom homogenates can be a cost-effective and efficient method for assessing and comparing insect diversity within fungal fruiting bodies. However, sequencing individual larvae provides deeper insight into ecological interactions such as host–microbiome and host–parasitoid associations.

Predator-induced stress increases insects' feeding rates in grasslands along elevation gradients

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Abstract

Top-down processes largely influence ecosystem functioning and composition. The presence of predators within an ecosystem is generally beneficial to primary producers by reducing herbivore abundance or altering herbivore behaviour. However, current climate-driven novel associations along temperature gradients, such as elevation, are challenging these conceptions.

Here, we tested the cascading effects of spiders (predators) on alpine plants (primary producers) via higher- and lower-elevation orthopterans (herbivores), in the context of novel interactions arising from climate-driven upward migration of lower-elevation insects. To assess these cascading effects under different climatic conditions, we used alpine plant communities translocated in field common gardens and climate chambers. We exposed them to different herbivore-predator communities and then recorded herbivory levels.

We revealed that top-down effects were strongest when lower-elevation orthopterans faced higher-elevation spiders under warmer temperatures, highlighting the cumulative roles of altered biotic interactions and warming in shaping the future of alpine ecosystems. Interestingly, our results further revealed that the presence of spiders almost systematically increases herbivory on plants, thereby exerting negative indirect effects on primary producers.

This recurrent pattern suggests that orthopterans fear spiders, which potentially increase their levels of stress, ultimately leading to higher feeding rates. This study describes a novel angle of the "ecology of fear", in which the risk of predation drives changes in herbivore behaviour (and physiology). These changes then affect ecosystem processes differently along climatic gradients.

Differential effects of baculovirus and parasitism on plant defense induction by specialist and generalist herbivores

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Ada FRATTINI LLORENS, Salvador HERRERO, Cristina CRAVA

Abstract

Multitrophic interactions among plants, insects, and the viruses that infect them shape plant defense responses. Viral infection can alter herbivore physiology and behavior, thereby affecting how plants perceive and respond to herbivory. These interactions become more complex when parasitoids are involved, as they can modulate both herbivore performance and plant defenses. Understanding these dynamics is particularly relevant in agroecosystems, where entomopathogenic viruses and parasitoids are used in combination and can influence plant defense responses.

To explore these interactions, we conducted herbivory bioassays using the generalist *Spodoptera exigua* and the specialist *Tuta absoluta*. Tomato plants were exposed to mock larvae and infected larvae with *Spodoptera exigua* multiple nucleopolyhedrovirus (SeMNPV) or *Phthorimaea operculella* granulovirus (PhopGV) for 3 and 24 hours. To incorporate a third trophic level, plants were exposed to mock- and parasitized *T. absoluta* larvae by *Dolichogenideia gelechiidivoris*. Across all experiments, we evaluated whether viral infection or parasitism modulated tomato defenses by measuring the expression of early- and late- response genes of the jasmonic acid pathway.

Our results revealed species-specific differences. In the generalist herbivore, viral infection significantly reduced the expression of JA-related genes, suggesting that SeMNPV modifies the plant-insect interaction. In contrast, the specialist herbivore did not induce significant changes in gene expression, indicating that PhopGV infection does not influence defense activation. Similarly, parasitism by *D. gelechiidivoris* did not alter defense activation, suggesting that the plant's perception of herbivory was unaffected.

In conclusion, baculovirus infection interferes with the activation of the jasmonate signaling pathway after *S. exigua* herbivory in tomato, but not after *T. absoluta*. These findings highlight how herbivore identity and degree of specialization shape plant defense responses and emphasize the relevance of considering multitrophic interactions.

Assessing invertebrate trophic networks through the lens of DNA: current state of the art and a look into the future

Michael TRAUGOTT (Department of Zoology, University of Innsbruck, Michael.Traugott@uibk.ac.at)

Abstract

Food webs have long captivated entomologists and ecologists as integrative frameworks linking species through feeding interactions. Quantifying these links is increasingly critical for understanding how communities and ecosystem functions respond to perturbations such as management interventions and climate change. Over the past two decades, DNA-based methods have transformed our ability to detect and quantify trophic interactions under natural conditions, with particular success in resolving the diets of insects and other invertebrates.

This presentation synthesizes the current suite of molecular approaches used to study insect food webs, including targeted assays and broader community-level analyses. I evaluate their practical applicability in entomological research, outlining the molecular skills and laboratory expertise required, as well as the associated temporal and financial costs. I also discuss emerging opportunities and persistent challenges in both DNA- and RNA-based analyses such as taxonomic resolution, quantification, and interpretation in ecological contexts. Together, these perspectives provide guidance on how to deploy molecular tools effectively and robustly to unravel insect trophic interactions, thereby advancing our capacity to monitor, manage, and predict changes in insect ecological networks.

From Leaf Mines to Food Webs: Resolving Plant-Insect-Parasitoid Networks with Long-Read DNA Barcoding

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Abstract

Tropical dry forests host highly diverse insect communities and complex trophic interactions, yet these networks remain difficult to resolve using conventional molecular or rearing-based approaches. Here, we integrate long-read DNA barcoding, non-target sequence co-amplification, and host plant taxonomy to reconstruct tri-trophic interactions among leaf-mining insects, their host plants, and associated parasitoids in a Mexican tropical dry forest. Using Single Molecule, Real-Time (SMRT) sequencing on the PacBio Sequel IIe platform, we generated high-fidelity barcodes from individual leaf-miner larvae and from parasitoid larvae and pupae recovered from leaf mines. Across 214 samples, we identified 92 operational taxonomic units spanning leaf-mining Lepidoptera, Diptera, Coleoptera, and their hymenopteran parasitoids. We detected 69 parasitoid sequences, corresponding to a parasitism rate of 32.2%. Of these, 40 sequences came from parasitoids dissected directly from leaf mines, while 29 were co-amplified from leaf-miner samples, showing that SMRT-based co-amplification enables direct detection of parasitism without rearing. Our molecular data revealed 156 trophic interaction types and 247 interaction events. Network analyses showed a highly modular tripartite network, with module structure primarily driven by host plant identity and a reduced set of influential leaf-miner and parasitoid taxa. Bipartite networks supported the hypothesis that interactions are more strongly compartmentalized between leaf miners and host plants than at higher trophic levels. These results demonstrate that long-read DNA barcoding with co-amplification detection provides a scalable framework for reconstructing multi-trophic interactions from individual specimens, overcoming key limitations of rearing-based methods and enabling robust biodiversity and ecological network assessments in species-rich ecosystems.

Assessing the potential of conservation biological control in fruit orchards using metabarcoding diet analysis

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Martine BJELLAND, Bonnie SAMBØL, Nuria AGUSTÍ, Lene SIGSGAARD

Abstract

Conservation biological control can play an important role in maintaining low pest pressure. Understanding trophic interactions is essential for evaluating the potential of conservation biological control by predatory arthropods. Our study analyzes the diet of several common predatory taxa in fruit orchards. A broad range of predatory taxa (Anthocoridae, Coccinellidae, Cantharidae, Chrysopidae, Forficulidae, Araneidae, Linyphiidae, Philidromidae) were collected from the canopy in apple and plum orchards during the fruitlet stage in early summer, a critical period when pest activity can cause significant fruit deformation and yield loss. Additionally, three species of ground beetles (Carabidae) were collected from the orchard floor during early season and short before the apple harvest in autumn to investigate their role in preying on pests overwintering at ground level. The gut content of collected predators has been analyzed using a multiprimer metabarcoding approach targeting arthropods, in addition to plants for the omnivorous predators. Results will be presented and discussed.

The work is part of the project “IPM strategies for future fruit production (IPM-fruit)”, funded by the Norwegian Research Council. The first authors PhD position is funded by the Norwegian University of Life Sciences.

Trophic cascades driven by invasive alien plants: consequences for aphid–parasitoid system

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Aude COUTY, Arnaud AMELINE, Géraldine DOURY

Abstract

Invasive alien plants pose a significant threat to biodiversity by disrupting trophic interactions, but they can also have important consequences for agroecosystems. By providing alternative food resources for phytophagous insects, these plants may sustain pest populations at the margins of crop fields and, through bottom-up effects, influence insect development and the performance of their natural enemies, such as parasitoids. Conversely, invasive plants may function as ecological barriers or traps for herbivorous insects, thereby altering trophic dynamics with cascading effects on higher trophic levels with potential implications for crop damage and biological control.

In this study, we investigated the bottom-up effects of three invasive plant species commonly occurring at the interface of agroecosystems (*Galinsoga quadriradiata*, *Reynoutria japonica*, and *Senecio inaequidens*) on the black bean aphid (*Aphis fabae*), a widespread polyphagous and economically important agricultural pest, and one of its parasitoids widely used in biological control, *Aphidius colemani*. We assessed key life-history traits to evaluate both aphid (developmental parameters) and parasitoid (developmental and behavioral parameters) fitness.

Our results show that invasive alien plants have contrasting functional roles: some act as reservoirs for aphid pests and enhance parasitoid development, while others function as ecological traps that impair both the aphids and their natural enemies.

Impact of Tillage on Trophic Interactions in Carabid Communities and Their Implications for Biological Control

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Michael TRAUGOTT, Oskar RENNSTAM RUBBMARK

Abstract

Food webs in agroecosystems are a central driving force of ecological interactions that govern the delivery of biodiversity-based ecosystem services, including natural pest regulation by predatory arthropods. Carabid beetles and other generalist predatory arthropods play a key role in complex food web dynamics, due to the diversity of their trophic links that include various sources of extra-guild as well as intra-guild prey. Such trophic interactions can be significantly altered through major disturbances caused by farming practices, such as tillage, which have a strong impact on community assemblages, habitat characteristics and agroecosystem stability. In this study we conducted a molecular gut content analysis to evaluate the effects of tillage on carabid diets, with an emphasis on extra-guild and intra-guild predation. Prey DNA was extracted from regurgitates of carabids collected in multiple fields across Europe, and analyzed using diagnostic multiplex PCR assays to determine the detection frequency of extra-guild and intra-guild invertebrate prey. These detections served as the basis to derive various metrics of food web complexity, including the extent of carabid specialization on different prey groups. The anticipated results unveil key trophic relationships among agroecosystem invertebrates with implications for the resilience of natural pest suppression. Such insights help inform sustainable farming practices by substantiating their effects on trophic interactions that affect ecosystem services in agricultural fields.

Sample type drives dietary reconstruction in the endangered alpine bush-cricket *Anonconotus italoaustriacus*

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Isabel MARTINEZ-SANUDO, Giacomo ORTIS, Arianna GENNARO, Cristina PORNARO, Filippo Maria BUZZETTI, Enrico VETTORAZZO, Luca MAZZON

Abstract

Understanding the trophic ecology of threatened insects is critical for developing effective conservation strategies, as diet directly affects survival, reproduction, and population stability. In this case study, we investigated the food plants exploited by *Anonconotus italoaustriacus* (Orthoptera: Tettigoniidae) by reconstructing its diet and comparing midgut- and feces-derived dietary data. This flightless alpine bush-cricket is endemic to the Eastern Alps, where it survives in four distinct populations, and is currently classified as Endangered by the IUCN. To evaluate the effect of sample type on the accuracy of dietary reconstruction, total DNA was extracted from intestinal and fecal samples and sequenced using the Illumina MiSeq platform, targeting the ITS2 region. Intestinal samples showed higher sequencing success and yielded more ASVs (32 ± 5) than fecal samples (14 ± 4). Beta diversity analysis revealed that samples clustered by matrix rather than by sampling site, suggesting that differences in taxonomic composition are primarily driven by sample type rather than environmental factors. Intestinal contents reflected a broader dietary spectrum integrated over digestion, whereas fecal samples showed a narrower dietary signal. Despite these differences, the two matrices provided partially complementary information: 45% of the detected taxa were shared, 40% were exclusive to intestinal samples, and 15% to feces. Across intestinal samples, *Rhododendron* spp. was consistently detected in all populations, suggesting either widespread availability or preferential exploitation. In contrast, fecal samples were dominated by a single plant genus, whose identity varied among sampling site, highlighting matrix-specific biases linked to physiological processes. Thus, using various sample types provides a more complete picture of the diet. These findings underscore the importance of selecting and, when feasible, combining different sample types to better capture dietary diversity. However, feces seem to represent a valuable, non-lethal source of dietary information, offering a practical approach for ecological studies on endangered species, where minimizing harm is essential.

eDNA in applied Entomology

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Christian MAUS, Henrik KREHENWINKEL, Arndt SCHMIDT

Abstract

The tradeoff between global food security and biodiversity protection is one of the main challenges of agriculture. Precision agriculture could be a solution to this problem. To fully leverage the potential of precision agriculture, reliable and cost-efficient biomonitoring approaches are of key importance. However, currently employed biomonitoring approaches are primarily detecting limited numbers of insect pest species, without incorporating the complex community structure in agricultural fields. Making use of the latest developments in molecular biodiversity research, namely eDNA metabarcoding, we are enabling unprecedented insights into the biodiversity of field-associated arthropods. With this tool we are not only able to uncover entire in-field arthropod communities, we likewise can monitor off-field communities, e.g. in flowering strips as success control for agri-environmental measures, both qualitatively and semi-quantitatively. In the case of in-field monitoring, eDNA analysis can e.g. be used to assess which pest species and which of their natural antagonists are present in a field. Furthermore, with eDNA analysis it may be possible to gain information about individual pest traits, e.g. insecticide resistance, or to measure gene flow between different populations, and to determine the developmental stage of present pests and beneficials. This will open the field for precision farming at dimensions that are not possible today. However, not only in agriculture this technology helps us to measure, understand and predict community and habitat changes, insect-plant or insect-environment interactions - these data and insights are crucial in advanced nature conservation as well.

Insect invasions in an era of globalization

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Abstract

Human-mediated transport has led to the establishment of more than 6700 non-native insect species with wide-ranging impacts on ecosystems, the economy, and human health. Insects are among the worst invasive species, and a better understanding of their anthropogenic spread is needed. They have been dispersed since the early beginnings of globalized trade and especially after the Industrial Revolution, following two waves of globalization. European colonialism has played a major role in accelerating invasions during the first wave of globalization, while emerging economies and trade networks play a more important role in more recent times. Many insect species have complex invasion histories, with multiple independent introduction events and frequent secondary spread. There are also new introduction pathways, including the emergent trade in insects as pets where invasive species are strongly overrepresented. As a result of global human-mediated dispersal of insects, communities worldwide are homogenizing, in particular on tropical islands. In the future, insect invasions could further accelerate due to intensifying global trade and climate change.

Inside the Black Box: Untangling Multi-Trophic Processes in Associative Cropping for Integrated Pest Suppression

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Abstract

The emergence of insecticide resistance in various insect pest groups coupled with neonicotinoid bans in certain regions of the world drives the need for efficient alternative control measures to sustain competitive yields. Associative cropping, traditionally used for weed control and nitrogen supply, has shown promising results in diminishing insect pest pressure across various crops. Mechanisms at play are often intricate and multifactorial, with diversified agroecosystems providing multi-trophic-levelled services leading to pest-suppressive environments. Results from both lab and field settings help shed light on complex inter-plant interactions shaping ecological outcomes in associative systems in various crop of major economic importance. However, recent findings also highlight the insufficient characterization of the multi-trophic processes involved, from inter-plant interactions and signaling to the contributions of environmental and biotic factors such as soil microorganisms and natural predators. Comprehensive understanding and optimization of these multifaceted interactions remains essential in order to fully leverage associative cropping as a robust and sustainable pest management strategy.

Drivers of overwintering carabid communities in arable crops and in flower strips: can we describe the effects of farming systems through disturbance intensity, resources and local habitat conditions?

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Abstract

Agricultural practices - such as pesticide use, soil tillage, organic inputs and plant cover - are major drivers of soil biodiversity in agroecosystems. Semi-natural habitats, including flower strips, contribute to biodiversity maintenance by offering overwintering refuges and complementary resources for arthropods. Carabid beetles, which play key roles in natural pest regulation, may particularly benefit from such habitats. Because agricultural practices vary strongly among fields and farmers, we compared categorical farming system typologies with more refined variables using a continuous field-level intensity gradient (PCA-based and continuous variables representing disturbance intensity, resources and local habitat conditions). Likewise, both study years were analyzed jointly to capture inter-annual variability without artificially separating community responses by crop type. Community metrics included total and species-specific abundance, taxonomic diversity, functional diversity and trait composition, derived from emergence tents placed from late winter to early summer inside crop fields and in adjacent flower strips. Across all models, agricultural management intensity emerged as the dominant driver of overwintering carabid communities. Farming system categories consistently produced strong directional shifts in trait composition: conventional systems were associated with higher abundances of large-bodied, granivorous and xerophilic species, whereas small-bodied, winter-active, hygrophilic and zoophagous taxa declined under more intensive management. Neither flower strips nor continuous management gradients provided explanatory power beyond farming system typologies. Overall, overwintering carabid assemblages were shaped primarily by broad farming system intensity rather than by individual practices or the presence of flower strips, highlighting the predominant influence of whole-system management on carabid communities. Similar patterns for overwintering spiders were observed and will be presented during the congress.

Beyond biocontrol: promoting functional biodiversity in agroecosystems to improve pest control

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Yulisa MORENO PATIÑO, Tobias GELENCSE, Roxane MULLER, Helena RÖMER, Franco WEIBEL, Paola CASSIANO, Flore BEAUSOLEI, Lukas PFIFFNER, Lara REINBACHER

Abstract

In this talk I would like to provide you with an overview on different strategies that we currently study and that aim at promoting functional biodiversity in agroecosystems to improve pest control. By diversifying farm landscape, pest control can be promoted and a more resilient cultivation system can be developed. While diversification measures in time such as crop rotation or cover crops are already well-established in agriculture, in-field diversification measures, such as companion plants and the implementation of flower reservoirs, remain largely unused due to economic concerns or technical aspects of integrating them into common cultivation practices. Promoting habitat for the establishment of biocontrol in agroecosystems can in fact reduce costs in the long run. In this talk, I will share with you how we think such strategies may be used to increase the diversity of beneficial insects on potatoes, which is subjected to rotation, as well as on cherry orchards, which is perennial cropping system. Our focus, in both cases, is on the promotion of generalist predators to improve the control of the most important insect pest in these systems, the Colorado potato beetle (CPB) and the black cherry aphids *Myzus cerasi*. During this presentation, I will walk you through the initial challenges, how far we got on the different projects, and well as the positive benefits we harvested so far. We use a flower mixture developed in house for this project in the case of flower reservoirs, and test two different companion plants in comparison with the potato plants monoculture. I will discuss how these strategies could be effective in the long run, requiring relatively low investments for farmers and is thus likely to increase their acceptance.

Synergistic Effects of Companion Plants and Beneficial Soil Fungi on Functional Biodiversity, Pest dynamics and Yield of Open-Field Tomatoes

APOSTOLOS KAPRANAS (Aristotle University Of Thessaloniki, Akapranas@agro.auth.gr)

Vasileia CHATZAKI, Anastasia KOKKARI, Vaya KATI, Nikolaos KOULOSSIS, Dimitrios KOVEOS

Abstract

Tomato is a crop of major importance globally. Agroecological farming practices aim to enhance functional biodiversity in order to support ecosystem services and reduce dependence on synthetic inputs. In this study, we investigated the effects of agroecological practices on functional biodiversity, major tomato pests and key natural enemies, as well as on tomato productivity in open-field cultivation systems in Thessaloniki, Greece. Over a three-year period, we evaluated agroecological practices based on the use of companion plants—phacelia (*Phacelia tanacetifolia*) and buckwheat (*Fagopyrum esculentum*)—planted alongside tomatoes, in combination with the application of the beneficial soil fungus *Trichoderma harzianum* T22. Insect sampling was conducted throughout the growing season, and data collection focused on beneficial insects visiting the companion plants, the main tomato pest species, and predatory insects of the family Miridae. Tomato growth and productivity were also assessed across treatments. Our results indicate that agroecological practices enhanced functional biodiversity by increasing the abundance and diversity of beneficial insects and reducing pest pressure. These effects were accompanied by improved tomato growth and higher crop productivity. Overall, this study highlights the synergistic effects of agroecological practices on crop protection and productivity. The proposed cultivation model strengthens functional biodiversity, enhances ecosystem services, and supports sustainable tomato production with minimal external inputs.

Diverting ants from aphids: service plants as a lever to enhance biological control of the rosy apple aphid in orchards.

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Abstract

Mutualistic interactions between ants and honeydew-producing Hemiptera involve ant-mediated protection in exchange for carbohydrate-rich resources, which interferes with natural enemies and constrains biological control. This represents a major ecological challenge for conservation biological control strategies targeting aphid pests. In agroecosystems, ant–aphid mutualisms are strongly influenced by the availability of alternative sugar resources. Manipulating plant diversity to provide accessible nectar sources may divert ants away from aphids and improve predator-mediated regulation. The rosy apple aphid, *Dysaphis plantaginea*, is one of the most damaging pests in European apple orchards, causing severe yield losses. In a context of reduced availability of authorized pesticides, there is an urgent need to develop sustainable management strategies based on ecological processes. However, the frequent association between *D. plantaginea* and ants often hampers the effectiveness of natural enemies. In this study, we investigated whether increasing plant biodiversity could disrupt ant–aphid mutualisms and enhance the natural regulation of *D. plantaginea*. First, we investigated the ant nest spatial distribution and seasonal nutritional requirements in apple orchards. Second, we evaluated the effects of introducing faba bean (*Vicia faba*), an extrafloral nectar–producing service plant, in border or inter-row strips on aphid populations and associated ant activity. Experiments were conducted in three apple orchards located in Angers (France), Avignon (France), and Lleida (Spain). Preliminary results show that nests of *Lasius niger* were preferentially located near apple trees associated with high availability of aphid-derived resources. The effects of faba bean strips differed according to their spatial implementation and the targeted ant species. Inter-row faba bean strips significantly reduced aphid abundance, colony longevity and *L. niger* attendance. In contrast, the presence of *Crematogaster scutellaris* within aphid colonies increased with proximity to faba bean border strips. Overall, these results indicate that the effects of plant diversification on ant–aphid mutualisms are species-specific and context-dependent.

Insectary plant species preferences of predators and parasitoid families in a Mediterranean horticultural agroecosystem

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Carmen DENIS, Valmir COSTA, Paula MOLINA, Judit ARNÓ, Jordi RIUDAVETS

Abstract

The use of insectary plants to provide alternative food and shelter resources for enhancing natural enemy activity has been established as a common practice in IPM. Candidate flowering plant species had been screened and evaluated for their contribution to enhance life parameters of beneficial insects. However, less information had been reported on the preference of these natural enemies to different insectary plant species in the field. The relative attractiveness of six insectary plant species to the key natural enemies groups on horticultural crops in the Mediterranean region was assessed by observing the relative frequencies of appearance on six plant species: *Achillea millefolium* L. and *Calendula officinalis* L. (Asterales: Asteraceae), *Daucus carota* L. (Apiales: Apiaceae), *Diplotaxis tenuifolia* (L.) DC. (Brassicales: Brassicaceae), *Fagopyrum esculentum* Moench (Caryophyllales: Polygonaceae) and *Lobularia maritima* (L.) Desv. (Brassicales: Brassicaceae). The presence of predators and parasitoids was evaluated by visual counts. Among predators, Syrphidae adults were evaluated by visual observation of inflorescence visits and/or hovering. The other predators recorded on the insectary plants were collected and divided into six groups; Aeolothripidae, Araneae, Chrysopidae, Coccinellidae, Dicyphini tribe and *Orius* spp. Parasitoids were also collected and grouped into families. The Syrphidae interacted the most with *D. tenuifolia*, *F. esculentum* and *L. maritima* being the last one the plant with higher proportion of visits after hovering on the inflorescence. Parasitoids were recorded the most on *A. millefolium* and *L. maritima*. Finally, significant differences were found on the preference of each group of predators for the six insectary plants. The different natural enemy groups preferences for the insectary plants are discussed in biological control context and of the key influencing factors that should be considered when assessing the relative attractiveness of natural enemies to the insectary plants.

A tailored mixed floral strip to reduce aphid numbers in smallholder's vegetable farms in Valdivia, southern Chile

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Khatrina MENESES, Blas LAVANDERO, Rodrigo BARAHONA-SEGOVIA, Javiera LAGOS, Manuel DIAZ

Abstract

Plant identity changes the flower-visiting insect community allowing for the screening and selection of plants that can be then used as part of floral strips to attract beneficial insects to promote biological control or pollination services across a variety of crops worldwide. The highly diversified agroecological conditions around the globe make impossible to simple “to cut and paste” successful flower strips strategies from one ecological zone to another. Since 2022 to 2025, several experiments were carried out in Valdivia and around Los Ríos region to assess the impact of flower strips on natural enemies and aphids in smallholder vegetable (lettuce and cabbage) farms. Initially, we tested flower strips made of buckwheat (*Fagopyrum esculentum*), calendula (*Calendula officinalis*), borraja (*Borago officinalis*), coriander (*Coriandrum sativum*), broad bean (*Vicia faba*) and alyssum (*Lobularia maritima*). Insects were assessed from August 2022 to March 2024 by visual observations, pitfall and pan traps. Our results suggested that broad bean could attract individuals early during the season probably by nectar production in extrafloral nectaries, while calendula and buckwheat attracted the highest proportion of natural enemies during mid-to-late season. Considering a long flowering period, high insect diversity and ease of agronomic establishment, a mixed floral strip composed of broad bean, calendula and buckwheat was sequentially established in 14 smallholder farms (7 agroecological, 7 conventional). Natural enemies were sampled by pan traps, while aphids counted and removed from vegetables. A generalized linear mixed effect model demonstrated a higher diversity of natural enemies and a lower aphid density in agroecological farms compared to conventional ones. Our mixed floral strip was more efficient in agroecological farms, probably due to a lack of pesticide applications. These results highlight the importance of farm management when using biodiversity-based strategies for pest control, and gives a tailored solution for aphid control in Southern Chil

Was the introduction of *Trissolcus japonicus* successful? Six-year field monitoring of *Halyomorpha halys* egg parasitoids in Northern Italy

Antonio MASETTI (Department of Agricultural and Food Sciences - University of Bologna, Antonio.masetti@unibo.it)

Giacomo VACCARI, Stefano CARUSO, Andrea ZANIBONI, Torreggiani DANIELE, Giovanni BURGIO, Michele VIOLI, Elena COSTI, Lara MAISTRELLO

Abstract

Halyomorpha halys Stål (Hemiptera: Pentatomidae) is a major invasive pest causing severe agricultural damage in Northern Italy. Since 2020, the release of the Asian egg parasitoid *Trissolcus japonicus* (Ashmead) (Hymenoptera: Scelionidae) has been promoted in the framework of one of the greatest classical biological control programs ever attempted in Italy. Between 2020 to 2023, approximately 160,000 *T. japonicus* individuals were released at about 300 sites in Emilia-Romagna region, and field surveys were carried out between 2019 (one year before the releases of the exotic parasitoid) and 2025. Egg masses of *H. halys* and other stink bugs were collected in semi-natural habitats, including both release and non-release sites. Long-term data revealed an exponential increase in parasitism rates by *T. japonicus* and a progressive range expansion, making it the dominant parasitoid in recent years. On the other hand, the exotic species *Trissolcus mitsukurii* (Ashmead) (Hymenoptera: Scelionidae), whose adventive populations have been detected in the sampling areas since 2018, exhibited a marked decrease over time. The native parasitoid *Anastatus bifasciatus* Geoffroy (Hymenoptera: Eupelmidae) remained widespread and abundant, with no evidence of competitive interactions with exotic species. The impact on-target stink bug species by exotic parasitoids was negligible. Overall, our results indicate that the introduction of *T. japonicus* in Emilia-Romagna has been successful and contributes substantially to the natural suppression of *H. halys* populations.

Conservation biological control and agroecosystem design to reduce *Psylliodes chrysocephala* damage in oilseed rape fields

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Abstract

Psylliodes chrysocephala is a major oilseed rape pest in Europe. With rising insecticide resistance and environmental concerns, promoting conservation biological control has become crucial. This approach involves redesigning cropping systems to enhance both bottom-up (plant-mediated) and top-down (natural enemy-driven) regulatory processes. In a network of French farmers' fields, we studied how crop management, local environmental characteristics, and flower strips influence *P. chrysocephala* populations and their regulation throughout their cycle. In early autumn, we tested trap crops to limit flea beetle colonization. Turnip rape proved more attractive than oilseed rape and much more than Daikon radish. Turnip rape suffered heavier larval attacks and thus acted as an effective trap, potentially protecting nearby oilseed rape fields. At the field scale, companion plants and weeds markedly reduced larval numbers—up to a threefold decrease as vegetation cover increased from 10% to 100%. However, previous crops residuals, intended to limit pest movement, did not significantly affect larval presence. In spring, about 30% of larvae were parasitized by microhymenopteran parasitoids. Parasitism was highest in insecticide-free fields with flower strips and lower in treated fields without such resources. Flowering weeds providing nectar within fields also increased parasitism rates. At the end of larval development, larvae dropped to the soil surface before pupating underground. Sentinel prey experiments revealed that 50% of larvae were consumed within 24 hours, regardless of the cropping system. Camera observations identified carabid beetles as main predators, followed by rove beetles, ants, and chilopods. In conclusion, intercropping oilseed rape with service crops in autumn and floral resources in spring were the main ways to enhance biological control of *P. chrysocephala*. While biological control only contributes to reduce pest populations in the following year, long-term and landscape-scale coordination of these practices is needed for an efficient management of *P. chrysocephala* populations.

Harnessing Plant- and Pest-Derived Semiochemicals to Enhance Biological Control: Insights from Predators and Parasitoids of Tomato Pest

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Abstract

Semiochemicals play a pivotal role in mediating interactions among plants, herbivores, and their natural enemies, offering opportunities to enhance sustainable pest management. Across five complementary studies, we investigated how plant- and pest-derived chemical cues shape the foraging behavior of key natural enemies of tomato pests. A conceptual review first highlighted the ecological and applied importance of kairomone-based strategies to improve biological control. Experimental evidence then demonstrated that herbivore-induced volatiles from tomato, particularly terpenes, attract the predatory mirid *Nesidiocoris tenuis*, enhancing its potential against multiple tomato pests. Focusing on the whitefly *Trialeurodes vaporariorum*, we showed that its infestation triggers tomato volatile emissions that are exploited by the parasitoid *Encarsia formosa*. Moreover, honeydew deposits and cuticular extracts from *T. vaporariorum* were identified as direct kairomonal cues guiding parasitoid host location. Finally, we revealed that the parasitoid *Dolichogenidea gelechiidivoris* eavesdrops on semiochemicals released by both tomato plants and the invasive moth *Tuta absoluta*, enabling efficient host detection. Together, these studies demonstrate the central role of plant- and pest-derived cues in tritrophic interactions and highlight their potential for developing novel, environmentally sound strategies to reinforce biological control in tomato cropping systems.

Increasing biodiversity in arable leek cultivation to stimulate biological control of the onion thrips

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Elke KLEIN HOLKENBORG

Abstract

Pest control is a key ecosystem service provided by insect predators and parasitoids, yet agricultural fields often fail to support these natural enemies due to pesticide use and the limited availability of alternative food sources and shelter present in monocultures. Recently, leek growers in the Netherlands have introduced the flowering plant *Lobularia maritima* as a banker plant, in combination with releasing the predatory bug *Orius majusculus* to suppress *Thrips tabaci*, the main insect pest in leek cultivation. We examined whether this natural-enemy system can provide an alternative for pest control with pesticides. During a two-year field survey we found that crop cultivation with the natural enemy-system is as effective in reducing thrips abundance and feeding damage as chemical pesticides. To study the system in more detail, we conducted a field experiment that compares the introduction of the banker plants with and without the release of *Orius* on thrips suppression to that obtained with the application of pesticides, or no pest control measures. We demonstrate that the introduction of banker plants and natural enemy release in the field is as effective as pesticide application for suppression of *Thrips tabaci*. Moreover, the presence of *Lobularia* enhances natural enemy abundance in the leek, which emphasizes the benefits of using *Lobularia* as a banker plant. Next to that, we showed that *Orius majusculus* disperses over 150 meters and can establish a population in the leek. Together, these findings provide compelling evidence that increasing functional biodiversity in crop fields stimulates ecosystem services like as pest control, and therefore provides a sustainable alternative to chemical pest control.

Multi-year evaluation of insecticide efficacy against *Bemisia tabaci* and parasitoid dynamics

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Çağlar KALKAN, Miraç YAYLA

Abstract

This study assessed the efficacy of six insecticides (Acetamiprid, Afidopyropen, Buprofezin, Cyantraniliprole, Pyriproxyfen and Spiromesifen) against *Bemisia tabaci* across two consecutive greenhouse cycles using X/2, X, 2X and 4X doses. Natural infestations were monitored at 1, 3, 7, 14 and 21 days after treatment for adult, egg, nymph and pupal stages, and parasitized hosts were recorded to evaluate non-target impacts.

Across both years, all insecticides rapidly suppressed adults, with Afidopyropen and Cyantraniliprole repeatedly achieving >90% reduction within 24–72 hours. Egg and nymph responses showed consistent year-to-year patterns: Afidopyropen produced the most stable cross-stage suppression, whereas Pyriproxyfen and Spiromesifen showed delayed or stage-dependent reductions, often followed by nymph resurgence at later sampling dates. Parasitoid activity increased in untreated controls but declined sharply in all treatments, frequently showing 80–95% suppression by days 14–21. Lower parasitoid counts in Afidopyropen- and Cyantraniliprole-treated plots were mainly attributable to strong host depletion rather than direct non-target toxicity.

These results demonstrate robust, multi-year consistency in insecticide performance and highlight the ecological trade-off between rapid chemical suppression and natural enemy conservation, providing key insights for IPM-driven decision making in protected cropping systems.

Responses of *Tetrastichus howardi* to temporary thermal stress: implications for biological control

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Evelyn Sales DA SILVA, Alice Vieira Carrazzone NUNES, Natalia Carolina BERMUDEZ, Jorge Braz TORRES

Abstract

Ectothermic insects rely heavily on temperature to regulate physiological processes, which directly affects the efficiency of biological control agents under current scenarios of climatic instability. Among these organisms, *Tetrastichus howardi* is a pupal parasitoid of Lepidoptera with recognized potential for pest management in several crops, including sugarcane. Understanding its response to thermal stress is therefore essential to optimize its use in integrated pest management programs. This study evaluated the effects of temporary thermal stress on the survival and parasitism performance of *T. howardi*. Parasitized pupae were exposed, at 10 or 15 days after parasitism, to temperatures ranging from 25–37 °C for 9 h and subsequently maintained at 25 °C until adult emergence. Female survival was assessed under semi-field conditions, as well as parasitism on pupae of the natural host *Diatraea saccharalis*. Results showed that female survival varied significantly among temperatures, with effects depending on the developmental stage at which stress was applied. When applied during the pupal phase, thermal stress resulted in survival equal to or higher than the control. In parasitism assays, prior exposure to stress did not affect progeny emergence or developmental time, although the total number of individuals produced varied with temperature. Sex ratio was not influenced by thermal stress. These findings demonstrate that controlled thermal stress can enhance the survival of *T. howardi* without compromising key parasitism parameters. Moreover, they suggest that similar approaches could be explored with other parasitoids and even different natural enemies, broadening the potential of biological control strategies across diverse agricultural systems.

Confirmation of The Presence of The Fruit Fly Parasitoid *Psytalia concolor* (Szépligeti, 1910) (Hymenoptera: Braconidae) Emerging from The Olive Fruit Fly *Bactrocera oleae* in Northeast Libya.

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Abstract

The olive fruit fly *Bactrocera oleae* (Rossi, 1790) (Diptera: Tephritidae) is an endemic fruit pest of the olive tree (*Olea europaea* L. (Lamiales: Oleaceae)) in the Mediterranean basin. In Libya, the olive fruit fly is widespread along the northern coastline, and its infestation reduces fruit and olive oil production. Based on the fruit fly biological control agents, the fruit fly parasitoid *Psytalia concolor* is used for release against the olive fruit fly *B. oleae* in some countries worldwide. Although some literature reviews referred to *P. concolor* presence in Libyan conditions as a native niche within North Africa, no data have been officially recorded about this wasp so far. This study aims to detect the braconid parasitoid *P. concolor* on its host *B. oleae* within the northeast region of the country. The experimental area was divided to three different locations (Ahlgregha, Ayn Marrah and Tobruk) in northeast Libya. A total of 250 *B. oleae*-infested olive fruits were randomly collected as samples from ten olive trees at each location. The presence of the fruit fly parasitoid *Psytalia concolor* was confirmed at the three locations with differences in parasitism level. A higher number of wasps emerged from infested olive fruits in Tobruk site compared to Ahlgregha and Ayn Marrah. The parasitoid *P. concolor* was photographed for morphological description. This study is the first documented data on the presence of the braconid fruit fly *Psytalia concolor* in Libya, which would enhance tephritid fruit fly control.

Predation of the invasive pea leaf weevil, *Sitona lineatus*, by an introduced generalist predator, *Pterostichus melanarius*, in pulse agroecosystems on the Canadian Prairies

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Maggie MACDONALD, Chulantha DIYES, Boyd MORI

Abstract

Conservation biological control (CBC) relies on the activity of natural enemies to suppress pest populations and secure ecosystem services in agricultural systems. Ground beetles (Coleoptera: Carabidae) are abundant, generalist predators that contribute to pest regulation but effectiveness depends on prey availability and temporal and spatial overlap with target pests. In this study, we examined the potential of *Pterostichus melanarius* (Illiger) as a natural enemy of the pea leaf weevil, *Sitona lineatus* L., a significant pest of field pea (*Pisum sativum* L.) and faba bean (*Vicia faba* L.) on the Canadian Prairies. We combined laboratory predation bioassays, field monitoring, and molecular gut-content analysis to assess trophic interactions between *P. melanarius* and *S. lineatus*. In laboratory assays, *P. melanarius* readily consumed *S. lineatus*, with consumption rates increasing with prey density. A diagnostic multiplex-PCR assay reliably detected *S. lineatus* DNA at low concentrations and up to 24 h post-feeding, demonstrating high sensitivity for use in field-collected specimens. Field trapping revealed higher *P. melanarius* abundance in field pea than in faba bean fields, and greater numbers in interior transects than at field edges, with seasonal shifts in within-field distribution. Screening of field-collected *P. melanarius* individuals detected *S. lineatus* DNA in 12.5% of samples overall, with higher detection frequencies in 2021 than in 2022. These results confirm that *P. melanarius* can prey upon *S. lineatus* under both laboratory and field conditions, highlighting its role as an opportunistic generalist predator with potential value for conservation biological control in pulse cropping systems.

Enhancing natural road verges to promote parasitism of Oak processionary moth (*Thaumetopoea processionea*) in urban landscapes

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Toon WILLEMS, Luc CREVECOEUR, Kathleen VERSTRAETE, Joost BLOEMBERG, Anne LEEFLANG, Jules SONDEIJKER, Johan NEEGERS

Abstract

The oak processionary moth (OPM), *Thaumetopoea processionea*, is a rather thermophilic species whose caterpillars feed gregariously on oaks (*Quercus* spp.). The caterpillars bear urticating hairs that can provoke severe allergic reactions upon contact or airborne exposure, affecting skin, eyes, and respiratory tracts. In the northern range, OPM predominantly occurs on urban and roadside trees, forest edges, and open woodlands—areas with high human (and pet) activity. Consequently, OPM is often controlled using biocides, which negatively impact biodiversity.

Recent hypotheses suggest that increasing habitat naturalness could enhance populations of natural enemies, particularly parasitoids, thereby improving biological control. Within the Life-OPM project (2021–2024), we tested this approach on 56 roadside verges in the Netherlands and Belgium, spanning a gradient of naturalness. Vegetation surveys quantified nectar plant availability, OPM nests were collected to assess parasitism rates, and population monitoring was conducted. Results indicate that parasitoids were dominated by Tachinidae flies. Parasitism rates ranged from 0% to 100%, with an average of 72.8%. Importantly, parasitism increased significantly with verge naturalness, characterized by higher herbaceous cover, species richness, and nectar index.

These findings demonstrate that promoting natural vegetation management along roadsides can substantially enhance parasitoid activity contributing to OPM management in human-dominated landscapes.

Are reduced fertilization and biological control compatible for pest regulation?

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Anne-Violette LAVOIR, Nicolas DESNEUX, Peng HAN

Abstract

In agroecosystems, arthropod communities may be influenced by bottom-up forces induced by environmental factors such as fertilization, which modify plant traits. While the influence of bottom-up forces on herbivores (the second trophic level) are well documented, their effect on natural enemies (the third trophic level) and their pest control efficacy remains less understood. This study investigates how tritrophic interactions among plants, herbivores, and natural enemies are influenced by fertilization as a bottom-up factor.

We conducted a greenhouse experiment using a tomato (*Solanum lycopersicum* L.) system to evaluate how two different fertilization regimes affected interactions among plants, the aphid *Macrosiphum euphorbiae*, the parasitoid *Aphidius ervi*, and the coccinellid predator *Adalia bipunctata*. We assessed plant traits, aphid population dynamics, and the biocontrol performance of the natural enemies.

Our findings indicate that although a moderate reduction in fertilization slightly reduced the parasitoid's biocontrol efficacy, aphid populations remained comparable across treatments. Additionally, the timing of fertilization affected both aphid and predator population dynamics. Leaf analyses revealed significant differences in nitrogen concentration and carbon-to-nitrogen (C/N) ratios among fertilization across treatments, which influenced aphid nutritional quality.

In conclusion, a moderate reduction in fertilizer can effectively suppress aphid outbreaks without compromising tomato yield. This study highlights the potential of nutrient management as a component of Integrated Pest Management (IPM). Fine-tuning fertilization not only supports the performance of natural enemies and enhances biocontrol efficacy but also reduces production costs, contributing to more sustainable agricultural practices.

Maize defence against *Ostrinia nubilalis* under drought: cultivar-specific stress interactions

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Ilka VOSTEEN, Mohammad ALHUSSEIN, Susanne NEUGART, Michael ROSTÁS

Abstract

Climate change is expected to intensify drought episodes in Europe, yet it remains unclear how water limitation interacts with *Ostrinia nubilalis* herbivory. Although drought stress and maize responses to *O. nubilalis* have been studied independently, their combined impact on plant defence signalling and herbivore performance has received little attention. We provide one of the first integrated assessments of drought x *O. nubilalis* interactions across two maize cultivars differing in drought tolerance, using a Plantarray lysimeter system. The cultivars, DKC 3400 (drought-sensitive) and SY Glorius (drought-tolerant), were exposed to either well-watered conditions or drought (seven-day irrigation cessation, followed by 90% replenishment). Plants were subsequently subjected to controlled herbivory: three days of foliar feeding by five L2 larvae and continuous stem feeding by two L3 larvae until harvest. Growth, transpiration, phytohormones, and larval performance were quantified. Drought strongly suppressed plant productivity in both cultivars, reducing kernel number, kernel and cob dry mass, stem dry mass, and final plant height. These reductions were accompanied by shifts in defence signalling. Absciscic acid and its glucosyl ester increased significantly under drought, alongside elevated salicylic acid and indole-3-acetic acid. In contrast, jasmonic acid peaked under well-watered x herbivory conditions. Defensive benzoxazinoids showed cultivar-specific patterns: DIMBOA accumulation increased only in well-watered x herbivory SY Glorius plants, whereas chlorogenic acid was consistently higher in DKC 3400. These physiological responses were reflected in herbivore performance. Early larval mortality was significantly higher under drought, and drought reduced larval weight in DKC 3400 despite unchanged larval passage length. Notably, the drought-tolerant SY Glorius produced the highest overall mortality, suggesting cultivar-specific defence strategies under combined stress. Our findings demonstrate that drought strongly modulates maize defence physiology and suppresses *O. nubilalis* performance, with cultivar-specific patterns. This work highlights the importance of integrating abiotic stress responses into future pest management strategies under climate change.

Assessing non-intended effects of exclusion nets on natural enemies at local and landscape scales

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Abstract

The use of insect-exclusion nets is rapidly expanding in perennial cropping systems, particularly as a means to reduce reliance on plant-protection inputs. However, the unintended effects of this practice on natural enemies remain poorly understood, and its landscape-scale implications have received even less attention. Between 2021 and 2023, we monitored 23 pairs of organic orchards, some protected by nets and some not, in the main apple-growing area of south-eastern France. This design allowed us to disentangle local and landscape effects of netting on soil-dwelling natural enemies (ground beetles, spiders) and canopy species (earwigs, lady beetles, mirid bugs). At the local level, nets appear to have little effect on the abundance and richness of most of the natural enemies studied. However, this practice is associated with a clear increase in the abundance of earwigs in the canopy, while the responses of spiders appear to vary depending on the communities and the time periods considered. At the landscape scale, netting effects were detected only for soil-dwelling natural enemies, with a negative impact on ground-beetle activity density and a positive influence on earwig presence. This study is, to date, the only large scale analysis of the unintended effects of exclusion nets in commercial orchards. The results, which reveal limited impacts on natural enemies, and even positive impacts for some, reinforce the interest in this technique as an effective agroecological option.

Cross effects of biopesticides, temperature and intraguild interactions on the predatory capacity of the natural enemy *Forficula pubescens* (Dermaptera : Forficulidae)

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Hazem DIB, Magali RAULT

Abstract

The earwig *Forficula pubescens* (Dermaptera) is a generalist predator that contributes to the biological control of several pest species in apple orchards. Mainly found in southeastern France, its ecological role could be constrained by two stress factors: pesticide exposure and rising temperatures linked to global climate change. In addition to these abiotic factors, biotic interactions between organism living in orchards could disrupt the predatory potential of natural enemies and need to be disentangled. In this study, we assessed the combined effect of pesticide exposure, temperature and intraguild interactions on the predation capacity of different stages of *F. pubescens*.

The effect of two pesticides authorized in organic farming (Catane® and Success4®) and two temperatures (20°C and 35°C) was studied in the presence or not of the natural enemy *Forficula auricularia*, commonly found in orchards.

We revealed an absence of intraguild predation between *F. pubescens* and *F. auricularia*, regardless of the developmental stage combinations tested and the abiotic stress applied. While the impact of each abiotic stress alone was stage-dependent, our results highlighted that the combination of pesticide exposure and elevated temperature had a significant negative effect on the predation ability of *F. pubescens*.

This study suggests that coexistence of these two earwig species in orchards does not lead to intraguild predation but that competition for food resource could occur between *F. pubescens* and *F. auricularia*. However, it highlights the importance of evaluating pesticide effects in a context of rising temperatures, particularly for natural enemies that play a key role in conservation biological control. Conducted under controlled laboratory conditions, this study provides an essential first step in understanding how *F. pubescens* could cope with changing environmental conditions in orchards. Integrating such knowledge into orchard management strategies must be taken into account in order to maintain effective and sustainable pest control services.

Pesticide resistance reduces host suitability for the parasitoid *Aphidius colemani*

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Marion JAVAL, Enric FRAGO, Gaylord DESURMONT

Abstract

The extensive and repeated application of chemical pesticides has led to widespread resistance in many insect species, reducing agricultural yield. This resistance often necessitates repeated applications of increasingly ineffective treatments, leading to cascading negative effects on ecosystems and posing health risks to agricultural practitioners and consumers. The use of parasitoids to control pesticide-resistant insect pests is considered a promising alternative to chemical pesticides. However, no study has tested the suitability of pesticide-resistant hosts for parasitoids.

In this project, we hypothesized that pesticide resistance and parasitoid success interact, but the nature and direction of this interaction remain unknown. A trade-off between pesticide and parasite resistance could increase host susceptibility to parasitoids, whereas cross-resistance could instead strengthen host defence against parasitoids.

To test this hypothesis, we studied the green peach-potato aphid (*Myzus persicae*), a major agricultural pest that has developed resistance to multiple pesticide classes. We used ten aphid lineages with varying resistance levels to the neonicotinoids imidacloprid and thiacloprid and exposed them to parasitism by their main parasitoid species, *Aphidius colemani*. We then measured several parasitoid performance parameters, including mumification rate, development time, sex ratio, and adult size.

We observed a lower mumification rate and adult size, as well as a longer development time, for parasitoids developing in neonicotinoid-resistant aphid lineages. These results suggest that neonicotinoid-resistant aphids are less suitable hosts for parasitoids than sensitive lineages. This study provides the first evidence that resistance to chemical stressors can affect host-parasitoid interactions and may help optimize biological control strategies for managing pesticide-resistant insect pests.

#10433

GLOBAL CHANGE: Biological invasion 1

30/06/2026 at 10:30, Descartes

Plants on the move: Enemy release and its erosion

Andrew LIEBHOLD (Czech University of Life Sciences, Forest Invasion Synthesis Centre, Aliebold@gmail.com)

Abstract

Globally, plants are increasingly growing outside of their range. This includes plants cultivated for purposes of agriculture, forestry and horticulture, but also invasive plants that increasingly dominate floras around the world. When a plant species is initially introduced to a new region, it typically experiences decreased herbivory as a result of the escape from insect herbivores that use it as a host in its native range. Enemy release is one of the most important mechanisms that contributes to the exceptional performance of non-native plants cultivated for agriculture and forestry but it also contributes to the invasiveness of many species. Over time, enemy release may diminish as a result of 1) native insect species expanding their range onto non-native plants and 2) invasions of specialist herbivores from the plant's native range as well as from other regions. Here I describe this phenomenon in several different systems and discuss the importance of the erosion of enemy release.

Malevolence in Eden: *Agrilus mali* yet another invasive buprestid?

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Zhaozhi LU

Abstract

Agrilus mali Matsumura (Coleoptera; Buprestidae) is knocking on the door of central Asia, the garden of Eden for wild apples, *Malus sieversii* (Ledeb.) M. Roem, the key ancestor of domestic apples. *Malus sieversii* grows in a few remnant pockets of a unique forest ecosystem in the mountains of Kazakhstan, eastern Uzbekistan, Kyrgyzstan, Tajikistan, Turkmenistan and Xinjiang in China. Wild apples were moved east and west along the “Silk Road” as early as the Neolithic, selected for various traits and deliberately crossed with local *Malus* species to produce domestic apple cultivars we enjoy today. The outbreak of *A. mali* in the Tien Shan of Xinjiang, first recorded in the 1990’s, has devastated the local wild apple forest, causing extensive branch dieback, greatly reduced yield and tree death with consequences for the wild apple forest ecosystem due to a reduced seed bank for forest regeneration. It has greatly impacted the destiny of this relic plant, the local economy and local indigenous communities. We summarise the literature on this species and the evidence for spread of *A. mali* from what was once a very limited distribution, the damage caused to the wild apple forest, management strategies and likelihood of continued spread.

Using genome skimming to track and manage the spread of an invasive lepidopteran

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Anna PLATONI, James KITSON

Abstract

Oak processionary moth (OPM – *Thaumetopoea processionea*) is a prominent invasive pest in several northern European countries, presenting threats to both oak health and biodiversity, through defoliation and numerical domination of hosts, and human health through the urticating hairs that later instar larvae develop. In Great Britain (GB), OPM has been present since 2006 establishing a breeding population despite biosecurity measures. Since this initial establishment there have been several outbreaks and the establishment of one satellite population outside of the currently defined established area which are too geographically distant to be the result of natural dispersal. Either, they have been spread via the transport of infested material internally, or they are further incursions across biosecurity measures at the border. Regardless of the mechanism the presence of these outbreaks suggests potential vulnerabilities in the national biosecurity effort against OPM.

To highlight where these vulnerabilities are we have taken a population genomics approach to better understand how genetically similar the separate groupings of OPM in GB are. Samples were taken from the established zone, the three outbreak sites, and from a variety of varying European countries where OPM is also present, to not only analyse GB populations but also to put this in the context of the wider European population of OPM. Population-level genetic analysis was undertaken comparing the DNA from samples at each site to each other and to populations from mainland Europe for a wider context view. This was done by extracting single nucleotide polymorphisms (SNPs) from annotated mitogenomes and comparing across populations. The resulting analysis has allowed us to make inferences about the relative number of incursions of OPM to GB and to hypothesis on the possible implications of these results to GB biosecurity and control of OPM.

Alien Phytophagous Mites in Europe: host plant adaptation, genetic pools, and potential range expansion for risk anticipation

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Abstract

Alien mites can represent a risk to plant health posing a threat to agricultural production. This study focuses on three alien spider mites with restricted distributions in Europe and potential to threaten new crops/areas: *Oligonychus perseae*, an avocado pest in Southern Europe; *Eotetranychus lewisi*, a quarantine pest present in Portugal; and *Oligonychus yothersi*, a polyphagous pest recently (2024) reported in Sicily, Canaries and the Azores. With the goal of anticipating risks, we conducted: (i) field surveys to verify range expansion, host plant adaptations, and population densities; (ii) molecular characterization (DNA sequencing) to assess invasive lineages; and (iii) species distribution modelling (SDMs) to predict distributions in Europe.

Oligonychus perseae, previously reported in mainland France, was also found in avocado orchards in Corsica, sometimes reaching high densities. Although previously reported from grapevine, no significant infestations or damage were recorded in vineyards in France or in Portugal. A very low genetic diversity is observed across invaded areas in Italy (Sicily), Portugal (Azores, Madeira) and France (Côte d'Azur, Corsica). The high densities in Corsica highlights the need to follow its pest status and to define management practices.

Eotetranychus lewisi, a pest in the Americas, has been found in Europe at high densities only on poinsettia and castor bean, raising questions about the introduction of a host-specific lineage. Molecular characterization of populations from Portugal and from a number of host plants in Mexico was carried out. Results do not evidence host-associated genetic structure, discarding the hypothesis of a host-specific lineage in Portugal. The ecological factors underlying the low population densities in crops in Europe require further study.

The development of SDMs is constrained by the limited number of occurrence records and requires careful parameterization. The results indicate that the species studied here have a large potential for expansion in Europe, particularly around the Mediterranean basin.

Invasion-driven changes in *Drosophila* and their parasitoid communities along a latitudinal gradient in the Rhône valley

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Abstract

Invasive species profoundly reshape ecosystems by altering trophic relationships and resource availability. Their impact is further modulated by ongoing climate and environmental change, which affect both the biotic and abiotic components of newly colonized habitats. One widely accepted explanation for invasion success is the Enemy Release Hypothesis, which suggests that invaders escape their natural enemies during colonization. While this hypothesis has been extensively tested, the reverse pattern where natural enemies follow and establish alongside their invasive hosts has been more rarely investigated. Here, we focus on a particularly promising model: the invasive crop pest *Drosophila suzukii* and its larval parasitoid *Leptopilina japonica*, recently detected in Europe. Unlike most *Drosophila* species that exploit decaying fruit, *D. suzukii*, native to East Asia and now widespread in Europe and North America, lays eggs in ripening fruits, causing major economic losses in berry production. Its invasion likely reshaped *Drosophila* communities in France, with potential cascading effects on associated parasitoids. Parasitoid wasps, major natural enemies of *Drosophila*, fall into two main guilds based on host stage preference: larval and pupal parasitoids. In Europe, only pupal parasitoids can develop on *D. suzukii*, as larval parasitoids succumb to a strong immune response. In its native range, however, *L. japonica* successfully parasitizes *D. suzukii* larvae, and its recent establishment in France provides a rare opportunity to study host–parasitoid co-invasion under contemporary environmental change. Using a long-term monitoring dataset (2009–ongoing) along the Rhône Valley, we characterized *Drosophila* and parasitoid communities across space and time to answer two main questions: how do environmental and climatic changes shape fly and parasitoid community composition, and how have the invasions of *D. suzukii* and *L. japonica* affected the structure and distribution of these communities? Our findings will highlight how natural enemy tracking might shapes communities under biological invasion and climate change.

Invertebrate invader in the South Atlantic: An ecological threat assessment

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Abstract

Entomological invasions are a global issue, raising concerns over food -production, biodiversity loss, and alterations to ecosystem functions. Ecological impacts of invasive species are often particularly acute in island ecosystems, and in the Southern Ocean Islands – where a number of key UK Overseas Territories lie – the frequency and scale of new introductions are anticipated to increase as a result of climate warming and growth of human activities.

In the Falkland Islands, European earwigs *Forficulana auricularia* have been reported in large numbers and become a serious horticultural and domestic pest. Despite being documented for over 20 years, no studies have examined the invasion biology or assessed the risk of ecological impact of this species. At present, domestic populations are controlled via commercial spraying; however nothing is known on the origins of this invader, the distribution, diet, phenology, habitat preferences, or social dynamics of this very unpopular invertebrate.

We set out to address some of these knowledge gaps and to present findings that will inform the ecological impact assessment that earwigs may have, which will form part of any future management strategy.

Over a 14 -month field campaign, we sampled across the Falklands Islands, in and outside the urban environment, gathering phenological, molecular, social and geographic data to record, publish, and assess the current situation and the threats that this invasion may pose.

An invader under pressure: exploring the consequences of an emerging fungal parasite on an invasive ant species in Europe.

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Simon TRAGUST

Abstract

Anthropogenic activities reshape ecosystems, notably through the intentional or accidental transport of species, which promotes biological invasions and the emergence of novel host-parasite interactions. As both processes intensify, understanding how invasive species and emerging pathogens interact and how these interactions affect native species has become a key challenge. Recently, the ectoparasitic fungus *Laboulbenia formicarum* has been observed infecting European populations of the invasive garden ant *Lasius neglectus*. The biological, ecological and evolutionary consequences of this novel interaction remain to be established, or especially for the invasive host, as well as for native ant communities. Within my PhD project, potential consequences of a *Lab. formicarum* infection were investigated across multiple biological levels. First the changes in invasive garden ant supercolony spatial dynamics and population genomics in relation to a *Lab. formicarum* infection were examined through a long-term field survey spanning over 10 years. Second, laboratory experiments were conducted to investigate colony development in terms of brood production under controlled conditions, while additional assays explored infection-related changes in individual behaviour and chemical signatures, and microbiota. Finally, impacts on native ant communities were evaluated by examining community composition around supercolonies and by experimentally quantifying the aggressiveness of *L. neglectus* towards native species. I am now presenting the latest results of these investigations providing an integrative view on how an emerging fungal parasite influences invasive *L. neglectus* ant populations across community, population, colony and individual levels.

Supercolonial ants – the making of a perfect invader

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Abstract

Most ant, bee, wasp, and termite colonies are well-defined families competing against other such families. However, some ants seem to have secondarily given up the fitness benefits of collaborating with close kin to form large networks of interconnected nests whose individuals are unrelated but fail to show territorial aggression. This can lead to the emergence of massive supercolonies that may extend over hundreds or even thousands of kilometres as seen in the most successful and problematic species of invasive ants. The iconic pest species is the Argentine ant *Linepithema humile* that I will use to demonstrate the life-history characteristics that appear to define supercolony-forming ants, and to argue that supercoloniality is a distinct category of social organisation. However, studies on other important pest species indicate that supercolonies may not always be as standardised as previously thought. The pharaoh ant *Monomorium pharaonis* has genetically extremely divergent colonies, even over a small spatial scale, suggesting that this species has efficient mechanisms to keep lineages of colonies separate. Nevertheless, after a brief initial aggression period, most colonies fuse readily in the laboratory. In contrast, the common red ant *Myrmica rubra* often forms populations with a mix of different colony types where local supercolonies may depend on recruiting new queens from isolated family-based colonies, and these may in turn expand to new supercolonies. These complexities suggest that there may be more than a single evolutionary and ecological route to supercoloniality. Importantly, the existence of alternative routes implies that the constraints from limited dispersal and genetic diversity faced by the “standard” supercolony can be overcome and may over time lead to increased invasiveness in the introduced ranges of supercolonial species. Most likely these insights are important for improving our ability to predict further ant invasions in the future.

Beyond Borders: The Silent Spread of Alien Thrips Across Europe

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Abstract

Global trade is continuously progressing and steadily increasing in volume every year, which facilitates the unintentional transport of exotic species. Updating lists of exotic species is therefore essential, given the dynamic nature of biological invasions and the growing number of introduced species. In this study, the list of Thysanoptera species alien to Europe was updated through a literature review, and about 480 national occurrences of 82 introduced species in 44 European countries (including main islands and Israel) were analysed.

Alien thrips to Europe belong to four different families, but two of them (Phlaeothripidae and Thripidae) include more than 96% of the alien species. *Frankliniella occidentalis* (Pergande), the western flower thrips introduced to the Netherlands in 1983, is now the most invasive species in Europe. It colonises 86% of the countries studied, with 5 other species colonising more than 50%. Conversely, 30 species are recorded in only one country. Five European countries (Portugal [Madeira], France, Spain, Italy, and the Netherlands) host more than 30% of the known alien Thysanoptera.

Alien thrips represent about 14% of the native European thrips fauna. They originate mainly from Asia, Central and South America, and North America, and are mostly phytophagous, seldom predators or fungus-feeders. Global trade is the prevailing pathway of introduction, and the main habitats colonised are cultivated areas (greenhouses, gardens, and parks). Since 1950, a clear acceleration of thrips introductions is evident, with a new alien species arriving on average every year between 2000 and 2025. There is no reason to assume a decrease in people's movements and restrictions on the transport of goods in the near future. Therefore, we can expect new thrips introductions in coming years, which means that European countries must maintain capabilities for quick and reliable identification of alien thrips through entomological quarantine expertise.

Darwin's naturalization conundrum in ants

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Cleo BERTELSMEIER

Abstract

Ongoing globalisation is accelerating the introduction of insects, posing threats to biodiversity and human well-being worldwide. A longstanding assumption is that species invasion is predictable based on the ecological similarity between native and alien species. However, it remains unclear how ecological similarity between native and alien species influences species invasions along invasion stages. Here, by integrating phylogenetic and functional information and leveraging ant species at different stages of invasion, we investigated the species- and community-level factors contributing to invasion success. We found that functional similarity to native species consistently increases the probability that alien ant species were introduced, established, and became invasive. In contrast, the effect of phylogenetic relatedness to native species was stage-dependent: phylogenetically distant species were more likely to be introduced, establishment success was higher when closely related native species were present, and successful invaders that spread widely tended again to be phylogenetically distant from natives. Greater native ant diversity reduced the occurrence probability of introduced ant species but increased establishment and invasion success. Overall, our global analysis of alien ant invasions highlights the different roles of phylogenetic and functional similarity at different invasion stages.

Evolution of the genetic load in invasive insects: insights from a genomic cross-species study

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Abstract

Biological invasions are a major component of global change, yet it remains unclear why some introduced populations become invasive while others do not. One hypothesis is the purging of deleterious mutations during the introduction process. When a small number of individuals colonize a new area, the interplay between genetic drift, inbreeding and natural selection can lead either to the fixation or to the purging of deleterious alleles, ultimately affecting fitness. We hypothesize that successful invasive populations are those that have reduced part of their genetic load.

We investigate this purge hypothesis across a broad taxonomic scale, analyzing ten insect species with well-documented invasion histories. For each species, we sampled between five and ten key native and invasive populations, representative of major stages in their invasion routes. We performed whole-genome pool-sequencing and developed a reproducible analysis pipeline to identify, annotate and categorize hundreds of thousands of SNPs per species. This framework enables quantitative comparisons of genetic load within and between species.

As expected, genetic diversity is generally lower in invasive populations than in native ones, reflecting introduction bottlenecks. However, we observe substantial interspecific variation in both bottleneck severity and estimated genetic load. No consistent trend emerges regarding the evolution of genetic load: some invasive populations show patterns compatible with purging, whereas others appear to have accumulated deleterious alleles. These contrasting outcomes highlight the complexity of evolutionary trajectories during invasions.

Our multi-species comparative approach suggests that genetic-load dynamics are highly context-dependent. While purging may contribute to invasion success in some species, it is not a systematic outcome. Ongoing work will refine these findings and test whether specific subsets of genes are more prone to purging. Altogether, our results call for a more nuanced understanding of how demographic and selective forces interact during biological invasions.

Temporal dynamics of species coexistence between invasive and native fruit flies sharing an ephemeral trophic resource

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Abstract

Rhagoletis completa (Tephritidae) is an oligophagous fruit fly from North-America, invasive in Europe since the 1990s and responsible for significant damage to walnut production. Its recent spread in northern France appears favored by climate warming and the multiplication of walnut trees, planted or spreading spontaneously along roadsides. By piercing the hard skin of unripe walnut fruit and altering its flesh, this alien species creates entry points and new trophic resources for other fruit flies. Its impact on Drosophilidae diversity and community composition has never been studied before.

This study aims to disentangle the relative roles of local environment, landscape and meteorological factors influencing the infestation success of *R. completa* and their effects on fruit Drosophilidae species coexistence and diversity. From July to December 2023, fruits were collected from the ground and canopy of 24 walnut trees (*Juglans regia*) in northern France. Around each tree, the local environment was characterized within a 20 m radius, the landscape composition was extracted from OSO database within buffers of 20 to 5,000 m and microclimatic and macroclimatic conditions were recorded.

In total, 2,433 walnut fruits were collected: 12,7% were infested by *R. completa* and 24,2% by 10 Drosophilidae species, including the two invasive flies, *Drosophila suzukii* and *Chymomyza amoena*. In September, 80% of trees were infested by *R. completa*, dominating the insect community living in unripe canopy fruits early in the season, while Drosophilidae species secondarily infested previously damaged fruits. Co-infestations were rare, suggesting a temporal partition in the use of walnut fruit, where small Drosophilidae avoided the competition with the large Tephritidae larvae. Marked differences among sites also indicate a strong environmental filtering. Finally, our study illustrates the invasional meltdown concept where positive interactions among non-native species could facilitate one another's invasion, even increasing their impact upon the native community.

Landscape and local factors shaping infestation rates of wild and garden cherry trees by the invasive fruit fly *Drosophila suzukii*

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Abstract

The spotted-wing drosophila, *Drosophila suzukii* (Matsumura), is an invasive fly that has been spreading in Europe since 2008. This pest infests cultivated fruit, particularly cherry crops, with large damage on fruit production. Beyond orchards, *D. suzukii* also infests wild cherry as well as sweet and sour cherry trees from gardens or abandoned lands. These alternative reservoirs scattered throughout the landscape could contribute to maintain its populations outside production areas. This study aimed to understand and quantify the relative influences of climatic, landscape, and local factors on the infestation rates of wild cherry and unmanaged domestic sweet and sour cherry trees. The study was conducted between May and July 2025 on 60 trees in Picardy and Normandy (northern regions of France). Fruits, sampled at different stages of ripeness, were collected both from the tree and from the ground. Upon collection, they were characterized morphologically and chemically (pH, sugar content) and then placed under laboratory conditions until the emergence of fruit flies which were identified to the species level. Local environment conditions (tree traits, vegetation structure and composition, meteorology, etc.) and landscape composition around cherry trees were also recorded. First results showed that *D. suzukii* was predominant on fruits sampled from the canopy, while native Drosophilidae communities were more diverse in fruits collected on the ground. The cherry fruit infestations peaked in early July and were positively correlated with fruit sugar content. Similarly, increased infestation by *D. suzukii* was associated with the presence of anthropized areas and habitats offering refuges (gardens, orchards). These results highlight the role of abandoned or unmanaged cherry trees in maintaining and dispersing *D. suzukii* populations which should be considered in IPM strategies.

Population genetic assignment to characterize long-distance dispersal of *Monochamus galloprovincialis*, vector of the Pine Wood Nematode

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Abstract

The pinewood nematode, *Bursaphelenchus xylophilus*, (PWN) is the causal agent of the Pine Wilt Disease, which blocks sap circulation and leads to the death of pine trees in less than two months. Native to North America, this species has caused considerable damage to pine forests in Asia, since its introduction to Japan in the early 20th century, and more recently in southern Europe, on maritime pine in Portugal, Spain and France. *Monochamus galloprovincialis* (Coleoptera Cerambycidae) is the main insect vector involved in the natural spread of the nematode in Europe, monitoring is based in part on a system for trapping adult insects in risk areas. These insects originate from local population, or could be immigrants from elsewhere, either by natural flight or by transport on contaminated wood. Being able to accurately identify dispersers and individuals' population of origin is therefore important.

This study aimed to improve current knowledge about the dispersive risk of the pinewood nematode, with a focus on the dynamics of insect vector propagation at large scale. By using genetic assignment methods, individuals with unknown genetic origin can be assigned to source populations. To provide tools for molecular assignment, Single Sequence Repeats (SSRseq) microsatellite markers, which have the advantages of codominant inheritance and of being hypervariable, are good candidates to characterize polymorphism among populations. Genotyping of individuals sampled within the natural range of *Monochamus galloprovincialis* were used as reference populations for assignment. These newly defined genetic clusters would help to identify the most likely source for trapped individuals, which provide significant help in assessing the potential pathways of PWN expansion across Europe.

Predicting and tracking invasive insects on the horizon

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Abstract

Invasive alien species (IAS) are a major and growing threat to people and nature. Target 6 of the Global Biodiversity Framework (GBF) commits nations to reduce the introduction of IAS by 50 percent and minimize their impact. Effective biosecurity, and specifically preventing the arrival of IAS, is critical to achieving Target 6. Collaborative horizon scanning studies, combining impact assessments and expert elicitation, are used to inform biosecurity by predicting which species might be the most likely to arrive and impact biodiversity and ecosystems. We have applied this approach to inform prioritisation of preventative actions for IAS in Britain and across the UK Overseas Territories. Here we provide an overview of the invasive alien insects that are considered to be amongst the high-risk species in different contexts including islands. Additionally, using the yellow-legged hornet, *Vespa velutina*, as an example, we highlight the importance of early warning and rapid response for mitigating the impacts of IAS. We call on everyone to contribute information about alien species rapidly through national and regional information systems ultimately sharing openly and following FAIR data principles. Such information is used in many different ways including informing horizon scanning and our understanding of progress towards Target 6 of the GBF. Enhancing information and data flows leads to improvements in predictions to inform prioritisation and action. Curbing the threat of INNS, including insects, is urgent but achievable.

Boring Business: Global Trade and Wood-Borer Interceptions in Great Britain

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Sarah FACEY, Anna PLATONI

Abstract

Global trade and the dispersion of wood products and wood packaging materials throughout the world has led to a number of economically-damaging invasions of wood-boring insects. Border interceptions represent one of the first lines of defence against such invasions and by identifying and risk-assessing such interceptions, countries can devise policy and practice to help protect trees and forests within their borders from the most impactful pests. Though the trade in wood packaging material is globally regulated through ISPM15, wood commodities are largely regulated at the country-level with the default legal position that trade is generally allowed unless restricted. As such many wood-boring pests have already become established in naive regions, and whilst only a small proportions of these are genuinely economically significant, the damage and impact they can have on the economy is immense. Unfortunately however there is little published data on interceptions of non-quarantine species at the border, even though these may be the quarantine species of tomorrow. This paper will look at long-term trends in the interception data of wood-boring insects through Great Britain's Phytosanitary Service, focusing on some case studies and the role of geopolitics in trade. Knowledge gaps will be highlighted, and recommendations made for effective at-border surveillance, whilst also acknowledging that such surveillance must be part of wider pan-country efforts to monitor and prevent the establishment of novel pests.

Implementing trapping networks with generic lures at ports-of-entry for early detection of non-native xylophagous species

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Abstract

Due to globalization and renewed trade routes, insect invaders are increasingly consisting of “emergent” species, which have never been observed before in areas other than their native ones, and thus often not included in the quarantine lists. The use of traps baited with blends expected to provide a generic attractiveness at insect-genus or -family level may enhance the possibilities to detect such unpredicted species at arrival. Since 2021, the National French project PORTRAP SORE deployed traps baited with a blend including 10 Cerambycidae pheromones at 29 sites considered as potential ports-of-entry in the country. The traps were additionally implemented with ethanol and (-) α -pinene, two plant volatiles known to have a generic attractiveness for bark and ambrosia beetles. The trapping design consisted in a pair of black and green traps installed in the port and a similar pair placed in nearby wooden areas located within a radius of 1 km from the port. The same trapping design was extended to Corsica, Sardinia and parts of continental Italy since 2023 under the ALIEM Apostrophe and ALIEM Vigil projects. Over the 5-year period, a total of 30 non-native xylophagous species were detected, including 12 Curculionidae (bark and ambrosia beetles), eight Cerambycidae, six Bostrychidae, two Dryophthoridae, one Anthribidae and one Zopheridae. Four of these species were intercepted for the first time in Europe. Quite all surveyed sites (82%) showed a recurrent arrival of non-native xylophagous species, with a maximum of eight species on the Corsican port of Bastia. Most species did not move outside the port they arrive but a few species did. The trapping network allowed to follow the dispersal of the Asian cerambycid *Xylotrechus stebbingi* within continental France, Corsica and Sardinia as well as those of the ambrosia beetle *Xylosandrus crassiusculus* and *X. compactus*, both likely vectored by domestic ornamental trade

Enhancing Lepidoptera Identification in EU Import Controls: towards an identification key for larvae

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Abstract

Regulation (EU)2019/2072 and its amendments define the quarantine plant pests prohibited within the European Union, including 39 Lepidoptera species whose introduction and spread must be avoided. In routine inspections of fruit and vegetable consignments imported from non-EU countries, plant products are rejected and reported to the European Commission when a quarantine organism is detected. However, these official records do not capture all occurrences of non-quarantine Lepidoptera, and many detections are only identified to higher taxonomic levels, limiting the completeness and usefulness of available data.

Lepidoptera are among the insect groups most frequently intercepted on imported plant produce, yet their real diversity remains underestimated when relying solely on official notifications. Identification is further complicated by the fact that most specimens arrive as larvae, for which detailed morphological descriptions and diagnostic tools are often lacking.

To better understand (a) which Lepidoptera species are encountered during EU import controls and (b) whether they can be rapidly and reliably identified through morphology, a dedicated project was launched. Through a collaborative network of National Reference Laboratories across all Member States, the project compiled the most extensive dataset to date on Lepidoptera interceptions from the past thirty years. Specimens were identified using COI barcoding, after which detailed morphological characterisation was carried out for the most frequently detected species, supported by high-resolution images.

Based on this work, a dichotomous key for larval identification is being developed to distinguish the selected species using relevant diagnostic characters. A draft version is already available and is continuously updated. Once finalised and validated, this key will provide a robust, tailored, and up-to-date tool for stakeholders involved in Lepidoptera identification at European border inspection posts. Furthermore, having more comprehensive and detailed data on intercepted non-quarantine lepidoptera will also contribute to risk assessment and early warning of future threats posed by these organisms.

Are declining forest stands stepping stones areas for exotic invasive species?

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Abstract

Forest decline (and dieback) is the process of progressive tree decline in a forest stand and can result in tree death. This phenomenon is increasingly observed globally, mainly because of the rising impacts of global warming and associated natural disturbances (e.g. droughts or pest outbreaks). Previous works have studied the consequences of forest decline and dieback on forest biodiversity, functioning, and services. Nonetheless, whether declining stands can be used as stepping stones by forest exotic invasive insects remain unclear. Stand decline alters habitat conditions creating suitable resources and microclimates, and destabilizes native communities which can favor colonization by invasive xylophagous and saproxylophagous species. However, the large range of habitats provided by these stands allows them to host rich species communities, including beetles, birds, and bats, whose complex network of interactions can modulate the colonization opportunities by exotic invasive species – e.g. via competitive exclusion or predation. To better understand how declining forest stands are affecting populations of exotic invasive species, we used several contrasting European case studies (i.e. lowland and montane forests, affected by different natural disturbances, i.e. droughts, windstorm and pest outbreak). We show how exotic invasive species populations respond to gradients of forest stand decline and subsequent salvage logging. We also demonstrate how potential biotic interactions can facilitate or hinder populations of those species, by studying the responses of potential competitors and predators/parasitoids.

Human-mediated dispersal of invasive termite pest species

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Abstract

While termites play important ecological roles, a fraction of species have strong invasive capabilities and represent urban pests of economic importance worldwide. Their invasive potential is exacerbated by human activities such as maritime transport, with privately owned boats serving as key vectors for local and global termite dispersal, particularly for *Cryptotermes* and *Coptotermes* pest species. Land establishment by invasive termites can remain undetected for decades, often making eradication attempts too late to succeed. Ultimately, invasive termite species will likely continue to spread at the global scale, and recent new invasive records point toward an underestimation of their actual current invasive status. Unequivocally, the ongoing global spread of invasive termite pest species is slowly leading to a partial homogenization of urban termite pests. While climatic conditions may be a primary restrictive factor for introduced species survival in non-native areas, the ongoing urbanization-associated changes at the local and global scale are conducive to augmented termite damage potential in the near future. The economic impact of invasive termites has been rising over the decades and will continue to intensify as they continue to establish in new locations, via human-mediated transportation, primarily by privately owned leisure boats.

Whole genome sequencing reveals multiple invasion routes of *Popillia japonica* in Switzerland

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Abstract

The Japanese beetle (*Popillia japonica*), native to Japan, is a damaging invasive insect species impacting agriculture and horticulture in North America and, more recently, Europe. Following its initial establishment in the Azores in the 1970s, the species colonized northern Italy in 2014 and subsequently reached southern Switzerland in 2017. In 2023, *P. japonica* was detected in three additional regions in Switzerland: Kloten (Canton of Zürich), Basel (Canton of Basel-Stadt), and eastern Valais near the Italian border. In 2024, several isolated individuals were recorded across further Swiss cantons. To trace *P. japonica* spread and origins in Switzerland, we investigated 42 individuals from infested areas, comprising scattered findings across the country. These new genomic data were analysed together with previously published datasets from Japan (native range), North America, the Azores, northern Italy, and southern Switzerland. Phylogenetic inference and population structure analyses revealed distinct *P. japonica* migration patterns. Populations in Basel, Valais, and central Switzerland likely originated from Ticino/Northern Italy via road or rail transport. Conversely, the population near Zürich Airport was identified as an independent introduction from North America, likely through unintentional air transport. These findings demonstrate that *P. japonica* is entering and spreading within Switzerland through multiple pathways and from different source populations. This highlights the importance of coordinated surveillance strategies, pathway-specific mitigation measures, and rapid detection to prevent further establishment and slow the beetle expansion across Europe.

Complexity in the plant-aphid molecular dialogue

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Abstract

Aphids are devastating insect pests of crops and pose a major threat to food security. These insects deliver effectors inside host plants during probing and feeding to suppress the plant's immune system and enhance susceptibility. We used a combination of “omics” approaches to identify and compare effector repertoires from economically important aphid species. Not only has this allowed us to prioritise effectors for functional characterisation, but it has also led to the discovery of a co-regulated effector pair that is co-located across aphid genomes. Recent data from our lab shows that the encoded effector pair can physically interact to form an oligomeric effector complex and targets host proteins involved in plant cell trafficking. Using computational biology, structural biology and protein interaction assays, we provide evidence for effector co-evolution across the aphid phylogenetic tree. Further characterisation of effector-effector and effector-host target complexes will not only reveal how effectors enhance host susceptibility but also provide novel insights into plant biological processes targeted during infestation. This, in turn, will enable the development of pest control strategies based on preventing effector activities.

Insect detoxification enzymes as key drivers of evolutionary adaptation to plant toxins

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Abstract

Phytophagous insects have evolved sophisticated detoxification systems to overcome the diverse chemical defences of their host plants, yet linking specific enzymes to ecologically relevant plant toxins remains a major challenge. Here we combine gene-cluster knockouts with in vitro metabolism to functionally connect defined detoxification enzymes to key plant allelochemicals in lepidopteran pests. (i) In *Helicoverpa armigera*, CRISPR/Cas9-mediated deletion of CYP6AE subfamily gene clusters, together with recombinant enzyme assays, identifies members of this family as key determinants of tolerance to the xanthotoxin and 2-tridecanone. We further show that xanthotoxin is initially converted to xanthotoxol and 5-hydroxyxanthotoxin by CYP6AE19, and that these metabolites are subsequently glucosylated by UDP-glycosyltransferase UGT33 family enzymes to form detoxified glucoside conjugates. (ii) In *Spodoptera frugiperda*, we identify SfUGT33F32-mediated glucosylation as a key mechanism enabling detoxification of DIMBOA, a potent insecticidal benzoxazinoid produced by poaceous plants, thereby facilitating adaptation to maize. This DIMBOA-detoxifying capacity is conserved in several generalist *Spodoptera* species, whereas the lily specialist *Spodoptera picta* has lost this function owing to a non-functionalising mutation in the orthologous SpUGT33F34. Together, our results provide new insights into the evolutionary adaptation of insect pests to plant toxins, and offers molecular targets for the the control of several notorious lepidopteran pests.

REPAT proteins as a bridge between caterpillar infection and plant defense response

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Abstract

Recent studies have revealed that lepidopteran orally secreted proteins can interfere with jasmonate-mediated plant defense pathways by targeting repressors or transcription factors within the JA-signaling cascade. Among these effectors, several proteins identified in *Helicoverpa armigera* and *Tuta absoluta* belong to the REPAT family, originally described in *Spodoptera exigua* approximately two decades ago due to their strong induction following microbial challenge, which led to their designation as REsponse to PAThogen proteins.

In this study, we identified a total of 397 REPAT genes across the genomes of eight moth species. Phylogenomic analyses indicate a marked expansion of the REPAT family in *Spodoptera* species. While some REPATs display strict one-to-one orthology and are widely distributed across chromosomes, those putatively involved in plant-insect interactions tend to be organized in genomic clusters. Additionally, *Spodoptera* genomes contain unique REPAT clusters lacking the characteristic multi-bridge factor 2 (mbf2) domain that is conserved in all other REPAT proteins.

To investigate the physiological role of REPATs and their involvement in pathogen infection and plant defense modulation, we focused on orally secreted REPATs in *Spodoptera exigua*. Differential proteomic analyses showed a reduction in specific REPAT proteins in the oral secretions of larvae infected with *Spodoptera exigua* iflavirus 1. This reduction was associated with a stronger activation of plant defense responses following herbivory by infected caterpillars. Together, these findings provide the first evidence that REPATs function as a molecular link between viral infection in the insect host and the activation of plant defense mechanisms.

From roots to populations: microbe-induced resistance alters herbivore life history

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Abstract

Mutualistic root associated microbes can indirectly influence herbivorous insects by enhancing plant immunity, a phenomenon known as Microbe Induced plant Resistance (MIR). Recent evidence shows that the display of MIR can compromise insect performance beyond the larval stage, creating a MIR-related fingerprint (so called MIR-imprint) in surviving insect individuals, as a sublethal effect, with potential consequences for herbivore population dynamics. However, the mechanistic basis of the MIR-imprint, and its consequences for insect population dynamics and its broader agroecological implications remain poorly understood. We hypothesized that MIR triggered in tomato plants by the mutualistic root-associated fungus *Trichoderma harzianum* triggers a MIR-imprint in *Spodoptera littoralis* surviving individuals, at molecular, metabolomic and physiological levels, affecting insect population dynamics. We first assessed whether and to what extent the expression of MIR in the plant affects insect development and demography relevant traits. Importantly, in the surviving insect population, we found that MIR was related to sublethal effects such as reduced larval growth, delayed pupation, diminished sex-specific differences in developmental timing, and altered pupal sex ratios. These changes affect critical components of insect demography, including development rate and sex structure, which are known to influence population dynamics. To gain insight into the mechanistic basis of these responses, we performed RNA-seq analyses of larval fat body and gut tissues. Transcriptomic profiling indicates shifts in metabolic, regulatory, and stress-related pathways, supporting the idea that MIR imposes systemic physiological constraints on herbivores. Overall, our findings indicate that MIR triggered by *T. harzianum* can shape insect life-history traits and demographic parameters, creating a MIR-imprint with potential consequences for population dynamics and agroecological interactions between insects and plants.

Funding:

This work was supported by ERC Consolidator Grant MIMIR_101124883 of the European Research Council.

Metabolic profiling of Agave species with varying susceptibility to the agave weevil *Scyphophorus acupunctatus* (Coleoptera: Dryophthoridae)

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Abstract

Scyphophorus acupunctatus Gyllenhal, 1838 (Coleoptera: Dryophthoridae), an invasive weevil native to Central America, is a major pest of Agave plants globally. Following its introduction into the Mediterranean region, it has emerged as a severe threat to ornamental agaves, particularly affecting botanical collections and urban landscapes. As Agave species exhibit varying degrees of susceptibility to this pest, this study was conducted to investigate the constitutive and induced metabolic traits potentially influencing host-plant compatibility.

An untargeted LC–MS metabolomic approach was employed to analyze eleven Agave species categorized into three levels of host suitability: susceptible (supporting larval development: *A. americana*, *A. americana* var. *marginata*, *A. mitis*, *A. attenuata*), intermediate (supporting adult feeding only: *A. fourcroydes*, *A. franzosini*, *A. salmiana* var. *ferox*), and resistant (not exploited by the weevil: *A. macroacantha*, *A. victoriae-reginae*, *A. nigra*, *A. stricta*). For each species, five healthy plants were sampled to evaluate constitutive metabolic profiles. Additionally, for susceptible species, five infested individuals were included to characterize the induced response to herbivory.

Multivariate analysis revealed a metabolic separation between healthy and infested samples within the susceptible group, suggesting an induced response. Pathway analysis indicated the involvement of defense-related mechanisms, such as α -linolenic acid metabolism and the biosynthesis of cutin, suberin, and fatty acids. Furthermore, constitutive profiling showed some divergence among the three susceptibility groups. Susceptible species were characterized by pathways associated with growth and development, such as sphingolipid and zeatin metabolism. Conversely, intermediate and resistant species showed a relative enrichment in pathways linked to energy metabolism and stress resilience, including the TCA cycle, carbon fixation, and ascorbate metabolism.

These findings highlight metabolic traits potentially associated with Agave resistance, providing a foundation for understanding host–plant interactions and supporting the future development of integrated management and preventive strategies against *S. acupunctatus*.

Rhythmic determinants of folioivory by the Brassica specialist pest Diamondback moth (*Plutella xylostella*).

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Abstract

Rhythmic determinants of folioivory by the Brassica specialist pest Diamondback moth (*Plutella xylostella*).

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Annually, the diamondback moth *Plutella xylostella* (DBM) causes losses to the global agricultural economy in the order of 5 billion US\$. Increasing resistance to and concerns about the use of insecticides make it imperative to identify alternative integrated pest management strategies for this invasive migratory Lepidopteran pest. We have investigated how DBM folioivory on host plants is regulated by pest-plant interactions. Laboratory experiments identified an impact of the alignment of the circadian phases of host plant and DBM clocks on both folioivory and DBM gene expression.

Consistent with the notion that rhythmic plant defences shaped rhythmic folioivory, significant changes were observed for caterpillars feeding on arrhythmic *Arabidopsis* mutants as well as those with defective Jasmonate signalling. Moreover, the arrest state of the plant circadian clock significantly impacted caterpillar feeding. Time-course RNA-seq and real-time PCR analyses of late instar DBM caterpillars demonstrated that transcript rhythms of core circadian clock genes were unaffected the circadian phase of host plants. However, the wider programme of caterpillar diel transcript rhythms and regulations of resistance genes in specific exhibited regulation by host plant phase. Thus, rhythmic plant defence shapes folioivory rhythms of DBM. We will discuss our results as well as the potential of reducing DBM-mediated damage to Brassica crops by changing the expression rhythms of specific defence genes.

Antibiosis resistance to *Tuta absoluta* in wild and cultivated tomato accessions

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Abstract

Tomato (*Solanum lycopersicum*) is a significant crop both nutritionally and economically, but faces threats from pests, particularly the tomato leaf miner (*Tuta absoluta*). With limited pest resistance in cultivated tomatoes due to genetic bottlenecks, wild relatives offer potential resistance sources. We evaluated 24 tomato accessions, including wild species and cultivated varieties, for resistance to *T. absoluta* through no-choice and choice assays under greenhouse and tunnel conditions, respectively. Antibiosis was measured through damage parameters including leaflet lesion type (LLT), percentage of attacked leaflets, and number of mines. No-choice tests revealed significant inter- and intraspecific differences. Principal component and clustering analyses grouped accessions into three categories based on resistance, with wild accession *Solanum habrochaites* 'PI24' demonstrating high resistance alongside other wild relatives, while cultivated varieties like Rose de Berne clustered as susceptible. In choice assays, 'PI24' sustained less damage and reduced larval progression compared to Rose de Berne. Early-stage larvae (L2) were more frequent on 'PI24', but few progressed to later stages (L3 and L4), indicating that 'PI24' defense mechanisms interfere with larval development. Untargeted metabolomics was conducted to characterize the leaf constitutive metabolic diversity of the 24 accessions. It revealed substantial differences between wild and cultivated species, with wild species like *Solanum pennellii* and *Solanum habrochaites* displaying greater metabolic diversity. Integrating antibiosis assays and metabolomic data highlighted metabolic classes putatively related to tomato resistance. Take together, this study highlights the value of integrating wild accessions traits into cultivated tomatoes for sustainable pest management, with 'PI24' emerging as a valuable resource for breeding pest-resistant tomato varieties.

In silico and in vitro analyses revealed odorant receptor divergence associated with host specialization in moths

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Abstract

Host specialization in herbivorous insects is often associated with divergence in chemosensory abilities. Here, we investigated the possible contribution of odorant receptors (ORs) in host plant specialization in the lily moth *Spodoptera picta*, a species specialized on Amaryllidaceae, compared to its polyphagous sister species *S. littoralis* and *S. litura*. Genomic annotation of *S. picta* ORs revealed a repertoire similar in size and composition to those of its sister species, suggesting that specialization did not involve major gene loss or expansion. To assess functional divergence beyond gene number, we developed an innovative large scaled structure-based virtual screening approach applied to the entire OR repertoires of these three *Spodoptera* species, generating ligand-binding profiles for over 120,000 volatile compounds. Among 69 1:1:1 OR orthologs, 24 exhibited divergent predicted binding spectra. We pinpointed one OR that we also found to be highly expressed in both male and female antennae of *S. picta* through a RNAseq approach. Functional assays demonstrated that this *S. picta* OR acquired heightened sensitivity to limonene, a volatile emitted by host Amaryllidaceae inflorescences. Site-directed mutagenesis revealed that amino acid substitutions localized within the predicted binding region underly this shift in sensitivity. These results suggest that host specialization in *S. picta* is not driven by large-scale OR repertoire remodeling, but probably by subtle molecular changes that fine-tune receptor sensitivity to ecologically relevant volatiles. Our findings highlight the evolutionary potential of small amino acid substitutions to shape chemosensory adaptation and suggest a broader role for receptor-level functional divergence in insect host specialization.

Azospirillum brasilense reconfigures maize-mediated defenses across herbivore and parasitoid trophic levels

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Abstract

Plant-microbe interactions play a central role in sustainable agriculture by reducing fertilizer inputs and reshaping pest dynamics. Although plant-associated microbes are known to influence plant defenses against herbivores, little is known about how the plant growth-promoting rhizobacterium (PGPR) *Azospirillum brasilense*, one of the most widely used biofertilizers in maize, affects maize defenses against the fall armyworm (FAW, *Spodoptera frugiperda*). Here, we investigated the cascading effects of the PGPR maize association on FAW oviposition behavior, attraction of the recently described larval parasitoid *Aleiodes ceres*, and maize volatile emissions. Oviposition preference was assessed in laboratory non-choice assays, parasitoid responses were evaluated in dual choice olfactometer tests, and maize headspace volatiles were collected from individual plants enclosed in glass chambers. Plants were exposed to herbivory by third-instar FAW larvae before the volatile sampling and behavioral assays. Females laid significantly more eggs on non-inoculated maize, whereas parasitoids were consistently more attracted to inoculated plants, even in the absence of herbivore damage. PGPR inoculation induced qualitative shifts in volatile profiles: inoculated undamaged plants emitted indole, a key herbivore-induced volatile and oviposition deterrent, while inoculated damaged plants additionally released α -copaene, a compound commonly exploited by natural enemies for host location. These results indicate that PGPR inoculation reconfigures maize chemical signaling in ways consistent with a priming-like defensive state, simultaneously deterring FAW oviposition while enhancing parasitoid attraction. Our findings highlight that, beyond improving crop performance, PGPR inoculation can generate complex and context-dependent outcomes across trophic levels, with both benefits and costs for plant defense against FAW.

Plant–insect–microbe interactions shape ethanol tolerance and foraging ecology in social wasps

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Abstract

Fermenting yeasts are common inhabitants of ripe fruits and floral nectars, where they convert plant sugars into ethanol (EtOH), altering both resource quality and accessibility for insect consumers. Social wasps (Vespidae) are key participants in this tri-trophic system: they forage on sugar-rich plant substrates, harbor fermentative yeasts in their guts, and act as vectors that disperse microbes among fruits and flowers. In the Old World, long-term associations with the highly ethanol-tolerant yeast *Saccharomyces cerevisiae* may have shaped wasp foraging behavior and physiological capacity to exploit fermented plant resources. In contrast, New World fermentations historically relied on low-ethanol-producing yeasts, potentially limiting the evolution of similar adaptations.

Using ¹³C-labeled ethanol, we show that Old World species rapidly oxidized yeast-derived ethanol, whereas New World species showed slower metabolism and reduced tolerance. Behavioral assays further revealed delayed sedation and greater resistance to ethanol vapor in Old World wasps. Hemolymph analyses indicate that Oriental hornets efficiently eliminate ethanol before they accumulate in circulation.

These findings suggest that evolutionary history with fermentative plant-associated microbes influences wasp foraging ecology, metabolic traits, and tolerance to microbially modified plant resources. Ongoing work integrates gut mycobiota analyses to test whether New World vespids can acquire and transmit *S. cerevisiae*, potentially reshaping plant–insect–microbe interactions in invaded ecosystems.

Natural and Synthetic Agents Shape Wireworm Behaviour: Responses of *Agriotes lineatus* and *A. litigiosus*

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Abstract

Wireworms (Coleoptera: Elateridae) are major subterranean crop pests whose hidden soil-dwelling behaviour and strong orientation toward plant roots complicate their control within Integrated Pest Management (IPM). We aimed to determine whether selected natural and synthetic agents could influence the behaviour of two wireworm species, *Agriotes lineatus* and *A. litigiosus*, and thus support more sustainable control approaches. Using dual-choice soil olfactometers and rhizotron assays, we quantified larval movement in response to two types of compost tea (CT16, CT19), the synthetic volatile organic compound 3-octanone, and the entomopathogenic fungus *Metarhizium brunneum* (strain 1868). Compost tea CT16 acted as a significant attractant, CT19 showed no significant effect, and both 3-octanone and *M. brunneum* significantly repelled larvae of both species. Furthermore, rhizotron observations confirmed reduced time spent in treated zones in the 3-octanone and fungal treatments, indicating strong avoidance behaviour. Species-specific differences were minor and limited to the lower overall response rate observed in *A. lineatus*. These findings highlight clear differences in wireworm behavioural responses to both natural and synthetic agents, offering promising tools for developing push-pull-based wireworm management. Future field studies are needed to validate their practical applicability and clarify underlying mechanisms.

Effects of two water regimes on leaf redox status, pest preference and performance (*Amrasca biguttula* and *Helicoverpa armigera*) in two cotton varieties under controlled conditions in Bénin

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Abstract

Plant defence responses are tightly regulated by redox signalling pathways, yet their influence on plant-insect interactions remains poorly understood. Cotton, one of the crops most heavily attacked by insect pests worldwide, relies on intensive insecticide use with major environmental and health impacts. Improving our understanding of cotton physiological responses to pest performance is therefore essential for developing sustainable pest management strategies.

This study examined how two redox-sensitive factors, respectively water regime (water stress vs. optimal conditions) and cotton variety (ANG956, moderately hairy; DeltaOpal, low hairiness), shape the preference and performance of two major yield-limiting cotton pests: the jassid *Amrasca biguttula* and the bollworm *Helicoverpa armigera*. Experiments were conducted under controlled conditions using a 2×2 factorial design (variety × water regime). For each pest species, we conducted adult female preference and nymphal/larval development assays, and measured plant morphological and redox parameters, and pest performance traits (female plant choice, development duration, mortality and larval weight for bollworms).

DeltaOpal attracted significantly more *A. biguttula* adults, hosting 70% of individuals after 48 h and exhibiting higher leaf damage (50% vs. 30% for ANG956), indicating greater susceptibility of the low-hairiness variety. For *H. armigera*, gravid females strongly avoided ovipositing on water-stressed plants, regardless of variety, though neither water regime nor variety affected larval development. Ongoing analyses of redox markers aim to identify physiological mechanisms underpinning these contrasting patterns.

Together, these results highlight pest-specific responses driven by varietal traits (jassids) and abiotic stress (bollworms), pointing to the need for integrated pest management strategies that incorporate plant physiological and redox-mediated mechanisms, particularly in the context of increasing climatic variability.

Plant Induced Responses to Insect Derived Airborne Signals

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Abstract

Plants can perceive and respond to volatile organic compounds (VOCs) emitted not only by other plants but also by insects. These airborne signals have the potential to modify plant physiology, influence defences pathways, and alter interactions with herbivores. While plant–plant volatile communication has been widely studied, the consequences of plant exposure to insect-derived VOCs, particularly pheromones, remain largely unexplored. Emerging evidence suggests that these cues may prime defences responses and affect traits relevant to herbivore performance.

In this study, we investigate how exposure of Brassica plants to the synthetic pheromone of the specialist pest *Plutella xylostella* influences plant physiology and subsequent plant–insect interactions. After controlled pheromone exposure, we assess plant responses at multiple organizational levels, including gas exchange parameters, volatile emissions, and behavioural and performance assays, including oviposition preference and larval feeding activity. Together, these data reveal whether insect pheromone cues induce or prime physiological shifts in the plant that ultimately shape herbivore behaviour and performance.

Plant phenology and VOCs signals mediating *Halyomorpha halys* (Hemiptera: Pentatomidae) host selection mechanisms

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Abstract

Volatile organic compounds (VOCs) emitted by plants are key mediators of plant–insect interactions and play a central role in host plant selection by polyphagous pests. In this work, we combined headspace chemical analyses and electrophysiology to investigate how the brown marmorated stink bug, *Halyomorpha halys* (Hemiptera: Pentatomidae), perceives and responds to host-derived volatiles. First, we characterized VOC emissions from five major host plants and identified 68 compounds, 13 of which were consistently shared across the selected species, suggesting the presence of a common chemical backbone that may underpin this insect’s extreme polyphagy. Consequently, we examined VOC profiles of kiwifruit (*Actinidia chinensis* var. *deliciosa*) across three phenological stages using GC-MS and GC-EAD. Distinct chemical blends were associated with each phenological stage, with compounds such as camphor, nonanal, sabinene, and α -pinene eliciting strong antennal responses in adults. Together, these findings reveal both the diversity and the commonality of host plant chemical cues exploited by *H. halys*, pointing to a synergistic mechanism of host detection, shaped by dynamic VOC landscapes. Ongoing behavioral assays aim to link chemical and electrophysiological activity with host-selection behavior, contributing to the identification of candidate semiochemicals for improved monitoring and management strategies.

Volatile chemicals mediate conifer-bark beetle-fungus interactions

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Abstract

The Eurasian spruce bark beetle, *Ips typographus*, is a lethal pest for Norway spruce (*Picea abies*) across Europe. These beetles have intricate relationships with a suite of ascomycete blue-stain fungi, likely providing multiple benefits to their vector beetles. These fungi act as phytopathogens, showing variable levels of virulence, ranging from highly aggressive to moderately or less harmful.

We investigated whether beetles could distinguish the virulence of fungi based on their volatile emissions and use these cues to associate with specific fungal partners. Analysis of volatiles emitted from beetle galleries revealed the presence of phenolic volatile styrene, which was absent in uncolonized bark. Furthermore, a symbiotic virulent fungus was identified as a source of styrene, producing it through the metabolism of trans-cinnamic present in the host conifer. Single sensillum recordings showed that adult beetles possess broadly tuned OSNs to detect styrene and other structurally similar chemicals. Short-range behavioral assays involving walking beetles demonstrated that beetles are attracted to styrene-producing virulent fungi, implicating the role of styrene in mediating the interaction between beetles and virulent fungi. These results suggest that beetles utilize specific volatile cues derived from the fungal metabolism of a non-volatile tree compound to identify and differentiate virulent from less virulent fungi.

Silicon as a tool to improve maize defenses against *Spodoptera frugiperda* (J.E. Smith, 1797) (Lepidoptera: Noctuidae) under climatic stress conditions

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Mateus Francisco O. DIMAN

Abstract

Insect–plant interactions are strongly influenced by plant nutritional quality and physiological status, factors that shape both plant development and the performance of herbivorous insects. Water and salt stress, conditions increasingly intensified by climate change, compromise plant growth and disrupt key metabolic processes, which can directly modify plant–insect dynamics. Silicon (Si) has emerged as a beneficial element capable of enhancing plant growth, modulating physiological and biochemical responses, and strengthening defense mechanisms, thereby reducing the impacts of both biotic and abiotic stresses. However, studies examining the role of silicon in plants subjected to simultaneous stresses remain scarce, particularly regarding their interactions with major insect pests. This study investigates how silicon influences the physiological responses of maize plants challenged by *Spodoptera frugiperda*, a key pest in maize production, under isolated water and salt stress. Our results indicate that silicon promotes a significant increase in maize plants growth under normal conditions and, when subjected to severe abiotic stresses, acts as a mitigating agent, partially attenuating the effects of water and salt stress, contributing to plant development under adverse conditions. However, neither of these stresses, applied separately or in combination with silicon, significantly altered the feed intake of *S. frugiperda*. Future research will focus on nutrient intake, digestibility, and food conversion efficiency to clarify whether stress conditions or silicon influence insect nutritional physiology beyond simple consumption metrics. Overall, this study provides insights into the complex interactions between maize, abiotic stress factors, and herbivory, contributing to improved understanding of silicon-mediated plant defenses. These findings aid the development of more sustainable pest management strategies and support advances in breeding programs aimed at enhancing crop resilience under changing environmental conditions.

Individual and interactive effects of drought, herbivory and developmental stage on Oak leaf chemistry

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Abstract

Climate change scenarios anticipate an increasing frequency and intensity of drought events in the coming years. Therefore, understanding how drought-stress alters growth-defence relationships in plants and their consequences for herbivory is highly relevant. Yet, despite a rich body of research, ecologists still struggle to come up with a conclusive mechanistic framework of how drought impacts plant-herbivore interactions. Moreover, variations in phytochemistry and resultant herbivore responses are also strongly influenced by tree phenology and by genetic differences among individuals. This study aimed to understand the implications of drought stress, oak developmental stage and their individual and interactive effects on leaf chemistry and herbivory, while controlling for among-tree genetic variation. To accomplish this, in 2024, we grew 108 pedunculate oak (*Quercus robur*) clone DF159 saplings under either moderate drought priming or control, overwintered them unstressed, and then transfer them to a glasshouse in spring 2025. In a full-factorial design, saplings were exposed to moderate drought, herbivory by *Lymantria dispar*, their combination, or control conditions, and sampled at two developmental stages. We assessed herbivore performance and quantified leaf damage using an AI-powered software, conducted multiple phytochemical analyses including targeted and untargeted metabolomics, tannin (HST and CT), plant hormone, and non-structural carbohydrate analyses and measured plant biomass and several physiological traits. Our results shed light into how drought priming, individually and interactively with oak developmental stage alter multi facets of oak's chemistry and physiology and consequently its' responses to subsequent drought and herbivory.

Plant–Microbe Interactions Between Entomopathogenic Nematode Symbiotic Bacteria and Tomato Plants

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Abstract

Entomopathogenic nematodes (EPN) of the general *Steinernema* and *Heterorhabditis* parasitize and kill their insect hosts with symbiotic bacteria of the genera *Xenorhabdus* and *Photorhabdus*. Recent findings suggest that EPN influence indirectly the plants sometimes by activating direct and/or indirect defences. Moreover, symbiotic bacteria from EPN interact with plant roots but their specific role in plants remain largely unexplored. Our aim is to investigate whether these bacteria are involved in plant's functions and metabolism, thereby altering their resistance to biotic and abiotic stresses. For this purpose, we evaluated several developmental and physiological characteristics of tomato plants, such as chlorophyll content and CO₂ assimilation under drought and spider mite infestation in the presence of EPN symbiotic bacteria. In addition, the performance of mites was evaluated under different treatments (bacteria, drought). Our preliminary results suggest that EPN symbiotic bacteria influence positively the development of tomato plants and indirectly lead to suppression of mite populations and their feeding activity in tomato plants. These findings indicate suggest that EPN can have important implications for overall plant health that go beyond their traditional role as biological control agents.

Independent and interactive effects of drought and herbivory on oak seedlings and their leaf fungal communities

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Heidy SCHIMANN, Bastien CASTAGNEYROL

Abstract

Leaf-associated microbiota are increasingly recognized as sensitive indicators of how plants respond to environmental stressors. While abiotic and biotic stresses often occur simultaneously, their combined impact on tree performance and associated microbial communities remains poorly understood. We hypothesized that drought increases oak susceptibility to insect herbivory, and that drought and herbivory jointly (i) reduce microbiome diversity and shift community composition toward pathogen dominance, and (ii) reduce tree performance.

We manipulated water availability and infestation of oak seedlings by the invasive oak lace bug *Corythucha arcuata* in a factorial experiment using four deciduous oak species. We monitored leaves for insect herbivory, characterized leaf endophytic fungal communities, and assessed the individual and combined effects of drought and herbivory on leaf physiology and tree growth.

The species diversity of the leaf endophytic fungal community was, on average, lower in seedlings exposed to drought treatment. Herbivory altered community composition depending on oak species, resulting in either turnover or nestedness patterns. Despite the low number of pathotrophic fungal species, their diversity increased with herbivory in one oak species.

Herbivory ranged from 0 to 99 % of leaf area discoloured by *C. arcuata*, regardless of the water regime. Drought, but not herbivory reduced tree growth. Herbivory, but not drought, was associated with reduced photosynthesis activity. Stem non structural carbon contents were only influenced by oak species.

Our results indicate that in the short term, the combined effects of drought and sap-feeding herbivory do not impair the performance of European oaks. However, they also suggest that repeated exposure to these stressors over multiple years could contribute to shifts in microbial communities, including an increased prevalence of pathogenic taxa, with potential consequences for tree health. Taken together, our findings emphasize the importance of considering longer-term stress combinations and their effects on tree performance as well as on microbial communities.

Insect symbionts used as seed inoculants establish endophytic interactions with maize: effects on the metabolomics of maize and the herbivore *Spodoptera frugiperda*.

Fernando CONSOLI (University of Sao Paulo - Luiz de Queiroz Colle of Agriculture, Fconsoli@usp.br)

Diandra ACHRE

Abstract

We have previously shown that bacterial insect symbionts can establish endophytic interactions with maize plants, affecting plant growth and the interactions of symbiont inoculated plants with the maize herbivore *Spodoptera frugiperda*. The effects of these symbionts on maize and *S. frugiperda* was species-dependent. Some induced plant growth, while others increased larval mortality of *S. frugiperda* or increased the plant oviposition stimulation to *S. frugiperda* moths. In here, we will demonstrate changes in the metabolome of maize plants and the interacting herbivore induced by the inoculation of insect symbionts that enroll in endophytic interactions with the host plant. The use of seed inoculants to regulate plant growth and aid in pest control is a great alternative to reduce the carbon footprint in agricultural systems.

Motor Flexibility: central and proprioceptive contributions to the generation of task-specific motor output for leg stepping

Ansgar BÜSCHGES (Institute of Zoology, University of Cologne, Ansgar.bueschges@uni-koeln.de)

Abstract

In goal-directed legged locomotion, animals modify the movements of their extremities and the coordination between them in specific ways to serve the presumed tasks. Examples for this comprise walking at different speeds, walking forward or backward, turning with different radii, and, finally, surmounting gaps and obstacles. The motor output for driving the associated contractions of leg muscles depends on the action of descending commands from the animal's brain onto the neural machinery for generating movements of single legs and their coordination. These circuits reside in the ventral nerve cord of arthropods or the spinal cord of vertebrates. Here, I will report with specific emphasis on the insect leg muscle control system on our recent advances in understanding the organization of these circuits and the role that proprioceptive feedback signals about movements and forces (or load) from the legs play in the task-specific control of single leg kinematics for walking and for inter-leg coordination.

Locomotion on granular media : insect stability on sandy inclines

Miguel PINEIRUA MENENDEZ (Institut de Recherche sur la Biologie de l'Insecte, Miguel.pineirua@univ-tours.fr)

Jérôme CASAS, Anna VERBE

Abstract

Insect locomotion on sandy media is very common in nature. The underlying physical principles governing the interaction between the insect and the granular medium are of great interest not only from an ecological perspective but also as a source of inspiration in biomimetics. The main challenge in dealing with granular media comes from its complex nature, as it can behave as a solid or a fluid depending on the stresses applied on it. Inspired by the case of the antlion pit, our work aims to shed some light on the understanding of insect locomotion stability on granular inclines. Through a series of model experiments mimicking artificial multilegged walkers, we show that the stability on a granular incline near the avalanche angle strongly depends on the applied pressure on the medium as well as on the distance between the different points at which pressure is applied. Based on a simple stability criterion, our findings suggest that mass to leg length allometric relations may play a crucial role on the locomotion stability of insects on inclined granular media.

Locomotion in Complex Terrains: Biomechanics to Bioinspiration

Kaushik JAYARAM (Imperial College London, K.jayaram@imperial.ac.uk)

Katrina ABROGAST, Heiko KABUTZ, Kimberley FUNG, Holly VISSER, Kendall WEBSTER

Abstract

High-speed locomotion on complex terrains, including confined space and lateral inclines, is an open challenge for both animals and robots alike. In this talk, we will discuss our group's efforts in understanding the role of body and limb shapes and their effect on biomechanics in the context of laterally confined gaps and laterally inclined terrains. To compensate for the effects of gravity or overcome environmental constraints, we hypothesize that multilegged organisms adapt their gait and posture during locomotion. Here, the terrestrial arachnid, *Schizocosa mcmilli*, was encouraged to laterally traverse a runway inclined at angles 0° , 15° , 30° , 45° , and 60° . To discourage wall-following behaviors, we developed a novel trackway with pneumatic jet 'airwalls'. Using high-speed videography and markerless tracking, we quantified kinematic and gait parameters as a function of inclination. Preliminary results showed a significant decrease in speed, from 16.67 cm/sec at 0° to 2.88 cm/sec at 60° , and lateral accelerations, from 147 cm/sec² to 45 cm/sec² over the same range. Notably, 61% of this decrease occurred after 45° , with limited changes in stride frequency (4-8 Hz). Qualitative postural observations indicate that unilateral leg adjustments across the sagittal plane become increasingly obvious on steeper gradients. The up-slope legs (legs that are elevated relative to the body) exhibited greater flexion, while the down-slope legs demonstrated greater extension. Additionally, we observed significant widening of the base of the support polygon, suggesting the need for increased stability at steeper inclines. Further investigating these biomechanical strategies across laterally inclined surfaces will not only provide insight into distinctive balance control techniques but will also inspire multilegged robotic designs and control architectures. We will also present how spider adapt their legs positions to fit through tight spaces and use a near-scale bioinspired robotic model to demonstrate novel applications in robotics.

Egg glue of the stink bug *Nezara viridula*: production site, mechanical properties, and surface interactions

Asmita BARAL (PhD student, Department of Chemistry, Biology and Biotechnology, University of Perugia, Italy., Asmita.baral@dottorandi.unipg.it)

Alessandra PASSERI, Silvia CAPONI, Maurizio MATTARELLI, Chuchu LI, Stanislav GORB, Elena GORB, Silvana PIERSANTI, Gianandrea SALERNO, Manuela REBORA

Abstract

Insect egg glue produced during oviposition functions as a natural adhesive that binds eggs together and anchors them to the substrate, providing protection and stability. The Southern green stink bug, *Nezara viridula* L. (Hemiptera: Pentatomidae), is a highly polyphagous pest that deposits eggs on plant surfaces with diverse structures and wettability.

This study investigates i) the site of egg glue production; ii) the adhesive strength on various plants and artificial substrates with different surface features and surface chemistry; and iii) mechanical characterization of the glue, along with the measurements of polymerization time and the humidity effects on the glue. Light and electron microscopy (SEM and TEM) revealed that the glue is synthesized by follicular cells within the ovarioles and conforms to substrate microstructures upon deposition. Adhesion assays demonstrated that attachment strength varied substantially across plant surfaces and artificial substrates. Among natural surfaces, *Brassica* species, characterized by dense tubular wax projections, exhibited the lowest adhesion forces, whereas smooth hydrophilic surfaces consistently showed the highest adhesion. Exposure to various humidity treatments, did not result in significant differences in adhesion strength. Correlative Brillouin Spectrometry revealed rapid polymerization within the first few minutes of air exposure, leading to the formation of a rigid material that corresponds with increased adhesion strength over time. The glue exhibited mechanical heterogeneity between thicker and thinner regions. Quantitative measurements of the Young's modulus and hardness of the egg glue were obtained using the SA2 Nanoindenter.

Collectively, these findings advance our understanding of the glue's effectiveness for insect adaptation and evolutionary success, providing also mechanistic insights relevant to pest-control applications and the development of novel bio-adhesives.

Flapping Flight in Diptera: From Evolution to Aerodynamics

Thomas ENGELS (CNRS & Aix-Marseille Université, Thomas.engels@univ-amu.fr)

Camille LE ROY, Ilam BHARATHI, Florian MUIJRES

Abstract

Flight has been a key innovation in insect evolution, yet the selective and mechanistic forces shaping their flight motor systems remain poorly understood. Here, we present a comprehensive comparative analysis of Diptera (true flies), integrating morphology, wingbeat kinematics, and aerodynamics within a phylogenetic framework. We quantified morphology in 133 species spanning the Dipteran phylogenetic and size range, and for a subset of 46 species, we combined high-speed stereoscopic videography with computational fluid dynamics (CFD) to characterize wingbeat kinematics and aerodynamic performance, respectively. Our results reveal that morphology is strongly structured by phylogeny, whereas wingbeat kinematics are broadly conserved across Diptera, reflecting dominant aerodynamic constraints. Two basal lineages, Culicomorpha (mosquitoes and midges) and Tipulomorpha (crane flies), exhibit strikingly divergent kinematics and aerodynamics, suggesting lineage-specific selective pressures. Scaling analyses show that smaller species compensate for reduced aerodynamic force production efficacy through relatively larger wings, and higher wingbeat frequencies. Moreover, miniaturization is constrained by increased viscous drag at low Reynolds numbers, causing a plateau in aerodynamic power reduction with decreasing size. We further demonstrate that mosquitoes exhibit disproportionately high aerodynamic and acoustic power, coupled with enlarged flight musculature, consistent with sexual selection favoring acoustic signaling during in-swarm mating. This trade-off highlights how reproductive pressures can override aerodynamic efficiency. By integrating comparative morphology, kinematics, and aerodynamics across a major insect radiation, our study uncovers the interplay between physical scaling laws, aerodynamic constraints, and ecological pressures in shaping the evolution of animal flight. These findings provide a mechanistic framework for understanding how complex locomotor systems diversify under multiple selective forces.

#12046

INSECTS AS SOLUTIONS: Biomimeticism - Bioinspired materials, sensory and actuation systems

30/06/2026 at 12:00, Montlouis

Nonlinear softening and resonance in odonata flapping flight

Ramiro GODOY-DIANA (PMMH, UMR 7636 CNRS, ESPCI Paris–PSL, Sorbonne Université, Université Paris Cité, Ramiro@pmmh.espci.fr)

Camille ARACHELOFF, Benjamin THIRIA, Romain GARROUSTE, André NEL

Abstract

We investigated the connection between the flight flapping frequency and the intrinsic wing properties in Odonata (dragonflies and damselflies). For such large flying insect species, it has been noted that the wingbeat frequency is significantly lower than the structural resonance of the wing itself. However, the structural resonance mechanism is often evoked in the literature for flying and swimming animals as a means to increase locomotion performance. Here, we show that the flight of Odonata is based on a nonlinear mechanism that strongly depends on the wingbeat amplitude. For large flapping amplitudes (as observed in natural flight), the resonant frequency of the wings decreases with respect to its value at low amplitudes to eventually match the wingbeat frequency used in flight. By means of this nonlinear resonance, Odonata keep a strong wing stiffness while benefiting from a passive energy-saving mechanism based on the dynamic softening of the wing.

Reference: Aracheloff et al. *Journal of the Royal Society Interface* **21**, 20240401 (2024). doi: 10.1098/rsif.2024.0401

Flight and swimming mechanics of miniature wasp *Tiphodytes gerriphagus* (Hymenoptera: Scelionidae)

Nadezhda LAPINA (Department of Entomology, Faculty of Biology, Lomonosov Moscow State University, Moscow, Russia, Nnadlappa@gmail.com)

Sergey FARISENKOV, Evgeny SHERBAKOV, Alexander TIMOKHOV, Dmitry KOLOMENSKIY, Alexey POLILOV

Abstract

Locomotion in two media with different viscosities provides a unique perspective on the evolution of movement and serves as a valuable source of inspiration for biomimetic engineering. Some hymenopterans use their wings both for flight and swimming underwater. Currently, their structural features and mechanics of locomotion in air and water remain poorly understood.

We compared the wing morphology of swimming and non-swimming hymenopterans to identify adaptations for locomotion in air and water. We found that the percentage of the wing area occupied by bristles is higher in swimming hymenopterans than in non-swimming. Additionally, swimming forms have a greater relative wing length and smaller relative venation length compared to non-swimming forms. These appear to be important adaptations for both flight and swimming.

The wasp *Tiphodytes gerriphagus* (Marchal, 1900) was chosen as a model organism. We conducted a high-speed recording of flight and swimming, a reconstruction of the wing kinematics of *T. gerriphagus* in air and water, computational fluid dynamics simulations, and a comparison of the morphological data with those of non-swimming species of comparable size. The wing kinematics of *T. gerriphagus* in air is typical for hymenopterans of similar size. However, the swimming kinematics combines features typical of flight in very small insects with those that seem to be specific only to swimming. The angle of attack during the upstroke reaches 90°, while during the downstroke it is limited to about 45°. The upstroke is strongly U-shaped. The recovery stroke is short in distance but very long in time. Swimming occurs in jerks during the wing strokes, alternating with drift during the recovery strokes.

The study of swimming hymenopterans allows identifying adaptations that arise during locomotion in media with varying viscosities, while minimizing the influence of interspecific differences. Our results could be useful in the design of miniature swimming devices.

Insects on the menu: Nutritional value and potential risks

Mik VAN DER BORGHT (KU Leuven, Mik.vanderborght@kuleuven.be)

Abstract

Edible insects have been part of traditional diets across the globe for centuries, harvested from nature and occasionally reared for consumption. Today, their potential to contribute to global food security is increasingly recognized, yet scientific research on their nutritional properties and safety remains relatively recent.

This presentation offers an introduction to global practices of insect consumption. Given the rarity of insect consumption in Europe, the presentation will also focus on a possible strategy to promote the acceptance and integration of edible insects into European diets. Research indicates that edible insects are a highly nutritious food source, rich in proteins, fats, essential amino acids, vitamins, and minerals. They also contain chitin, a compound that functions as a dietary fiber. This presentation will offer insights into the nutritional composition of insects, the analytical challenges in accurately characterizing their composition and representation of this data. Furthermore, a methodology is put forward to obtain unambiguous nutritional data, to ensure its reliability and enabling comparison of nutritional data.

As with any food source, insect consumption entails certain risks. A concise overview of key chemical hazards related to insect consumption will be provided. Particular attention will be given to the presence of microplastics in the insect value chain, with a focus on how their size and shape may influence potential health risks.

Mapping the effects of diet protein, carbohydrate, and lipid composition on black soldier fly (*Hermetia illucens*) larval outcomes

Kim JENSEN (Aarhus University, Department of Animal and Veterinary Sciences, Kj@anivet.au.dk)

Abstract

Larvae of the black soldier fly (*Hermetia illucens* (L.)) can exploit a wide array of waste substrates and therefore have huge potential to convert organic side streams into feed. However, knowing the composition of nutrients that matches requirements is essential to exploit side streams optimally. Studies on macronutrient balancing in insects and other animals have focused on protein (P) and carbohydrate (C), while the influence of dietary lipid (L) has been largely ignored. In black soldier fly diets, L is kept at a low level as higher concentrations have appeared harmful. Using pure, synthetic ingredients, we applied nutritional geometry to produce full macro-nutritional landscapes going from 0 to 100% for each macronutrient in diets systematically varying P, C, and L composition in a complete grid of 166 combinations, while keeping all other dietary components constant. We then let two replicates of 100 larvae of 5-6 days of age develop on each diet at 28°C for eight days, and produced thin-plate spline landscapes for larval outcomes over dietary macronutrient compositions. Results show a peak for larval dry mass production at 35% P, 30% C, and 35% L, a peak for L production at 30% P, 40% C, and 30% L, and a peak for P production at 90% P, 10% C, and 0% L. Survival was high on all diets but highest on low P, where growth was limited but P utilization was maximal. Using agar to maintain similar structure across diets, we show that L can be beneficially included at a much higher level than has been the general norm, probably due to its negative effect on diet structure rather than its nutritional value. Our results give optimal dietary nutrient combinations for different larval growth parameters, which is useful when designing an optimal diet e.g. from different available side streams.

Functional expression of PET-degrading enzymes in *Drosophila melanogaster*: a proof-of-principle study exploring insects for plastic biodegradation

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Valentina PIRILLO, Federica BARCA, Daniele BRUNO, Sara CARAMELLA, Claudia FONTANA, Matteo BATTISTOLLI, Elena CATELAN-CARPHIO, Davis ROMA, Morena CASARTELLI, Silvia CACCIA, Alessandro GRAPPUTO, Gianluca TETTAMANTI, Gianluca MOLLA

Abstract

Plastic contamination in organic municipal waste is an increasing challenge that current recycling systems have difficulty managing efficiently. Although insects convert organic material, they display a limited ability to degrade synthetic plastics such as polyethylene terephthalate (PET). To explore whether engineered insects could be improved for this capability, we used the model organism *Drosophila melanogaster* to generate transgenic lines expressing *in vitro*-evolved variants of PETase and the leaf-branch compost cutinase LCC. Both enzymes, fused to a gut-targeted secretion signal, were produced and secreted in active, soluble form in cell cultures and whole organisms. Biochemical assays on larval extracts demonstrated that a modified LCC variant was active in depolymerising 10% of PET nanoparticles within 48 hours. Transgene expression did not impair larval or adult performance: developmental timing, adult fertility, gut morphology and digestive activity in larvae remained comparable to wild-type insects, indicating that the metabolic burden of enzyme production was well tolerated. These results provide a proof-of-principle that insects can host functional PET-degrading enzymes. Therefore, this approach will be transferred from *D. melanogaster*, whose physiological traits, including small larval size and growth temperatures, are not optimal, to more thermotolerant and industrially relevant insect species, providing a basis for the future development of insect-based strategies for plastic-waste bioprocessing.

BEYOND LINEAR NUTRITION: EVIDENCE FOR CIRCULAR, MICROBIALLY DRIVEN NUTRIENT DYNAMICS IN BLACK SOLDIER FLY LARVAE

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Nate SIBINGA

Abstract

There is significant interest in better understanding the nutritional requirements of Black soldier fly larvae (*Hermetia illucens*), yet many foundational principles of classical animal nutrition do not fully translate to this system. Traditional nutrition models assume a linear flow of nutrients from feed to animal biomass, with excreted wastes representing irreversible losses. In contrast, BSF larvae develop within microbially dynamic substrates where nutrient transformations are continuous and strongly mediated by microbial activity. Larval feeding rapidly depletes specific limiting nutrients, which in turn imposes selective pressure on the substrate microbiota, favoring taxa capable of synthesizing, mobilizing, or recycling those nutrients. Larval waste products (e.g. exuviae, uric acid, and partially digested feed) are converted in situ into microbial biomass and can immediately re-enter the larval food supply. Microbial communities thus play an active role in mediating nutrient availability and can compensate for nutritionally deficient substrates.

This can confound carefully executed studies, as larvae exhibit robust growth on substrates that are designed to fail. This talk examines how such microbial feedback loops challenge conventional nutritional models and highlights the need for nutritional methods that can account for larva–microbe–substrate interactions. Using an axenic (germ-free) rearing model that does conform to classical nutritional assumptions, we determined the “true” nutritional requirement of BSF larvae for lysine using a broken-line model based on substrates with graded inclusion levels. This approach holds promise for increasing mechanistic understanding of the specific functional contributions of microbes to BSF larval nutrition and is expected to lead to improved selection of substrates and probiotics, thereby promote performance on suboptimal substrates.

Uncovering genes regulating female fecundity in *Tenebrio molitor* L: a transcriptomic analysis.

Maria XANTHOU (University of Thessaly, department of Biochemistry and Biotechnology , Mxanthou@uth.gr)

Eirini BARA, Panagiota PELKOUDI, Konstantinos MATHIOPOULOS

Abstract

The yellow mealworm, *Tenebrio molitor* L., is a key species for industrial mass rearing, aligning with the principles of circular economy due to its capacity to convert low-value substrates into high-value products with minimal environmental footprint. In large scale rearing facilities, female fecundity is one of the primary traits determining production efficiency. However, the molecular mechanisms that regulate fecundity remain largely unexplored, limiting the development of targeted strategies for improving reproductive output.

To investigate the molecular basis of fecundity, we combined comparative transcriptomics with RNA interference (RNAi) to identify and functionally validate candidate genes associated with reproductive output. Transcriptomic analysis was conducted on reproductive tissues [ovaries and female accessory glands (FAGs)] from two strains with markedly distinct reproductive performance: the more fecund Greek strain, and the more poorly performing German strain. This comparison revealed 62 upregulated and 17 downregulated genes in the Greek strain relative to the German one. From these, two genes with contrasted expression patterns were selected. Both genes, *15-hydroxyprostaglandin dehydrogenase* (15PGDH) and *farnesol dehydrogenase* (FDH), are linked to pathways involved in diverse physiological processes, including reproduction. However, their specific roles in fecundity remain to be functionally defined. RNAi-mediated knockdown in adult females resulted in efficient gene silencing, demonstrating that both genes significantly affected oviposition.

This study provides the first functional evidence that *15PGDH* and *FDH* contribute to female fecundity in yellow mealworm, directly linking gene expression differences to reproductive outcome. Beyond advancing the molecular understanding of insect reproduction, these findings identify candidate molecular targets that may support future strategies for enhancing fecundity in mass rearing systems.

Mining plastic-degrading enzyme in the gut microbiota of *Hermetia illucens*

Davis ROMA (University of Milan, Davis.roma@unimi.it)

Conor SCOTT, Giuseppina SEQUINO, Bellicini AURORA, Martina MARZARI, Daniele BRUNO, Gianluca TETTAMANTI, Francesca DE FILIPPIS, Matteo BRILLI, Morena CASARTELLI, Silvia CACCIA

Abstract

Plastic pollution represents a global concern, dramatically impacting ecosystems and human health, as plastic wastes are exceptionally persistent and pervasive. Considerable scientific efforts have been directed toward developing innovative strategies for plastic waste reduction and valorisation, with enzymatic plastic biodegradation as a promising and environmentally sustainable approach. Despite the chemical inertness of plastic polymers, several plastics degrading microbial species have been isolated from disparate sources, such as marine ecosystems, soil, plastic landfills, and even the gut microbiota of some invertebrates, including insects. Among promising insect species, the larvae of the dipteran *Hermetia illucens* (Black Soldier Fly, BSF) displayed the ability to grow and degrade polyethylene (PE). Our recent research aimed to develop protocols for the rearing of *H. illucens* larvae on plastics-based substrates to select for plastics-degrading microorganisms, focusing on: i) characterization of the shifts in the taxonomic composition of the gut microbial communities caused by the ingestion of different plastic polymers; ii) reconstruction of an in silico functional profile of the gut community, focusing on enzyme families enriched in plastic containing diets and therefore potentially associated with plastic biodegradation; iii) select a panel of enzymes for further characterisation, gaining essential knowledge for their optimization through protein engineering and synthetic biology approaches.

Don't cry over spilled milk: Repurposing wet byproducts from the dairy industry as alternative moisture sources in *Tenebrio molitor* rearings

Christina ADAMAKI-SOTIRAKI (University of Thessaly, Greece, Cadamaki-s@uth.gr)

Christos G. ATHANASSIOU, Ioannis VRONTAKIS, Sofronios ZAFEIRIADIS, Georgia V. BALIOTA, Theodora GOGOU, Georgios KARAGIORGIS, Christos I. RUMBOS

Abstract

The dairy industry produces large amounts of wet byproducts from dairy processing wastewater to expired dairy products, whose disposal remains an environmental and economic challenge. Although many agri-food byproducts have been successfully tested as feeding substrates for *T. molitor*, bioassays assessing wet dairy wastes and their effects on larval growth, feed conversion, and final product quality have not been published yet. In this study, we explored whether wet dairy wastes can be reused as moisture sources in the rearing of the yellow mealworm (*Tenebrio molitor*), creating a direct link between dairy waste management and insect production. Seven liquid byproducts were tested: expired milk, kefir, plant-based milk, as well as acid lactose (UC), sweet lactose (UF), whey byproduct, and acid whey lactose. Two different gelling agents (i.e., agar and starch) were utilized to alternate their texture and make them suitable for *T. molitor* larvae consumption. Overall, the larvae performed well across all treatments tested. The larval survival and weight were not affected negatively and remained high until the end of the bioassay. Differences were observed in larval development time, which were reduced up to 48 days. Larvae fed with milk and kefir based moisture sources developed faster, while those receiving whey byproduct developed slower. Larval protein content remained stable among treatments, while lipid content was affected by the type of dairy waste. The higher values of lipids were observed in larvae reared on milk, plant milk, and lactose byproducts. These findings highlight the potential of *T. molitor* rearing as a practical and "green" solution for the management of wet dairy byproducts.

Financial support for this research has been provided by PRIMA, a program supported by the European Union, under grant agreement No 2231, project CIPROMED (PRIMA Call 2022 Section 1 Agri-food IA).

Survival of spore-forming bacteria during black soldier fly larva *Hermetia illucens* (L.), Diptera: Stratiomyidae), waste conversion

Christina NIELSEN-LEROUX (INRAE, Christina.nielsen-leroux@inrae.fr)

Agnès REJASSE, Christophe BUISSON, Ludovic BRIDOUX, Isabelle POQUET, Vincent SANCHIS BORJA

Abstract

The Black soldier fly, *Hermetia illucens*, larva (BSFL) is considered as a sustainable animal feed ingredient. BSFL can grow on a variety of naturally microbe-rich substrates, like waste streams. BSFL are also known for their capacity to eliminate some human animal pathogens. However, little is known about BSFL ability to eliminate spore forming bacteria, that can survive routine hygiene treatments. In this study, we first evaluated the nutritional value and natural presence of spores in human opportunistic pathogens *Bacillus cereus* (Bc), insect pathogen *B.thuringiensis* (Bt) group bacteria and human opportunistic pathogens *Clostridioides difficile* (Cd). Five waste streams, three from plant material and two containing animal proteins were tested. To assess the capacity of BSFL to reduce the spore load, the waste (70% waste+30% wheat bran) was spiked with 10^6 spores/g. 5 mg larvae were reared on the waste (1 larva /g feed), and larval weight and spore concentration were recorded, after 3 and 7 days, in the larvae and in the frass. All waste allowed a good larval growth; larval weight was ≈ 35 mg at day 3 and up to ≈ 180 mg at Day 7 for an animal protein waste. Some of the waste naturally contained *B. cereus* ($\approx 10^4$ cfu/g), but no detectable Cd. The spiked Bt were recovered mainly as spores, in both the larvae and frass, without any significant difference in their final concentration. However, a small, difference in the total Bt counts, was found at day 3 or 7 as compared to day 0, indicating presence of the bacterial vegetative form as well; spiked Cd spores were not reduced. In conclusion BSFL could not reduce Bc/Bt, Cd spores during waste bioconversion, thus the presence of spore-forming pathogens must be monitored in both larval diet and in the final larva /pupal stage ensure safety of insect products.

Profiling the resistome and virulome of the *Hermetia illucens* midgut microbiota

Conor SCOTT (Department of Biosciences, University of Milano, via Celoria 26, 20133, Milano, Italy, Conorscott2204@gmail.com)

Davis ROMA, Matteo BRILLI, Francesca DE FILIPPIS, Giuseppina SEQUINO, Silvia CACCIA, Morena CASARTELLI

Abstract

The spread of antimicrobial resistance has become a crucial global health threat. Agricultural practices and livestock production have contributed greatly to the spread of antibiotic resistance genes (ARGs) in the environment. However, the spread of ARGs is not the only challenge facing the agri-food sector which requires urgent innovation for the adoption and development of more sustainable processes. The larvae of the Black Soldier Fly (BSFL) *Hermetia illucens* are mass-reared to produce animal feed and fertilisers, yet the resistance and virulence encoded within their midgut microbial communities remain underexplored. To elucidate the risk associated with their use, the profiles of antibiotic resistance genes (ARGs), virulence factors (VFs), and plasmids were predicted from the midgut bacterial community of BSFL reared on a standard diet for Diptera. Shotgun metagenomic sequencing revealed the presence of genes encoding resistance against 26 classes of antibiotics, and genes encoding virulence by nine mechanisms. Three horizontally-mobile ARG-encoding plasmids were also identified. Taxonomic classification of shotgun metagenomic contigs revealed that Pseudomonadota phylum taxa were the dominant members of the resistant and virulent communities in the BSFL midgut. Metagenome reconstruction was performed to achieve higher taxonomic resolution and revealed taxa harbouring multiple genes for resistance and virulence, including a *Pseudomonas* species with 42 VFs and seven ARGs. To contextualise the bioinformatic classification of the resistome, culturable antibiotic-resistant strains of bacteria were isolated from the BSFL midgut and identified using MALDI-TOF mass spectrometry. Altogether, this analysis represents the most comprehensive profile to date of the midgut microbiota resistome in *H. illucens*. It will provide both a valuable tool to the research community working on BSF larvae, and for the assessment of the antibiotic resistance risk posed to the environment and to public health through their use.

Gas Exchange as a Predictive Tool for Growth and Nutrient Allocation in Black Soldier Fly Production

Mattias SCHOW-MADSEN (Department of Bioscience, Zoophysiology, Aarhus University, Mattiasschow@hotmail.com)

Kim JENSEN, Maja LERMARK SCHØN, Johannes OVERGAARD

Abstract

Large-scale rearing of Black Soldier Fly larvae (*Hermetia illucens*) requires non-invasive monitoring tools that relate environmental and nutritional conditions to growth performance, metabolic efficiency, and product composition. Here we present evidence that continuous measurements of oxygen consumption, carbon dioxide production, and respiratory exchange ratio (RER; VCO_2/VO_2) can serve as reliable indicators of growth and metabolic dynamics under varying environmental and dietary conditions.

After validating that small-scale respirometry chambers replicate metabolic patterns observed in large-scale facilities, we used these chambers (400 larvae per 1 L chamber) to investigate how (i) temperature, (ii) macronutrient balance (protein:carbohydrate), and (iii) amino acid balance influence development, growth rate, metabolic trajectories, and associated respiratory parameters.

Our findings indicate that (i) oxygen consumption rate correlates strongly with biomass accumulation, providing a robust estimator of yield without invasive sampling; (ii) gradual fluctuations in oxygen consumption signal instar transitions, offering valuable guidance for harvest timing; and (iii) RER serves as a reliable proxy for lipid assimilation, increasing when carbohydrate-driven lipogenesis predominates.

We further show that the main energetic costs of growth are linked to protein assimilation, while lipid assimilation is less costly. Growth efficiency (energy cost per gram of protein assimilated) increases under unfavorable conditions, such as extreme temperatures or suboptimal diets. Overall, these findings underscore the potential of respirometry as a non-invasive tool for monitoring growth and diagnosing limitations (e.g., heat stress, macronutrient imbalance, amino acid deficiency) that enabling producers to optimize for faster growth, reduced CO₂ emissions per unit yield, or enhanced protein content according to production goals.

#11159

INSECTS AS SOLUTIONS: Insects as feed and food 2

30/06/2026 at 15:00, Bourgueil

Pangenomics of the Black soldier fly

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Abstract

The black soldier fly, *Hermetia illucens*, is at the centre of a rapidly expanding livestock feed and waste management industry. The ability of the larvae to consume a variety of organic waste products, and their high protein content, make it a prime target for industrialised mass rearing as an alternative protein source.

Despite this, understanding of the genetics of the species is still limited. Here, we present the first pangenome of the black soldier fly (BSF), incorporating multiple *de novo* genome assemblies from across the species' global distribution. We identify patterns of structural variation and gene absence-presence (GAP) variation between genomes and use this to identify regions of potential interest for future experiments involving selective breeding, and to investigate gene duplication events associated with BSF larvae's generalist detritivore lifestyle. We also show an improvement in mapping quality when mapping short reads to the pangenome graph, when compared to the published single reference genome, enabling future population genetic studies involving resequencing individuals from diverse populations.

Finally, we perform short read sequencing of single individuals from other *Hermetia* species to produce the first molecular phylogeny of the genus, in order to identify the closest sister species of BSF to use as an outgroup for phylogenetic analysis and enable future comparative genomic studies between the two species.

Breeding of the black soldier fly (*Hermetia illucens*) for high temperature adaptation and resistance to the entomopathogen *Paenibacillus thiaminolyticus*.

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Abstract

Increasing susceptibility to entomopathogens in insect breeding facilities linked to rising temperatures driven by global warming stand out as a major challenge for the insect mass rearing industry. Among the species currently used, the black soldier fly (*Hermetia illucens*, Diptera: Stratiomyidae) is particularly notable due to its remarkable efficiency in converting organic waste into high-value feed ingredients. In this context, the selection and breeding of insect lines capable of growing at higher temperatures and exhibiting increased resilience to emerging entomopathogen-induced diseases represents a promising strategy to enhance the economic and environmental sustainability of insect-based protein production.

After twenty-four generations of selecting larvae for fast growth at 35 °C, we obtained a colony (Sel35) that shows a reduction in the larval developmental time at 35 °C and in the duration of its reproductive cycle when reared at 35 °C and at 28 °C. In addition, the selected strain was tested for its susceptibility to a *Paenibacillus thiaminolyticus* strain associated with larval mortality (previously isolated from BSF larvae exhibiting a characteristic infection phenotype). Compared with the non-selected strain, Sel35 exhibiting higher resistance against the bacterial infections and was additionally selected for resistance to this pathogenic bacterial. In this presentation we will report the selection procedure and the catheterization of different biological parameters of the selected colony, revealing the potential of BSF breeding for the generation of new strains with improved properties contributing to a more sustainable and cost-effective insect production.

Investigating viral and bacterial pathogens associated with black soldier fly (*Hermetia illucens*) larval mortality in a French industrial production facility

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Abstract

Black soldier fly (BSF) rearing has gained popularity as a sustainable protein source for animal feed production. However, high-density rearing conditions may facilitate pathogen transmission and disease outbreaks, possibly leading to mortality and economic losses. While BSF-associated pathogens have been increasingly documented in recent years, comprehensive pathogen surveys in commercial facilities remain limited. This study investigated a French industrial BSF production site experiencing an episode of larval mortality. We employed two complementary approaches to characterize the pathogen community associated with larval mortality. First, targeted molecular screening was performed on asymptomatic and symptomatic larvae sampled at two developmental stages to detect and quantify six previously described BSF-associated viruses (HiIfV, HiSgV, HiLbV, HiSvV, HiInV, and HiCV) and *Paenibacillus* 16S rRNA gene. Detection rates varied considerably among pathogens, with HiInV being the most prevalent and HiCV absent from all samples. Second, metatranscriptomic analysis was conducted on the same samples. RNA-seq reads of asymptomatic and symptomatic larvae were mapped against the genomes (WGS) of two bacterial species isolated and sequenced from symptomatic larvae at the same facility: *Paenibacillus thiaminolyticus* and *Bacillus thuringiensis* subsp. *israelensis*. Differential expression analysis revealed no upregulation at 6 days post-hatching, but significant transcriptional responses at 14 days, with symptomatic larvae showing upregulation of multiple transcripts when mapped against *P. thiaminolyticus*, including genes potentially associated with virulence, while no differential expression was observed against *B. thuringiensis*. These findings reveal a complex pathogen landscape in commercial BSF production, with *P. thiaminolyticus* showing the strongest transcriptional association with larval symptoms, while tested viral pathogens appear unlikely to be primary mortality drivers. The ubiquitous presence of certain viruses regardless of health status, combined with species-specific bacterial responses, underscores the need for integrated pathogen surveillance strategies in the expanding BSF industry.

Probiotic-assisted farming: a microbiome-based approach to insect health

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Abstract

In these years, the identification of potential probiotics within microbiome of farmed insects and their application in mass reared environments have been investigated for recording the effects on insect growth, reproduction and health with the aim also to mitigate the presence of multiple stressors such as entomopathogens, temperature and high densities. Probiotic administration could be helpful to exploit insect farming, by reducing the time required to obtain the larval biomass, by sustaining the rearing and by obtaining healthy and high-quality insects beside the presence of mixed stressors. The PRIN 2022 Project InProFarm (Insect Probiotic-assisted Farming: a promising tool to enhance edible insect health and performances) explored the interactions of beneficial bacteria symbionts on *Tenebrio molitor* and *Hermetia illucens* and their ability in preserving insect health by selecting potential probiotics strains. In vitro and in vivo tests through probiotic feed administration and the evaluation of insects' performances and microbiota composition were applied for unravelling mechanisms underneath the host-microbe-diet interactions. Moreover, genes related to growth and immune pathways were analyzed for uncovering the effect of probiotics provision on insect traits of interest for breeding purposes.

The study underlines the importance to promote the development of healthy production of insects as feed and food.

Nudivirus domestication in Campopleginae wasps allows the production of Virus-like-Particles ensuring versatility of wasp virulence strategies

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Abstract

Nudiviruses, large dsDNA viruses related to baculoviruses, can be endogenized in the genomes of certain parasitoid wasp species, allowing the production of viral particles essential for parasitism success. *Venturia canescens*, an ichneumonid wasp of the Campopleginae subfamily, has endogenized in its genome dozens of alphanudivirus genes. These viral genes allow the production of Virus-like Particles (VLPs) containing virulence factors which will be injected into hosts of these wasps at the same time as wasp eggs. The description of many species phylogenetically related to *V. canescens*, in particular from the Campoplex genus, offers the opportunity to describe evolutionary processes involved in viral domestication and VLP production.

The sequencing of two Campoplex species (*C. capitator* and *C. nolae*), together with the exploration of the genome of another Campopleginae species *Rhimphoctona megacephalus*, allowed the identification of endogenized nudiviruses corresponding to the same endogenization event as the one described in *V. canescens*. Results obtained for *V. canescens* suggest that nudivirus endogenization in these parasitoid wasps has repeatedly led to the conservation of the viral RNA polymerase function, allowing the production of functional VLPs. Furthermore, electron microscopy and proteomic approaches revealed that the particles produced by *V. canescens* and *C. capitator* parasitoid wasps are very similar in morphology and composition. However, strikingly, the set of virulence proteins contained within the particles was shown to be completely different, probably due to the different selection pressures exercised by the hosts of these wasps, which have led to the recruitment of different virulence proteins to alter immune defenses. More broadly, it seems that VLPs offer wasps the opportunity to shift readily from one molecular strategy to another in the context of host-parasitoid evolutionary arms races.

Unraveling the origins of Ichnoviruses: metagenomic discovery of a relative free-living virus

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Abstract

Understanding PolyDNAviruses evolution requires tracing back their viral ancestors. While bracoviruses evolved from nudiviruses, ichnoviruses have, to date, no known viral homologs. Their viral origin is thus assumed from particle morphology and their mechanistic similarity to bracoviruses. To clarify the evolutionary origin of ichnoviruses, we searched for homologues of ichnovirus structural protein-encoding regions (IVSPERs) among the metagenome assemblies of 20 ichneumonid species, including 17 newly sequenced species. This led to the discovery of an ichnoviriform virus infecting a Cremastinae species. This virus shares sequence similarities with several families of large dsDNA viruses infecting insects, and encodes 22 homologues of Ichnovirus Structural Protein Encoding Regions (IVSPER) genes, making it the first free-living virus related to the ichnovirus donor. This finding provides the first strong genomic evidence that ichnoviruses are indeed of viral origin. Finally, based on the high sequence divergence between this virus and others, we propose that it constitutes the first member of a previously unknown viral clade that provided ichneumonid wasps with the raw material for a major genetic innovation.

Characterization of endogenous viral genes required at different stages of viral life cycle in ichneumonid wasps

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Abstract

Among endogenous viral elements that have been retained and repurposed by eukaryotic hosts, one of the most striking examples is the domesticated endogenous viruses (DEVs) used by parasitoid wasps, which enable their offspring to develop by manipulating host tissues. DEVs have been identified in thousands of wasp species and consist of multiple viral loci dispersed throughout the wasp genomes. Nevertheless, DEVs loci are activated exclusively in a specialized type of ovarian cells known as calyx cells, where viral particles are produced. However, the mechanisms and molecules involved in key steps of virion morphogenesis remain largely unknown. Our research focus on the ichneumonid wasp *Hyposoter didymator* that produce Ichnoviruses (IVs). Unlike others DEVs, IVs do not derive from a known virus integration but from an unknown viral ancestor. Thus, functional predictions for IV genes cannot be guided by sequence homology, making the study of IVs genes challenging.

To unravel the function of endogenous viral genes, our rational was to select candidate genes by identifying viral gene products associated to IVs virions. To do so we performed proteomic analysis on IV purified particles. Viral particles were chemically separated into two fractions, one fraction corresponding to the viral envelopes, and the other fraction containing the nucleocapsids. The analysis of the two fractions separated allows us to identify viral gene products associated specifically with the envelopes and/or with the nucleocapsid. Then, we used Transmission Electron Microscopy combined with RNA interference and quantitative approaches to study viral gene functions. Thus, two genes (U29 and U33) associated to the nucleocapsid fraction were shown to be involved in nucleocapsid formation. Four genes (IVSP2-2, U30, U37 and U39) involved in viral DNA replication and virion morphogenesis were identified. Together, our results allow us characterize previously unknown IVs genes involved at different steps of IVs replication cycle.

Role of bracovirus and transposable elements in a parasitoid wasp ongoing speciation.

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Abstract

Endoparasitoid wasps lay their eggs and develop at larval stages inside a specific host. Within the host, the braconid wasp reproductive success relies on highly regulated molecular host-parasite interactions involving an endogenous virus (bracovirus) used to circumvent host immune response. Recent studies have shown that endoparasitoid wasp species often constitute a complex of sister species, each one resulting from the adaptation to a particular host. This project aims to determine whether a TE is involved in the ongoing speciation of two host races of the parasitoid wasp, *Cotesia congregata* (CcC and MsT), that specialize on different hosts and often occur in sympatry. The CcC population parasitizes the caterpillar *Ceratomia catalpae* which lives on the catalpa tree, and MsT population parasitizes the caterpillar *Manduca sexta* which lives on tobacco. Differences in reproductive behavior and genetic differentiation (microsatellites and COI) indicate these two host races are beginning a speciation process.

Interestingly, a reproductive defect is observed which could contribute to reinforcing barriers between the two populations. The cross between CcC ♀ and MsT ♂ gives a fertile offspring while the reciprocal cross (MsT ♀ X CcC ♂) gives a nearly sterile offspring showing ovarian atrophy. We hypothesize that this phenotype corresponds to hybrid dysgenesis previously described in *Drosophila*, which would be induced by a TE present and active in CcC and not in MsT wasps or a more global deregulation of TE control. Hence, the TE could contribute to speciation by limiting genetic exchanges between the two populations.

Here, we present results identifying TE candidate potentially involved in dysgenesis among those showing piRNA repression in CcC and not in MsT. We present a study of ping-pong repression against TE thanks to piRNA sequencing of samples collected over several years.

This study provides the first analysis of ping-pong-mediated repression across germinal and somatic tissues.

RISC-bound small RNA-seq and degradomics in three leaf beetles reveal evolutionary insights into gene regulation

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Abstract

Diverse small RNAs (sRNAs) play important roles in gene regulation and immunity in insects. sRNA sequence studies have been instrumental in identifying diverse sRNAs, including microRNAs (miRNAs) and small interfering RNAs (siRNAs), that are differentially expressed across conditions such as developmental stages. However, cross-species sRNA investigations and their functional validation, including target regulation, remain major gaps in the literature. Here, we performed RISC-bound sRNA seq to investigate biologically active sRNAs in the adult stage of three leaf beetles, namely the cabbage stem flea beetle (*Psylliodes chrysocephala*), Colorado potato beetle (*Leptinotarsa decemlineata*), and hop flea beetle (*Psylliodes attenuatus*), which are all economically important pests in Europe. This analysis enabled us to identify both divergent and conserved sRNAs across these three leaf beetles. Next, we performed RNA degradomics in the same beetles to capture nascently cleaved RNA transcripts in order to validate the targets of the identified sRNAs. This analysis also identified common and divergent RNA targets of the RISC-bound sRNAs. Overall, this is the first study to investigate both RISC-bound sRNAs and their targets across related insect species, and it reveals novel molecular insights with implications for innovative pest control strategies.

Catching them all: Assessing the diversity and evolution of Iflaviridae genomes found in publicly available Lepidoptera sequencing data

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Abstract

The Iflaviridae family consists of small, non-enveloped, positive-sense RNA viruses. They primarily infect insects, including honeybees and agriculturally important species of the order Lepidoptera, including butterflies and moths. Some iflaviruses can alter the susceptibility of their host to other viruses or can potentially be used as biological control agents. Here we use the Serratus infrastructure to identify publicly available RNA sequencing data from the order of Lepidoptera that indicate to contain Iflaviridae. We develop a pipeline including host genome mapping, assembly, and a BLASTx search to reconstruct Iflaviridae genomes and to assess their completeness. We found 1,548 complete genomes across 1,483 transcriptome data sets that span 56 different host species (nine species with at least 30 data sets). Based on the ICTV species criteria, 835 virus genomes can be assigned to one of seven Iflavirus species and 170 do not have a closely related genome in NCBI, constituting potentially novel Iflaviridae species. Additionally, we developed an innovative patching approach based on a reference genome to include incompletely assembled contigs, resulting in 240 patched genomes. We reconstruct a comprehensive Iflavirus phylogeny and highlight potential host switches, where highly similar viruses have been found in the transcriptomes of different host species. To zoom into the evolution of selected iflavirus species, we then infer selection and recombination in the 4 iflavirus species with at least 30 genomes available. Our study helps to create a better understanding of the diversity of known iflaviruses, the host range of the viral family, and the evolution within iflavirus species. Our approach highlights the opportunity to reconstruct (novel) virus genomes from publicly available sequencing datasets incidental to the goals of the original studies, which can be applied to further viral families in the future.

Widespread and diverse densovirus-derived endogenous viral elements reveal evolutionary insights in the whitefly *Bemisia tabaci*

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Abstract

Endogenous viral elements (EVEs) are viral sequences integrated into host genomes and represent molecular records of historical virus-host interactions during evolution. The whitefly *Bemisia tabaci* is a globally important agricultural pest and a model of rapid evolution, consisting of more than 40 cryptic species. Among them, the MEAM1 and MED cryptic species are the most invasive and widely distributed.

In this study, we conducted a systematic analysis of 51 *B. tabaci* genomes, including 15 published reference genomes and 36 additional genomes assembled de novo from raw sequencing data retrieved from NCBI. We identified numerous EVEs derived from densoviruses (subfamily *Densovirinae*) in whitefly genomes. Comparative genomic analyses revealed substantial variation in the integration patterns of these EVEs among *B. tabaci* cryptic species. Phylogenetic and orthology-based analyses further indicated that densovirus-derived integration events have recurrently throughout the diversification of *B. tabaci* cryptic species.

Notably, we identified an ancient integration event that can be traced to the common ancestor of all *B. tabaci* cryptic species, giving rise to an EVE that is highly conserved across the entire species complex. Furthermore, several integration events were found to be specific to *B. tabaci* MEAM1 and MED. These EVEs are capable of encoding complete open reading frames or producing small RNAs. Functional analyses using RNA interference demonstrated that these EVEs play biological roles in *B. tabaci* MEAM1 and MED, suggesting that EVEs may contribute to the invasiveness and adaptive differentiation of whiteflies.

Finally, extending our analysis to 484 high-quality arthropod reference genomes revealed the widespread presence of densovirus-derived EVEs across arthropod lineages. Together, our results provide new insights into the evolutionary significance of EVEs in arthropods.

Tracing Thermal Adaptation in *Aedes albopictus*: Evidence from a North–South Gradient in Europe

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Abstract

The Asian tiger mosquito (*Aedes albopictus*) has rapidly expanded across Europe, establishing stable populations from southern to northern latitudes. Understanding whether this species exhibits local thermal adaptation within its invasive range is crucial for better understanding biological invasions, improving predictive models of *Ae. albopictus* spread and for designing targeted control strategies. In this study, we investigate potential adaptive differentiation among *Ae. albopictus* populations collected along a latitudinal gradient spanning from southern Italy, northern Italy and central Germany. Laboratory colonies have been established for each of the three populations using either wild-caught females continuously introduced during the summer season or from sampled eggs. We quantified key life-history traits (e.g., development rate, survival, fecundity) under both constant and fluctuating temperature regimes (13°C–33°C), representing different ecological realities across Europe. By comparing performance across these thermal conditions, we aim to identify whether local populations exhibit divergent responses indicative of thermal adaptation. The results will provide empirical evidence on the role of thermal variability in shaping population-level differences, contributing to a better mechanistic understanding of *Ae. albopictus*'s invasive success under ongoing climate change.

Larval environments reshape mosquito disease risk via phenotypic and molecular plasticity

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Abstract

Early-life environmental conditions can exert profound, lasting effects on adult phenotypes, with major consequences for fitness and disease transmission, especially in holometabolous insects such as mosquitoes, which are key vector species. Yet the molecular mechanisms by which juvenile environments shape adult physiology and behavior through transstadial effects remain largely unresolved. Here, we varied intraspecific competition levels to quantify adult body size, survival, reproductive output, host-seeking behavior, olfactory neurophysiology, and vector competence in the mosquito *Aedes aegypti*. Using transcriptomic profiling and integrative network analyses, we identify seven regulatory hub genes whose expression is strongly associated with size-dependent variation in olfactory behavior, reproductive investment, and Zika virus transmission potential. These hub genes belong to gene modules enriched for functions in chemosensory processing, metabolic regulation, and signal transduction, revealing a molecular framework mediating environmentally induced plasticity across metamorphosis. Integrating these empirical findings into a transmission model, we show that incomplete larval control can inadvertently increase outbreak risk by producing larger, longer-lived, and more competent vectors. Our results uncover molecular mechanisms underpinning phenotypic plasticity in disease vectors and highlight the critical need to account for transstadial effects in models of vector-borne disease transmission.

Characterization of the immune gene *Aea102* in *Aedes albopictus* larvae and analysis of transcriptional changes in larvae exposed to *Bacillus thuringiensis*

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Abstract

Mosquitoes are responsible for vector-borne diseases not only in humans but also in livestock and pets. Species such as *Aedes albopictus*, the Asian tiger mosquito, are now largely spread across the world, due to globalization and climate change. As they are vectors of many arboviruses, their control is a priority in an integrated vector management strategy. This is mainly achieved thanks to the use of bioinsecticides targeting aquatic larvae, especially those based on the entomopathogen *Bacillus thuringiensis* var. *israelensis* (*Bti*). However, the scarce persistence of these formulates in the environment is leading to frequent applications and higher effective doses, which cause a decrease in insect susceptibility and may promote resistance outbreaks. In phytophagous insects, the toxicity of *Bt* formulates has been successfully enhanced with RNA interference (RNAi), a mechanism that allows to silence specific immune genes through the oral administration of dsRNAs. To exploit a similar strategy to control mosquito populations with *Bti*, identification of immune genes involved in the larval response and a better understanding of the RNAi mechanism are needed. Transcriptomic analyses on *Bti*-exposed larvae were conducted to unveil larval response to the entomopathogen and individuate potential target genes to be silenced by RNAi and enhance *Bti* products efficacy. Research in our laboratory has highlighted the importance of the immune gene *Aea102* in *Ae. albopictus* larvae. RT-qPCR performed on mosquito larvae exposed to different doses of *Bti* showed the involvement of this gene in immune responses. Its mature mRNA sequence has been reconstructed, revealing the presence of two alternative transcripts at the 5'UTR end, differentially expressed during the development of the insect and between males and females. Research on its function is ongoing, but expression analyses and in situ hybridization in mosquito larvae support the idea that this gene might have other roles besides the immune one.

Assessment of Wolbachia Circulation in Wild Sand Fly Populations from Northern Italy

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Abstract

Vector-borne diseases are emerging and re-emerging infections transmitted by haematophagous arthropods such as sand flies, mosquitoes, and ticks, causing more than 700,000 deaths annually. Increasing attention has focused on vector control strategies targeting endosymbiotic bacteria—particularly Wolbachia—due to their ability to manipulate host reproduction, alter vector competence, and serve as self-disseminating platforms for introducing transgenes into natural populations.

Given its potential applications in vector management, this study investigated natural Wolbachia infections in field-collected sand fly populations from the Lombardy region of Northern Italy. Sand flies were collected using CO₂-baited traps between June 2023 and September 2025 across multiple sites. Samples were pooled (1–28 specimens) by sex, collection date, and location; males were identified morphologically, while females were screened molecularly for Wolbachia.

Positive samples were characterized using Multi-Locus Sequence Typing (MLST) targeting five genes (*coxA*, *gatB*, *ftsZ*, *fbpA*, and *hcpA*) and sequenced using the Oxford Nanopore MinION platform. Among the 124 pools analyzed, *Phlebotomus* populations exhibited a 38.7% Wolbachia infection rate, with *Phlebotomus perniciosus* being the predominant species collected, based on identification of males. Twelve positive samples were successfully sequenced, and COI analysis confirmed that all belonged to *Ph. perniciosus*. Their multilocus profiles fell within supergroup B and did not match any known sequence type (ST), showing the closest similarity to the Wolbachia strain reported from *Tribolium confusum*. However, sequencing of the *wsp* gene revealed 100% identity with a previously described *Ph. perniciosus* Wolbachia *wsp* sequence. MLST profiles were consistent across sex, location, and collection date. Sequences were deposited in GenBank under accession numbers PX531184–PX531242.

To our knowledge, this is the first report of natural Wolbachia infections in sand fly populations in Italy. Expanding our understanding of these associations is crucial, as future vector-borne disease control strategies may increasingly rely on Wolbachia-based approaches as alternatives to chemical insecticides.

CLIMOS – a coordinated effort to study sand flies and sand fly-borne pathogens under the ongoing climatic change in Europe and adjacent regions

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Abstract

CLIMOS project (Climate Monitoring and Decision Support Framework for Sand Fly-borne Diseases Detection and Mitigation with Cost-benefit and Climate-policy Measures) studied climatic, environmental, demographic, and epidemiologic characteristics associated with sand fly presence and abundance at different geographical scales across Europe and neighbouring countries. It collated historical datasets and active sand fly field surveillance in a coordinated and standardized effort, followed by screening for sand fly-borne pathogens. This data fed into epidemiological-climatic predictive mathematical models of realistic human-induced climatic changes scenarios to develop an early warning system for infection and disease, designed with the input from partner public health ministries for public use.

A coordinated and standardized sampling effort using a common protocol for sample trapping and processing was performed in 12 countries (Portugal, Spain, France, Italy, Slovenia, Croatia, Greece, Germany, Austria, Czech Republic, Turkey and Israel) during the 2023 and 2024 sand fly seasons (April-November), providing a unique standardized dataset on sand fly distribution, species composition and seasonality. Identification of host blood in engorged females revealed trophic affinities of various species in different regions. Screening for sand fly-borne pathogens, namely *Leishmania* spp. and phleboviruses, was performed after an external quality assessment (EQA) among participating partners. Presented data represent a unique dataset of sand fly occurrence, feeding patterns and involvement in circulation of sand fly-borne pathogens.

The CLIMOS consortium was co-funded by the European Commission grant 101057690 and UKRI grants 10038150 and 10039289. The six Horizon Europe projects, BlueAdapt, CATALYSE, CLIMOS, HIGH Horizons, IDAlert, and TRIGGER, form the Climate Change and Health Cluster.

Influence of land use on mosquito communities in central Panama

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Abstract

With the highest mosquito species diversity of Central America, Panama offers a unique opportunity to study how a diverse mosquito assemblage responds to forest degradation. Land use changes, in particular, reforestation projects, naturally recovering forest areas, and human settlements, are strongly associated with vector-borne disease risk. However, a basic understanding of how specific land use types influence mosquito ecology in a mosaic of tropical forest landscapes is still lacking.

This research assesses the mosquito community at the Smithsonian Tropical Research Institute's Agua Salud Project, a research site focused on biodiversity restoration, ecosystem services, and disease ecology. Agua Salud encompasses lowland tropical rainforest habitats of varying ages and land use histories, making it an ideal location to investigate how naturally and artificially regenerating forest habitats influence mosquito ecology. We focus on species that lay their eggs in natural (tree holes, bromeliads, and plant leaves) or artificial (tires and buckets) water-holding containers. Forest disturbance is expected to have an impact on mosquito demography by altering the availability of these containers and their water chemistry. This shapes oviposition opportunity for vector and non-vector species at different sites, determining the odds of disease epidemics.

We accomplished this by establishing four discrete land-use types (plantation, secondary forest, mature forest, and town) and completed three rounds of oviposition trap collections (bamboo, coconut, and plastic container) during the rainy season of 2025. Preliminary results suggest that there are differences in the species composition and abundance pattern of vector and non-vector species across land-use types. Findings can provide insights for preventing vector-borne disease outbreaks by implementing restoration strategies that reestablish forest biodiversity but lessen mosquito breeding opportunities.

How temperature shapes life-history traits and infection potential in an emerging invasive mosquito

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Abstract

Over the past decade, Europe has witnessed the invasion and establishment of several *Aedes* mosquito species, including *Aedes koreicus*, first detected in Belgium in 2011 and now established in multiple temperate regions, notably northeastern Italy. Its ability to colonise cooler climates, likely driven by higher cold tolerance, raises concerns regarding its invasive potential and ecological and public health impacts. Temperature is a fundamental driver of insect survival, development and reproduction, and therefore plays a central role in shaping mosquito population dynamics and geographic spread.

Here, we examined how temperature influences both the thermal biology and pathogen susceptibility of *Ae. koreicus*. Laboratory rearing conditions were optimised, and the effects of constant temperatures ranging from 16 °C to 32 °C were assessed. Temperatures above 28 °C were suboptimal, whereas temperate conditions between 20 °C and 24 °C supported optimal performance across multiple life-history traits, including development time, survival, adult size and reproductive output. These findings align with the species' successful establishment in cooler regions of Europe.

We then assessed whether *Ae. koreicus* can support viral infection across environmentally relevant temperatures. Mosquitoes maintained at 20 °C, 24 °C or 28 °C were orally challenged with a model insect alphavirus. Viral infection and dissemination were assessed across multiple post-infection time points using molecular and cell-based assays. Infectious virus was detected in the salivary glands of a subset of mosquitoes at all temperatures tested, indicating that *Ae. koreicus* can support viral replication and potential transmission even under cooler conditions.

Together, these results show that *Ae. koreicus* is well adapted to temperate environments and remains biologically competent across a broad temperature range. This work highlights how temperature-driven life-history traits can shape the invasion success and ecological relevance of emerging mosquito species in Europe.

Mosquito sugar feeding: a neglected aspect of their biology and tool for their control.

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Abstract

Feeding on plant-derived sugars is an essential component of mosquito biology, affecting key aspects of their lives such as survival, metabolism, and reproduction. *Aedes aegypti*, *Ae. japonicus* and *Ae. albopictus* are three invasive mosquito species in the US, and are vectors of diseases such as dengue fever, chikungunya, and Zika. These species live in heavily populated, (sub)urban areas, where they have high accessibility to various hosts, including humans, as well as to plants in backyards and public landscapes. However, the range of plants that are suitable sugar sources for these species remains to be described, despite the importance of understanding what plants may attract or repel mosquitoes to inform citizens and municipal authorities accordingly. In this talk, I will be summarizing some of the work we have conducted in the field as well as under laboratory conditions, showing that (native and) invasive mosquito species can exploit a broader range of plants than originally suspected, including wild and ornamental plants from diverse phyla, throughout the Spring, Summer and Fall seasons.

Unlocking crosstalk regulations in *Aedes aegypti* mosquitoes

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Abstract

As a vector of several human pathogens, *Aedes aegypti* mosquitoes represent a serious public health threat worldwide. We have been investigating the mechanistic regulation of ammonia metabolism in *Ae. aegypti* using a multidisciplinary approach involving the application of target mass spectrometry-based metabolomics, stable-label isotope tracing and reverse genetics. We have found unique pathways and crosstalk signaling regulation within ammonia pathways and between glucose and ammonia fixation, assimilation and excretion pathways. We recently reported that RNAi-mediated knockdown of ornithine decarboxylase (ODC) triggers an impaired nitrogen metabolism causing high mosquito mortality. To better understand the metabolic networks between polyamines and ammonia pathways, we are evaluating the role of spermidine synthase (SdS) and spermine synthase (SmS) using qPCR, western blotting, RNAi and target mass spectrometry metabolomics. We have observed that the enzymes SdS and SmS exhibit differential gene and protein expression patterns in mosquito tissues dissected from sugar- and blood-fed mosquitoes. RNAi-mediated silencing of SdS causes a pronounced decrease in SdS protein expression as expected, but also a significant reduction of SmS protein expression. RNAi-mediated SmS deficiency results in a significant decrease in SmS and SdS protein expression. Moreover, the silencing of SdS or SmS in blood-fed females impairs blood meal digestion, delays serine protease expression and reduces nitrogen waste excretion. In addition to altering nitrogen metabolite profile, ODC knockdown decreases SdS and SmS gene and protein expression. In correlation with these data, SdS or SmS silencing results in a reduction of transcript levels of ODC and several other transcripts of genes encoding proteins involved in polyamine and ammonia pathways. Our findings reveal how mosquitoes tightly regulate polyamine metabolism by crosstalk signaling mechanisms and highlight the complexity of the metabolic networks in *Ae. aegypti* mosquitoes.

Molecular basis of TRPA-dependent sensory modulation in Triatomines

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Abstract

Chagas disease is amongst the ten most important vector-borne human diseases, affecting the health of millions of people across the Americas. Its etiological agent, the protozoan parasite *Trypanosoma cruzi*, is hosted and transmitted endemically by triatomine insect vectors (Hemiptera: Reduviidae) notably species of the genera *Rhodnius* and *Triatoma*. These specialized haematophagous vectors seek human hosts relying on diverse sensory stimuli including heat^{1,2,3}.

TRPAs, Transient Receptor Potential Ankyrin channels, are a diverse insect gene family of cation-gated thermosensitive sensory receptors (e.g. Painless, Pyrexia, TRPA1, TRPA5), typically also activated by diverse natural chemical ligands. If the number and types of TRPAs vary depending on insect Orders, their physiological properties also reflect the diversity of insect sensory adaptations. However, despite the strong thermal reliance of triatomines for host seeking⁴, little is known about the molecular properties of triatomine TRPAs in temperature sensing, or their chemical ligands^{4,5}. Recently, we showed that the TRPA5 subfamily, absent in dipteran genomes, has diversified in other Orders including Hemiptera. Specifically, we revealed that in *Rhodnius prolixus*, TRPA5, a channel broadly expressed in peripheral sensory organs^{5,6}, exhibits high thermosensitivity when expressed *in vitro*⁵, suggesting a role in heat sensing.

Here, we establish stable TRP-FlpIn293 cell lines and leverage pharmacological fluorescent calcium assays to further examine the activation of *R. prolixus* and *Triatoma infestans* TRPA channels (TRPA1, Pain, TRPA5) and their isoforms by natural ligands, including biologically active, candidate repellent compounds recently identified in behavioural assays. Overall, our findings offer new insights into triatomine TRPA channel thermochemical sensitivity and help advance our understanding of the molecular mechanisms underlying triatomine sensory biology.

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Lifespan and biodemographic characteristics of *Aedes albopictus* and *Culex pipiens* biotypes

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Abstract

Aedes (Stegomyia) *albopictus* and *Culex pipiens* biotypes (*Culex pipiens* f. *pipiens*, *Culex pipiens* f. *molestus*) transmit pathogenetic arboviruses such as West Nile virus, Zika virus, chikungunya dengue fever affecting millions of people worldwide. They have anthropophilic (*Ae. albopictus*, *Culex pipiens* f. *molestus*) and ornithophilic (*Culex pipiens* f. *pipiens*) habitats with diurnal and nocturnal blood feeding regimes, necessities for egg production. Their biology determines the disease transmission and the development of effective control strategies. The purpose of the present study was to clarify how mating affects adult lifespan (male, female) and how blood meal frequency affects not only adult lifespan (females) but also their reproductive characteristics: egg production, number of pupae, pupation percentage, number of male offsprings, number of female offsprings, ratio of male/female offsprings. The population was collected at the vicinity of Volos and Larissa, Thessaly, Greece and the experiments were conducted under controlled laboratory conditions. Lifespan had a significance between virgin and mated males and females among all the species. The number of blood meals (one) significantly reduced lifespan of *Culex pipiens* f. *molestus* and *Culex pipiens* f. *pipiens* compared to *Ae. albopictus* almost 25, 13 days respectively. Lifespan of *Ae. albopictus* after two blood meals was lower than those of *Culex pipiens* f. *molestus*. There are significant differences in egg production among species. *Culex pipiens* f. *pipiens* with one blood meal produced almost 20 more eggs than *Culex pipiens* f. *molestus* and 30 more than *Ae. albopictus*. *Culex pipiens* f. *molestus* without blood meal produced more eggs than these of each species with one blood meal. The second blood meal of *Ae. albopictus* doubled egg production. The knowledge of the biology of mosquitoes and especially as far as the effect of blood meal provides valuable information for the development of mosquito population models and effective mosquito control programs.

Spiroplasma alters male fitness and reproduction in the tsetse fly *Glossina fuscipes fuscipes*

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Abstract

Glossina fuscipes fuscipes (*Gff*) is a riverine species of *Glossina* (commonly known as tsetse flies) reported as the primary vector of Human African Trypanosomiasis in Uganda, a disease caused by trypanosome. Tsetse flies display several peculiar characteristics, including adenotrophic viviparity as reproductive strategy, where females give birth to fully developed larvae, a strictly hematophagous diet, and a highly streamlined microbiota. Among microbes characterizing their microbiota, *Wigglesworthia*, *Sodalis* and *Wolbachia* are the most studied, as they are involved in fly physiology, survival, reproduction and vector competence. Recently, a new bacterium, *Spiroplasma*, has been identified in some population of tsetse flies belonging to the *Palpalis* subgroup where it renders the host fly refractory to trypanosome co-infection. In this study, we mainly investigated the effect of *Spiroplasma* on *Gff* male reproduction, focusing on mating fitness and molecular aspects, where we found that the infection has a profound impact at multiple levels. We observed modulation of mating behavior, indicative of non-random mating, as well as an alteration in the cuticular hydrocarbons profile. Moreover, transcriptomic and proteomic analysis on *Gff* reproductive tissues revealed a significant negative influence of *Spiroplasma* on testes, affecting processes involved in spermatogenesis, sperm motility, male fertility and energy metabolism. Interestingly, we also detected alterations in the composition of the testicular microbiota related to *Spiroplasma*-infection. In conclusion, this study provides new insight into the *Gff*-*Spiroplasma* interaction and represents an important finding to consider in the development of potential control strategies against tsetse flies and in efforts to limit trypanosomiasis.

The virome of *Culex modestus* mosquitoes changes during early generations of laboratory colony establishment

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Abstract

Arthropod-borne viruses (arboviruses) and their vectors have garnered increased attention over the last decades, with globalisation and climate change aiding their spread and infectivity. Whether or not a given mosquito species is a suitable arbovirus vector depends on multiple factors, including the mosquito microbiome. Especially the impact of insect-specific viruses (ISVs) has been of interest for their potential in arbovirus control. In turn, the microbiome is influenced by the mosquito environment, complicating the representative power of experiments performed on laboratory-reared mosquitoes. Nonetheless, early generations of lab-reared mosquitoes are frequently used as proxy for field-caught specimens to allow for larger sample sizes and homogeneity. So far, few experiments have investigated the changes during lab colonization, especially in the mosquito virome.

In the case of *Culex modestus* mosquitoes, a species that has lately been reported as a possible vector for Usutu virus, its microbiome composition and the influence of lab-rearing is still widely understudied. We investigated both bacteriome and virome composition of field-caught *Cx. modestus* mosquitoes during the first nine generations of laboratory colony establishment. For this, single mosquitoes were processed to allow for both 16S and virus-enriched whole transcriptome NGS analyses in parallel.

While the bacteriome seemed to remain stable across the investigated generations, virome diversity decreased rapidly very early on. While eight RNA viruses were found in total, by the third generation only two could still be detected. These suspected insect-specific viruses are one picorna-like virus closely matching an ISV known to infect mosquitoes, as well as one potentially novel toti-like virus. Their prevalence and relative abundance increased progressively across generations, indicating a vertical transmission mode. Further research into these ISVs holds promising future perspectives for understanding the complex interplay between arboviruses and the mosquito microbiome, as well as for the implementation of ISVs in arbovirus control.

Harnessing bacteriophage-derived endolysins to reduce mosquito attractiveness by selectively killing skin bacteria

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Abstract

When approaching potential blood hosts at close range, body odours play a critical role in the final host selection of mosquitoes. Many of these odours are produced by skin bacterial communities, and studies indicate that mosquitoes are more attracted to hosts with lower diversity and higher density of skin bacteria. Specific bacterial species or strains can further enhance or reduce mosquito preference. Especially, the presence and abundance of *Staphylococcus epidermidis* is well known to increase the attractiveness of humans towards mosquitoes.

In this study, we investigated the influence of *S. epidermidis* the attraction of the yellow fever mosquito *Aedes aegypti*. For this purpose, we used a two-choice video tracking setup to study *Aedes aegypti* preferences for bacterial and (humanised) mouse volatiles. Additionally, we harnessed newly developed bacteriophage-encoded lysins to selectively kill *S. epidermidis* to potentially reduce attractiveness to mosquitoes. We evaluated the killing efficiency of these endolysins and studied how their application affected the mosquito attractiveness and volatile profiles of bacterial suspensions. Hereby our study sheds light on how selective changes in bacterial communities directly influence mosquito preference.

Bringing worms and flies together: *C. elegans* as an experimental platform for the characterisation of insect behaviours and pesticide targets

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Abstract

New approaches for the control of insect pests are urgently required. This is in part due to the emergence of resistance to the chemicals that are used as pesticides. This demands a better understanding of the distinct properties of neural signalling that are essential to invertebrate survival as well as the modifications that lead to resistance development. Currently this goal is largely served by highly specialised labs with access to an insectarium. Moreover, characterisation of insect receptors engaged in neural signalling is technically challenging given the large and divergent gene families involved. To facilitate this, we are developing a new transgenic platform for characterisation of insect receptor ion channels using the model genetic organism *Caenorhabditis elegans*. We, and others, have previously shown that *C. elegans* will support the functional expression of ion channels from other nematodes, molluscs, *Drosophila* and even human. We are extending this approach to include expression of non-model insect receptors. As a proof of concept, we have chosen the well characterised GABA receptor subunit Phh-RDL from the human louse *Pediculus humanus humanus* for expression in the *C. elegans* pharyngeal system. Ivermectin is a widely used pesticide for invertebrates and one of its main targets is the RDL pentamer of the GABA receptor in insects. This paradigm permits functional readouts of receptor activation with the natural ligand GABA and ivermectin using the electrophysiological recordings from the *C. elegans* pharynx called electropharyngeograms (EPGs). This approach has potential to be hugely informative in understanding key features of drug-receptor interactions as well as the modifications on the receptor leading to resistance development.

This project benefited from support from Le Studium.

Insecticide resistance status of Spanish medfly populations over the last twenty years

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Abstract

The development of resistance to available insecticides is one of the main threats for Medfly control in citrus orchards in Spain. Current management strategies rely on the application of the insecticides spinosad and lambda-cyhalothrin as bait sprays (mixed with a food attractant) and the deployment of bait stations (traps that attract medflies by olfactory and visual stimuli) coated with pyrethroids (deltamethrin, lambda-cyhalothrin or esfenvalerate). We have analyzed the resistance status of field populations from eastern Spain to available insecticides for the last 20 years, and found resistance to malathion from 2004, to lambda-cyhalothrin from 2009 and to deltamethrin traps from 2018. In all cases, resistance was already widespread when first detected, probably related to the high rates of gene flow among Spanish Medfly populations. Field resistance to spinosad has not been reported, but resistance alleles to this insecticide have been detected in field populations. Thus, we are in a situation in which insect resistance management (IRM) strategies need to be implemented to prevent control failures. The elucidation of the mechanisms of insecticide resistance to malathion (a point mutation and a heterologous duplication in the acetylcholinesterase gene) and spinosad (mutations and/or deletions generating premature stop codons at the gene coding for the target alpha 6 subunit of the nicotinic acetylcholine receptor) has allowed the development of molecular tools for the detection of resistant alleles in field populations. In addition, the identification of the main factors involved in resistance evolution has contributed to the generation of evolutionary models aimed to forecast the efficacy of different IRM strategies. Our contributions intend to optimize the efficacy of insecticide-based treatments and the design of appropriate IRM strategies that avoid unnecessary pesticide applications.

Identification of mutations and associated intron variants in mosquitoes resistant to insecticides

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Abstract

Mosquitoes of *Aedes* and *Anopheles* species are important vectors of Dengue virus and malaria, respectively, as well as other diseases. Vector control by the use of insecticides is still a major strategy in managing these diseases. However, the effectiveness of insecticides is being undermined by resistance. In Cambodia, metabolic resistance specifically involving P450 monooxygenases appears to be predominant in *Ae. albopictus* mosquitoes as shown by piperonyl butoxide (PBO) restoring the efficacy of deltamethrin and permethrin [1]. These mosquitoes showed a lack of resistance-conferring mutations in the voltage-gated sodium channel gene (*vgsc*). In contrast, *vgsc* mutations are highly prevalent in *Aedes* mosquitoes from the neighboring country, Lao People's Democratic Republic [2]. Also, almost every *Anopheles* mosquito from Nigeria harboured at least one *vgsc* mutation as well as mutations in the GABA receptor gene, *Rdl*, and the glutathione S-transferase gene, *gst**e*2. In both *Aedes* and *Anopheles* mosquitoes, *vgsc* mutations were associated with particular variants in the preceding intron. Knowledge of the prevalence and mechanisms of insecticide resistance can prove invaluable for informing future strategies for vector control.

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Using functional genetics in malaria transmitting mosquitoes to validate the role of genes in insecticide resistance and provide insight into the phenotype's complexity

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Abstract

Despite significant progress, malaria remains a major cause of mortality and morbidity in Africa causing an unacceptably high number of 597,000 (in 2024) deaths annually. Prevention of malaria relies primarily on controlling the mosquito-vectors through the use of insecticides, applied as insecticide treated bed-nets and indoor residual spraying. However, the extensive and prolonged use of a limited number of insecticidal compounds has exerted intense selection pressure on mosquito populations, driving the rapid emergence and spread of insecticide resistance. Research into the factors underlying insecticide resistance has shown in most cases the co-existence of multiple mechanisms, including target site mutations and over-expression of detoxification enzymes (eg. P450s). More recently additional genes have been associated with resistance including ABC transporters and genes involved in the cuticle formation. We are using functional genetics (CRISPR, Gal4-UAS system) to validate the role of genes and single nucleotide polymorphisms in pyrethroid resistance, as well as measure their relative contribution. We also combine different resistance mechanisms within a susceptible genetic background and evaluate their combined impact on the resistance phenotype. Our findings enhance the understanding of the genetic basis of insecticide resistance and provide important information on the diagnostic value of various markers, whether present individually or in combination, in field mosquito populations. Ultimately, this work provides a stronger foundation for evidence-based strategies in insecticide resistance management.

Advances in Genetic Engineering of *Frankliniella occidentalis*

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Abstract

The discovery of CRISPR-Cas9-based genome editing has revolutionized genetic engineering in various fields. However, its application can still be challenging, particularly in non-model organisms, including many major agricultural pests. Thrips (order Thysanoptera), especially *Frankliniella occidentalis*, are among the most damaging agricultural pests worldwide. They transmit plant viruses of the family Tospoviridae, cause extensive feeding damage across a wide range of crops, and are notorious for their rapid development of insecticide resistance. In addition, their microscopic size and complex biology have limited the development of precise genome-engineering tools.

Recently, a highly efficient CRISPR/Cas9-based approach (SYNCAS) was developed that allows efficient gene editing in *F. occidentalis*. We used this method to knock-out the acetylcholine receptor $\alpha 6$ subunit (nAChR $\alpha 6$), thereby validating its role in spinosad and spinetoram resistance.

Because the knock-in of specific mutations is still more challenging with relative low frequency, we studied the DNA repair pathways of *F. occidentalis* with the aim of improving knock-in efficiencies. Several knockout lines in double-strand DNA break repair pathways were created. To facilitate rapid and reliable phenotyping of these lines, we developed a reporter system that enables efficient screening of both gene knock-out and knock-in events. This study aims to fill a pre-existing gap in molecular entomology and to support new perspectives for both fundamental research and sustainable pest management.

Investigation of the response of western flower thrip, *Frankliniella occidentalis* to pesticides in pepper cultivation facilities treated with recommended concentrations of pesticides

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Myeonghwan KIM, Yi-seul KIM, Donghun KIM, Do-Ik KIM, Young Cheol KIM, Gyung Moo KIM, Na Young JIN, Doo-hyung LEE, Jun Soo PARK

Abstract

Chili peppers are one of the most important seasoning vegetables worldwide. The insecticidal responses of the western flower thrips (WFT) collected from 180 pepper farms in 60 cities and counties across South Korea to eight insecticides (abamectin 1.8% EC, acrinathrin 5.7% SC, acetamiprid 5% SL, dinotefuran 10% SL, cyclaniliprole, chlorfenapyr 5% EC, emamectin benzoate 2.15% EC, spinetoram 5% WG) were investigated. The insecticide response of the WFT varied depending on the type of insecticide and the farm when the WFT were collected. The proportion of farms with insecticidal rates below 30% at recommended concentrations was in the order of acrinathrin > acetamiprid > cyclaniliprole > dinotefuran > abamectin > spinetoram > chlorfenapyr > emamectin benzoate. The proportion of farms with insecticidal rates above 80% at recommended concentrations was in the order of spinetoram > emamectin benzoate > chlorfenapyr > abamectin > cyclaniliprole > acetamiprid > acrinathrin. The degree of pesticide response of individual farms showed a similar tendency to the degree of pesticide response in the region.

Spatio-temporal spread and evolution of pyrethroid resistance in cabbage stem flea beetle, *Psylliodes chrysocephala*, a major pest in European winter oilseed rape

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Abstract

Cabbage stem flea beetle, *Psylliodes chrysocephala* L. (Coleoptera: Chrysomelidae) is a major pest of winter oilseed rape in several European countries such as Germany, France, UK and Poland, and particularly feeding on young emerging plants in autumn. Over the last decades, pyrethroid insecticides have been foliarly applied to control flea beetle outbreaks. Recent pyrethroid control failures, especially triggered by the widespread ban of neonicotinoid seed treatment applications, confirmed the continuous evolution of target-site mutations in voltage-gated sodium channels. Over the last decade we genotyped more than 2000 field-collected cabbage stem flea beetle populations and detected - along with the well-known kdr (L1014F) allele - an increasing abundance of novel super-kdr mutations (L1014F + M918L, L925I and/or T929N/I) conferring much higher levels of pyrethroid resistance than kdr in isolation. Indeed, these mutations are sex-linked in cabbage stem flea beetle (X0 sex determination system), i.e. one resistance allele in males confers high levels of resistance. This study reviews previous and more recent findings on polymorphisms in the para-type voltage-gated sodium channel gene of cabbage stem flea beetle and their impact on pyrethroid resistance. Furthermore, we recombinantly expressed different mutant variants of flea beetle voltage-gated sodium channels to investigate the impact of individual mutations and combinations thereof. Effective and sustainable control of cabbage stem flea beetle in European winter oilseed rape is an increasingly challenging task due to the lack of effective alternative modes of action.

The mode of action of neonicotinoid insecticides on insect nicotinic acetylcholine receptors highlights complex intracellular calcium mechanisms

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Abstract

Insect neuronal nicotinic acetylcholine receptors are transmembrane receptors that play a key role in the development and synaptic plasticity of both vertebrates and invertebrates, and are considered to be major targets of neonicotinoid insecticides. We used dorsal unpaired median neurons, which are insect neurosecretory cells, in order to explore the intracellular mechanisms leading to the regulation of insect neuronal nAChRs in more detail. Insect nicotinic acetylcholine receptors are up- and down-regulated by different protein kinases, such as protein kinase A, C and G. Other kinases such as calcium calmodulin-dependent protein kinases (CaMKII) and CaMK kinase are also involved, leading to the release of calcium through the endoplasmic reticulum, or the dysfunction of mitochondrial activity. This complex intracellular mechanism influences nicotinic acetylcholine receptor function, and neonicotinoid pharmacology. Our studies expose the importance of intracellular calcium pathways in the regulation of insect neuronal nicotinic acetylcholine receptors, and their role in the mode of action of neonicotinoid insecticides. We propose that these intracellular mechanisms could be essential for the development of more specific compounds in the future, and should therefore be studied further.

Insecticide resistance in a major invasive species, *Spodoptera frugiperda*, the role of CYP9As

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Abstract

Spodoptera frugiperda is a polyphagous lepidopteran and a major crop pest. Native to the American continent, it has gradually invaded the world in recent years and has been detected in Europe since 2023. With resistance detected for 47 active ingredients listed on the Arthropod Pesticide Resistance Database website, it is ranked among the top 15 most resistant arthropods on the planet. Among the resistance mechanisms developed, detoxification enzymes play a major role. We focused on cytochromes P450, phase 1 detoxification enzymes, and more specifically those of the 9A subfamily in the acquisition of resistance. The *S. frugiperda* genome codes for 14 genes of the CYP9A family, twelve of which are organised in clusters and have evolved rapidly within lepidoptera. CYP9As have been found to be overexpressed in several insecticide-resistant field populations. We then investigated the role of these enzymes using various techniques, such as gene knockout in the Sf9 cell model using the CRISPR/Cas9 technique, and heterologous expression to determine their ability to metabolise insecticides.

Comparative molecular mechanisms of chlorantraniliprole resistance in three major lepidopteran pests: Insights from target-site mutations and metabolic detoxification

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Abstract

Diamide insecticides function as modulators of ryanodine receptors (RyRs) in insects and are categorized under group 28 by the Insecticide Resistance Action Committee (IRAC). Since their introduction in 2007, insecticides such as chlorantraniliprole and flubendiamide have been widely used to manage a variety of pests, particularly within the order Lepidoptera. By 2025, high-level resistance to diamide insecticides had been reported in two lepidopteran pests (*Plutella xylostella* and *Spodoptera exigua*) in Korea. Recently, high-level resistance to chlorantraniliprole was confirmed in *Diaphania indica*. Comprehensive analysis of these three lepidopteran pests reveals that for *P. xylostella*, the G4946E mutation in the ryanodine receptor (RyR) target site is the primary factor, exhibiting a largely recessive mode of inheritance (degree of dominance of -0.82 to -0.93), while metabolic resistance, such as cytochrome P450, appears to be of minor contribution. In *S. exigua*, the I4790M mutation within the RyR has minimal impact on resistance development; instead, overexpression of CYP9A40 is identified as the primary factor driving resistance. In *D. indica*, not only was the I4790K mutation within RyR identified, but various detoxifying enzymes were also differentially expressed after chlorantraniliprole treatment, indicating complex, multifactorial resistance. This suggests that the underlying mechanisms of diamide resistance development vary significantly across species, underscoring the need for a precise understanding of these mechanisms for comprehensive pest management. Practical strategies for resistance management are also discussed.

Synergistic effect of S-methoprene and piperonyl butoxide against susceptible and resistant strains of the lesser grain borer, *Rhyzopertha dominica* (F.) (Coleoptera: Bostrychidae)

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Mariastela VRONTAKI, Marina GOURGOUTA, Graham MOORES, Christos ATHANASSIOU

Abstract

The lesser grain borer, *Rhyzopertha dominica* (F.) (Coleoptera: Bostrychidae), remains one of the most damaging pest of stored cereals worldwide. Resistance to insect growth regulators such as S-methoprene has been reported in several populations, raising concerns about the long-term sustainability of control strategies. This study investigated the effects of S-methoprene applied alone and in combination with the synergist piperonyl butoxide (PBO) on susceptible (Lab-S, QRD14) and resistant (Met-R, QRD551) strains. Wheat was treated with strain-specific concentrations of S-methoprene and two PBO doses. Treatments were applied either simultaneously or sequentially, and their impact on adult mortality and progeny production was assessed. Adult mortality remained low (<30%) across all treatments, confirming that S-methoprene has limited lethal action on *R. dominica* adults. Nevertheless, the addition of PBO produced a slight increase in mortality in the susceptible strain, indicating some enhancement of acute toxicity. In contrast, progeny suppression was substantial and emerged as the key determinant of treatment success. For the susceptible strains, progeny production was nearly eliminated in all combinations of S-methoprene and PBO. For the resistant strain, suppression was strongly dose-dependent. The greatest reduction occurred when the high S-methoprene dose (30 mg/kg) was combined with the higher PBO concentration (1.35 g/kg), suggesting that PBO can improve the performance of S-methoprene in strains with reduced susceptibility. Overall, the results indicate that S-methoprene primarily affects immature stages rather than adult mortality. Moreover, the incorporation of PBO enhances its performance, particularly in resistant strains. These findings highlight the potential of S-methoprene–PBO combinations as a valuable tool for integrated stored-grain protection, especially in systems where resistance threatens the effectiveness of conventional insect growth regulator treatments.

The physiological changes induced by exposing insects to sublethal doses and compensatory phenomena are two key factors to take into account in pest management.

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Alexandre BANTZ, Delphine GOVEN

Abstract

Contemporary agriculture is facing a new challenge that is to ensure quality production able to meet the growing food needs. Until now, the crop protection and the increase of their yields was mainly based on the use of pesticides such as insecticides¹. However, their use raises concerns about the impact on the environment and on human health. Furthermore, their use is also being questioned, particularly due to the emergence of resistant insects, leading to a loss of efficiency in insecticide treatments. Insect pest management is then a major challenge in preserving food resources. To improve pest management, it is essential to understand all the mechanisms put in place by insects to circumvent insecticide treatments.

The mechanisms of resistance such as behavioral avoidance, thickening of the cuticle, increased activity of detoxification enzymes or mutation of the insecticide targets have been well studied². Compensation phenomena have been observed in insects displaying these resistance mechanisms. Then, these mechanisms could help insects offset the fitness cost or functional disruption caused by mutations, allowing resistant insects to survive even under insecticide pressure. However, compensation phenomena can also occur in insects exposed to different abiotic factors such as sublethal doses of insecticides or light pollution. Further studies will be necessary to increase our knowledge of these mechanisms and to take them into account in the development of new strategies for controlling insect pests.

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Impact of organisms' origin and sensitivity to target pesticides on the outcome of residual pesticide exposure in a plant-aphid trophic system

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Abstract

Due to agricultural intensification and the associated increase in pesticide use, pesticide residues are omnipresent in agricultural landscapes. Terrestrial biodiversity, notably including plants and their cohort of herbivorous insects, is thus chronically exposed to low doses of various toxic molecules such as herbicides and insecticides. However, the direct and cascading effects of pesticides on terrestrial trophic interaction systems, such as plant-herbivore systems, are still poorly understood, especially in the case of non-target effects (e.g., the effect of an herbicide on an insect). In addition, the variations in organisms' sensitivity to pesticides, often linked to resistance or tolerance mechanisms, are widely ignored in the context of sublethal effects of pesticides on trophic interactions. This study thus aimed to assess the responses of a trophic interaction system (*Dactylis glomerata* [Poaceae] – *Sitobion avenae* [Hemiptera: Aphididae]) typical of ecosystems adjacent to crops to various sublethal doses of an herbicide (Flufenacet) and an insecticide (Pirimicarb). These effects were assessed on two plant lines and two aphid lines with contrasting origins (conventional vs. organic farming) and sensitivities to target pesticides. The different trophic system combinations were chronically exposed to four increasing doses of each pesticide, ranging from environmentally relevant non-lethal concentrations to higher sublethal doses, and various morphological traits were measured after four weeks of exposure. While deeper mechanistic analyses are yet to be conducted, our results already indicate that both organisms' sensitivity and the presence of herbivores shape the responses of plants to the herbicide as well as to the insecticide. In addition, while they display less contrasted responses to pesticides, these two factors also influence the outcome of insecticide exposure on aphids. Overall, our results suggest that residual doses of pesticides can alter plant-herbivore trophic interactions, and that these effects highly depend on each organism's sensitivity to pesticides and on the trophic interaction.

Dark Taxa Are Not an Inconvenience: Designing Biodiversity Science for Reality

Emily HARTOP (Norwegian University of Science and Technology, Trondheim, Norway, Emily.hartop@ntnu.no)

Abstract

As the biodiversity crisis accelerates, the future of insect systematics hinges on integrating classical taxonomic expertise with emerging technological approaches. Dark taxa—hyperdiverse, abundant, and largely undescribed groups—are not a nuisance of modern data pipelines; they are central to revealing the true scale and structure of biodiversity.

This talk highlights how systematics can be reshaped to meet contemporary challenges. Linking historic collections with modern molecular inventories using computer vision allows high-throughput species identification while preserving invaluable historical context. Ethical and targeted sampling and sustainable molecular workflows enable efficient sampling. Studies of species communities and rarity provide insight into ecological roles and guide sampling and conservation priorities. Community science extends both spatial and temporal coverage, adds ecological context, and engages the public with biodiversity research.

Together, these approaches demonstrate that traditional taxonomic expertise remains indispensable, guiding interpretation, validation, and integration of complex datasets. By centering dark taxa, this work provides a pragmatic, scalable framework for insect systematics—one that reduces harm, improves reproducibility, and enhances our ability to document, understand, and ultimately conserve insect diversity before it is irretrievably lost.

Hidden diversity and evolutionary uniqueness of gracillariid leaf-mining moths in the Ogasawara (Bonin) Islands, Japan

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Abstract

The Ogasawara (Bonin) Islands are oceanic islands located approximately 1,000 km south of mainland Japan (Honshu Island) and have been designated a UNESCO World Natural Heritage Site since 2011. Despite their small total land area (104 km²), the islands harbor a highly distinctive insect fauna, with a relatively high level of endemism (approximately 28%). As such, the Ogasawara Islands provide an exceptional natural laboratory for studying evolution, comparable to the Galapagos and Hawaiian Islands. Nevertheless, insect diversity and their evolutionary distinctiveness in the archipelago remain poorly documented. Since 2022, we have investigated the diversity of gracillariid leaf miners (Lepidoptera) in the Ogasawara Islands and have so far discovered nearly 20 undescribed species. These taxa represent 11 genera across six subfamilies, and several exhibit striking morphological and biological novelties, including unusual wing patterns and leaf-mining behaviors. Molecular phylogenetic analyses indicate that the putative sister taxa of these undescribed species are predominantly distributed in mainland Japan and/or Ryukyu Islands, suggesting a predominantly Palearctic origin of gracillariid leaf mines in the Ogasawara Islands. In this talk, I will highlight several undescribed species with particularly distinctive morphology and life histories and discuss potential evolutionary forces driving the unique diversification of gracillariid leaf-mining moths in the Ogasawara Islands.

Latitudinal diversity gradients in the globally dominant flying insect clades

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Amrita SRIVATHSAN, Karen NEVES, Rudolf MEIER

Abstract

Latitudinal diversity gradients are a key concept in ecology, but the available data are skewed towards large-bodied, charismatic taxa, excluding most multicellular species. To address this bias, we analyzed DNA barcode data for 1.35 million specimens of flying insects collected using 101 Malaise traps in 27 countries across six continents. We find that ten families consistently contribute more than half of all specimens and species across climates, habitats, and continents. Contrary to canonical expectations, five families have inverse or non-significant gradients while the remaining five exhibit only weak to average gradients compared to 470 other terrestrial datasets. These results reveal surprising convergence in the globally dominant insect clades across continents and illustrate that textbook latitudinal diversity gradients cannot be assumed for the poorly studied invertebrate taxa that make up most of the Earth's biodiversity. Therefore, broadening the taxonomic scope of macroecological studies is essential for understanding global biodiversity patterns.

Molecular systematics and island diversification of flightless beetles of the genus *Oxycara* (Coleoptera: Tenebrionidae) in Cabo Verde

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Abstract

Oceanic archipelagos serve as natural laboratories for studying evolutionary processes in isolated environments. The darkling beetle genus *Oxycara* (Tenebrionidae), which consists of flightless beetles adapted to xeric habitats in northern Africa and western Asia, exhibits a notable radiation in Cabo Verde islands, where 16 endemic species are currently recognised. These beetles, whose dispersal is constrained by their flightlessness, provide an excellent model for understanding colonisation patterns and diversification in fragmented island systems. Despite their singularity, these lineages remain understudied from a phylogenetic perspective. In this study, we infer phylogenetic relationships within *Oxycara* across the islands of Cabo Verde using mitochondrial (cox1) and nuclear (ITS2) DNA sequence data and extensive sampling throughout the archipelago. Our results reveal a complex biogeographic history characterised by multiple inter-island dispersal events. Several islands harbour more than one *Oxycara* species belonging to distantly related lineages, indicating that local diversity largely reflects independent colonisation events rather than in situ diversification. Phylogenetic patterns suggest that the earliest colonisation likely occurred on the eastern islands, followed by subsequent dispersal across the archipelago. Furthermore, one clade grouping species from the northern, eastern, and southern islands shows limited phylogenetic structure, consistent with a relatively recent diversification. Our results also imply a re-evaluation of the current taxonomic classification of the group.

New perspectives in the study of insect phenotypes: A semantic solution to the problem of data integration

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Abstract

Research in insect taxonomy produces thousands of new species descriptions each year. Systematics literature is a vast source of knowledge about insect phenotypes, from morphology to behavior, often available as phylogenetic characters. Ecological studies frequently produce large amounts of data on individual organisms or species, often linking measurements of functional traits to environmental information. Experimental biology connects wild and mutant phenotypes in insect model organisms to candidate genes. However, these varied sources of phenotypic information on insect biodiversity are mostly disconnected from each other, scattered across domains of knowledge, often spanning hundreds of years of research. What if we could integrate all phenotypic data into a shared framework? How can we solve the problem of data integration? One possible solution to this problem is to employ a common data model to represent insect phenotypes within and across different domains of knowledge. Ontologies—structured controlled vocabularies formalizing concepts in a domain of knowledge—and other semantic web technologies offer the tools necessary to achieve such a solution. In this talk, I will discuss some ideas about how ontologies and semantic web technologies in general could support the interoperability of phenotypic data in the context of phylogenetics. First, as proof of concept, I will present PhenoBees: A knowledge base and workflow for studying bee phenotypes. Next, I will demonstrate how adopting a common data model to represent insect phenotypes allows us to combine phylogenetic datasets from different studies and synthesize new phylogenetic data. I will also present potential applications of semantic phenotypic data in modeling the evolution of insect traits, emphasizing integration between different domains of knowledge. Finally, I will conclude with a discussion of the promises and challenges of semantic approaches to insect phenotypic data in the context of Big Data and the Biodiversity Crisis.

Multilocus phylogeny of *Dorcadion* and related taxa (Coleoptera, Cerambycidae)

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Abstract

Dorcadion, a species rich genus in the subfamily Lamiinae and with a wide distribution across the Palearctic, currently includes six subgenera delimited based on the external morphological characters, the structure of the endophallus and chorology. Only a few recent papers included DNA sequences for some species of *Dorcadion* in their analyses. We have reconstructed the first molecular phylogeny that includes besides *Dorcadion* four out of the five related genera, using eight molecular markers: two mitochondrial (COI and Cytb) and six nuclear (Histone 3, Wingless, Elongation factor 1 α , 18S, 28S and ITS2). For COI, 28S and ITS2 we have also developed short versions of these markers for samples with degraded DNA. Sequences from 91 individuals from *Dorcadion*, *Iberodorcadion*, *Neodorcadion* and *Politodorcadion*, including all of the currently valid subgenera and several big species groups, were analysed and used to reconstruct the phylogeny. Additionally, sequences from over 60 other longhorned beetles were used as outgroup. Our results show that the morphological classification is mostly consistent with the phylogeny with one exception and most of the subgenera were recovered as separate groups within the genus *Dorcadion* apart from *Cribridorcadion*. The exception is *Politodorcadion*, a genus that according to our phylogeny should be downgraded to subgenus. Furthermore, *Eodorcadion* is confirmed as not being closely related to *Dorcadion*, in our analyses this genus being more closely related to *Lamia textor*. Our study generated 659 new sequences, 85 of them being COI – the standard DNA barcoding region. This study also brings new insights about evolution, intra- and interspecific relationships, with proven cases of hybridisation even between distinct subgenera, introgression, reticulated evolution and so much more that warrant future research. Financial support provided by the Romanian Agency UEFISCDI through the grant 2D-3B (PN-IV-P7-7.1-PED-2024-1951).

Ancient routes, modern hotspots: phylogenomics illuminates the evolutionary journey of Saturniidae (Lepidoptera: Bombycoidea) across continents

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Astrid CRUAUD, Pierre ARNAL, Liliana BALLESTEROS-MEJIA, Thibaud DECAËNS, Marianne ELIAS, Delphine GEY, Paul D. N. HEBERT, Ian J. KITCHING, Sébastien LAVERGNE, Carlos LOPEZ-VAAMONDE, Jérôme MURIENNE, Yves CUENOT, Sabine NIDELET, Fabien CONDAMINE, Jean-Yves RASPLUS

Abstract

Wild silkmoths (Saturniidae) are among the most iconic moth families, yet their evolutionary history has remained poorly understood due to the absence of a comprehensive phylogenetic framework. We used cutting-edge phylogenomics approaches – analysing 1,024 ultraconserved elements (UCEs) across 338 species representing all described subfamilies, tribes, and genera – to reconstruct the evolutionary history of saturniid moths in space and time and propose the most complete systematic treatment of this family to date.

Our analyses reveal a complex biogeographic history originating during the Paleocene-Eocene, with an ancestral range spanning Neotropical, West Nearctic, and East Palearctic regions. Beringia played a crucial role as a dispersal corridor connecting the New and Old Worlds during the Eocene climatic optimum. Early saturniid lineages exhibit remarkable geographic conservatism, remaining confined to their ancestral regions for tens of millions of years. The notable exception is Saturniinae, which achieved a cosmopolitan distribution across all continents except Antarctica through multiple dispersal events.

This new robust phylogenetic framework leads us to propose substantial revisions to saturniid classification, including the description of one new subfamily and two new tribes, alongside several generic reassignments. Our results illuminate the evolutionary journey of saturniid moths across continents and open new perspectives of research about the origin and drivers of the diversity patterns observed today, with pronounced diversity hotspots in tropical regions, particularly the Andean mountains.

Temperature variability homogenized thermal responses in an ectotherm community along a European longitudinal gradient

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Abstract

Climate change, through rising temperatures, greater variability, and more frequent extremes, is reshaping insect phenology and thermal niches, with profound effects for pest outbreaks. Predicting these impacts requires a clear understanding of species and communities' responses across geographic gradients. We assessed thermal tolerance (CT_{max}, CT_{min}, CCRT) of three cereal aphid species *Sitobion avenae*, *Rhopalosiphum padi*, *Metopolophium dirhodum* from 30 populations along a 1200 km longitudinal gradient in Europe, comparing autumn and spring collections. We measured guild-level functional diversity to assess thermal trait patterns along the longitudinal gradient. We tested whether 1) eastern populations experiencing greater seasonality and harsher winters exhibited broader thermal ranges, 2) autumn aphids were more cold-tolerant and less heat-tolerant than spring aphids 3) stronger seasonality facilitated thermal trait convergence within the guild. Across the longitudinal gradient, autumn populations in eastern Europe exhibited broader thermal ranges, supporting the climatic variability hypothesis (CVH). In contrast, spring populations displayed a counter-gradient pattern, with stronger cold tolerance in the milder western winters, likely reflecting differences in overwintering strategies (active adults in the west versus diapausing eggs in the east). Additionally, autumn aphids were less heat-tolerant than spring individuals. Eastern communities exhibited trait convergence driven by large intraspecific variation, whereas western communities showed interspecific divergence, indicating differential environmental filtering. Increasing climate variability may drive thermal traits homogenization (negative standardized effect size of functional diversity for all traits) in ectotherm communities. Climate change may intensify season-dependent physiological changes, shift eastward the geographic range of aphids overwintering as active adults, and homogenize thermal niches, potentially altering pest dynamics and diminishing the effectiveness of integrated pest management strategies. Our study underscores the importance of integrating seasonal dynamics and intraspecific trait variations when predicting climate change responses, highlighting how changes in temperature variability – not just warming – may reshape ectotherm communities during the growing season.

Key drivers of bee occupancy and distribution in disturbed tropical montane landscapes in Malaysia revealed through multi-species occupancy modelling

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Abstract

Wild bee communities in tropical montane forests (TMFs) are still poorly documented, despite their ecological significance and vulnerability to land-use change. We surveyed bees across a fragmented agricultural landscape in Peninsular Malaysia, sampling primary and secondary forests, tea plantations, and urban–rural habitats to assess the environmental factors affecting their distribution. Using Bayesian multi-species occupancy modelling, the results show that although floral resources influence bee occupancy, habitat structure and landscape context play a more vital role in supporting diverse bee communities. Furthermore, group-level responses highlight the significance of specialisation, nesting strategy, and sociality in determining bee species distribution across the landscape. These findings illustrate how habitat structure shapes TMF bee assemblages and emphasise the vulnerability of rare and specialist taxa, as well as the habitats needed to support them. By identifying the factors that influence bee occupancy, this study provides vital evidence for conserving pollinator diversity in Malaysian TMFs and other threatened montane ecosystems.

From dense cities to protected semi-natural areas: large-scale homogenization of wild bee communities across Western Europe

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Abstract

Growing anthropogenic pressures threaten pollinator diversity, yet our understanding of how bee communities respond to human-modified landscapes remains fragmented, often biased by limited spatial scales, habitat types, or a focus on taxonomic metrics alone. Comparative evidence integrating protected semi-natural and urban habitats within a unified, trait-based framework is still scarce. Here, we compiled a large dataset of wild bee assemblages from 708 sampling points across Western Europe, encompassing 14 protected semi-natural habitats and 22 urban environments in three countries. Species composition, conservation status, and functional trait diversity were compared using a three-step analytical framework that controlled for biogeographical variation and explicitly targeted ecological drivers. Results reveal a general homogenization of bee communities between urban and semi-natural habitats in terms of taxonomic composition and conservation status, likely driven by pervasive human impacts and the underrepresentation of highly selective environments. In contrast, functional trait analyses clearly differentiate the two habitat types: semi-natural habitats support greater morphological and ecological diversity, whereas urban environments host more functionally constrained yet compositionally comparable communities dominated by common, generalist species. Notably, even protected natural sites show evidence of anthropogenic filtering, favouring less threatened taxa. This widespread biotic homogenization raises conservation concerns and underscores the importance of safeguarding habitats that retain regional functional diversity and support the most threatened species. Effective pollinator conservation, therefore, requires reducing human pressure across the entire landscape gradient, from urban to semi-natural systems, while improving habitat quality and resource availability to sustain both taxonomic and functional diversity, including within urban ecosystems.

Mosquito Community Shifts Along urban environments in a global south city.

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Elisabet BENITEZ, Andrés VISINTIN, Florencia SANGERMANO, María ASAR, Francisco LUDUEÑA-ALMEIDA

Abstract

Urbanization profoundly alters habitat structure and resource availability, reshaping insect communities and influencing vector-borne disease risk. This study assessed how mosquito community composition and diversity vary along an urbanization gradient in Córdoba, Argentina. Adult mosquitoes were collected at 30 sites using CO₂-baited light traps (24 h) to sample overall assemblages and sticky traps (one week) to target gravid *Aedes aegypti*. Sampling was conducted over six periods between April 2021 and February 2022, covering all seasons.

Because Córdoba is a heterogeneous urban mosaic not structured solely by distance from downtown, the urbanization gradient was defined using remotely sensed environmental variables and Local Climate Zone (LCZ) classification. Normalized Difference Vegetation Index (NDVI) and Normalized Difference Built-up Index (NDBI) derived from Sentinel-2 imagery, LCZ land cover proportions, and distance to downtown were integrated using Principal Component Analysis. Three urban environment groups were proposed: highly urbanized (G1), intermediate (G2), and vegetated/peripheral (G3), and validated using Discriminant Analysis.

Only LCZ Built types 6 (open low-rise), 10 (industry), land cover types A (dense trees) and B (scattered trees) significantly contributed to group differentiation. Alpha diversity was quantified using Hill numbers (species richness and effective numbers of common and dominant species), with comparisons accounting for sampling completeness.

A total of 4,821 mosquitoes, representing 4 genera and 14 species, were collected. *Culex quinquefasciatus* (71.7%) and *Aedes aegypti* (9.9%) dominated. Richness and diversity increased along the urbanization gradient: richness in G3 was 50% higher than in G1, and species diversity was 22% higher than in G1 and 17% higher than in G2. *Aedes aegypti* was absent outdoors during winter, whereas *Cx. quinquefasciatus* persisted year-round.

This city-wide assessment shows that urbanization reduces mosquito diversity while favoring dominant vector species, underscoring the need for strengthened surveillance under continued urban growth and climate change.

Loss of predators drives cascading effects in termite-mediated wood decomposition in tropical forests.

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Daniel MURCIA, José RODRÍGUEZ, Roderick VALDÉS

Abstract

Termites play a fundamental role in wood decomposition, nutrient cycling, and energy flow in tropical forests. However, the ecological consequences of predator loss on the processes they drive are still poorly understood. In this study, we examined how the absence of the Northern Tamandua (*Tamandua mexicana*), a specialized termite predator, affects termite spatial ecology and wood consumption in Panama. We compared colony density, nest characteristics, and wood consumption rates between predator-free and predator-infested habitats, using arboreal termites as focal taxa.

We found that predator-free sites showed significantly higher termite nest density, lower nest height, and greater wood consumption. For example, nest height was not explained by tree height or other structural variables, suggesting a selection process in response to predation pressure. Conversely, nest volume did not differ between habitats, indicating a consistent investment in nest construction, regardless of predator presence. Despite being the most frequent termite in wood blocks, *Microcerotermes arboreus* showed similar colonization rates in both habitat types, implying that increased wood consumption in predator-free areas was not due to species turnover, but rather to increased foraging activity, resulting from at least a higher colony density. Our findings demonstrate that the loss of a vertebrate predator can impact detritivore communities and alter fundamental ecosystem processes, such as wood decomposition and carbon flux. This study underscores the importance of trophic interactions in shaping ecosystem processes in tropical forests, and the ecological consequences of defaunation, as potential mechanisms that help to understand some of the processes of climate change.

Can the density of managed honey bees influence the presence of wild pollinator visitors?

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Abstract

Several recent studies demonstrate that managed honey bees can influence wild pollinators through direct displacement, aggressive interactions, and competition for floral resources. However, reported outcomes are highly context dependent, with negative, neutral, and occasionally positive effects on wild pollinator abundance and diversity. These inconsistencies make it difficult to generalise findings beyond individual study systems. In Scotland, the Pollinator Strategy (2017–2027) aims to make the country more pollinator-friendly, improve understanding of pollinator ecology and pollination services, and reverse declines in pollinator populations. To support these objectives, it is crucial to identify the honey bee densities at which adverse effects on wild pollinators may occur. To date, most assessments have relied on presence–absence data or simple measures of honey bee abundance, providing limited insight into density-dependent responses. Consequently, it remains unclear whether increasing honey bee densities elicit different responses among wild pollinator communities, particularly across landscapes where small-scale and large-scale commercial beekeeping coexist. Wild pollinators (bees and hoverflies) were surveyed during the spring and summer of 2024 and 2025 on oilseed rape fields and heather moorlands across 29 sites throughout Scotland, spanning a gradient of managed honey bee hive densities. Pollinators were identified to species level and quantified. This talk presents the relationships between honey bee density and wild pollinator abundance, species richness, and Shannon diversity, providing new evidence for density-dependent interactions between managed honey bees and wild pollinator communities.

Spatial Structure of Springtail Communities in Iran's UNESCO Hyrcanian Forests

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Abstract

The Hyrcanian Forests of Iran, a UNESCO World Heritage Site straddling the Caucasian and Iranian-Anatolian biodiversity hotspots, harbor exceptional diversity and endemism, yet their soil fauna remains underexplored. This study examines the spatial distribution and community structure of Collembola across sites and microhabitats in Bula Protected Area (eastern Hyrcania). Over two years, 89 samples from three forest sites—preserved natural (PNF), preserved anthropized (PAF), and non-preserved natural (NPF)—targeted moss, litter, and dead wood microhabitats. Results document 73 morphospecies across 39 genera and 12 families, with estimated gamma diversity of 80-110 species. Alpha diversity varied spatially, especially among microhabitats, the dead wood supporting the highest richness. Beta diversity was high but did not vary much depending on the spatial scale, while community evenness varies at landscape scales. Occupancy-abundance relationships show high interspecific variation but limited habitat specialization—most species exhibit broad spatial distributions without strong fidelity to microhabitats. Co-occurrence analysis indicate predominantly neutral interactions, with positive associations (likely shared niches/food preferences) outnumbering negative exclusions suggestive of competition, underscoring niche overlap as a coexistence driver. These spatial patterns suggest that forest management and fine-scale heterogeneity shape springtail communities, positioning dead wood as a critical diversity reservoir. The findings also highlight the need for a more in-depth investigation into the ecological factors influencing the spatial variation in the presence, absence and abundance of collembolan species.

Stratification of saproxylic beetle communities up top the canopy atmosphere interface under the influence of dieback in temperate forests

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Abstract

In the context of climate change, the forest canopy is at the forefront of atmospheric warming. Crown dieback and mortality can alter vertical structure and associated environmental gradients in the upper strata.

Due to their difficult access, the canopy and the interface between the canopy and the atmosphere are understudied ecological edges. In the canopy of temperate forests, the stratification of saproxylic beetles, a functionally important guild involved in wood decay and nutrient cycling, has been poorly documented.

In this study, we characterized the vertical distribution of saproxylic beetle communities across four strata: the understory, the lower canopy, the upper canopy, and the canopy–atmosphere interface located 2 m above the canopy. We further examined how forest dieback alters this stratification, e.g. through changes in deadwood pattern related to declining crowns.

Although taxonomic diversity was similar across strata, community composition differed markedly due to a strong species turnover. The two upper strata hosted more abundant assemblages and included more rare beetle species compared to the lower strata. All strata exhibited comparable levels of functional richness, but communities sampled above the canopy showed lower functional evenness than those from the lower canopy. Beetles were generally larger and displayed greater size heterogeneity in the upper canopy than in the other strata.

Across a gradient of dieback level, the between-stratum dissimilarities were reduced from healthy stands to strongly declining stands.

Overall, our findings highlight that restricting saproxylic beetle surveys to the understory substantially underestimates their true vertical diversity and overlooks unique canopy-associated assemblages.

Distribution, habitat preferences, and life-history traits of *Eriogaster catax* in Umbria (Italy): implications for conservation management

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Enzo GORETTI, Gianandrea LA PORTA, Lorenzo GIULIVI, Silvana PIERSANTI, Manuela REBORA

Abstract

Eriogaster catax (Linnaeus, 1758) was studied to enhance knowledge of its distribution, ecological characteristics, habitat requirements, and life-history traits in Umbria, Italy, supporting conservation actions under the LIFE IMAGINE UMBRIA project (LIFE19 IPE/IT/000015). We updated *E. catax* regional distribution through bibliographic review and field surveys; the database increased from 17 records (1994-2017) to 123 by 2024. *E. catax* is now documented in 17 10×10 km squares (89% increase) and in 12 Natura 2000 sites (71% increase). We analysed oviposition site selection by recording host plant species, oviposition height, shrub height, and branch diameter. Egg batches and larval nests occurred almost exclusively on *Prunus spinosa*. Mean oviposition height was 74 cm (range 20–175 cm), with 41–60 cm most used. Shrub height averaged 124 cm (range 60–300 cm), with 51–100 cm most frequent. Branches used for oviposition averaged 5 mm (range 2–10 mm). Most plants hosted a single larval nest. We conducted an ex-situ rearing study using field-collected egg batches to investigate the species life-history traits and phenology under laboratory conditions closely replicating its natural environment. Body length, head capsule width, and weight were recorded across larval instars. Average larval length and head width increased from 4.29 mm and 539 µm (instar I) to 38.97 mm and 3117 µm (instar V), with average weight increasing from 0.0018 g to 0.7206 g. Development from hatching to pupation averaged two months. Pupae were measured, weighed, and individually aestivated. Adult emergence occurred from 9–27 October for females and 16 October–6 November for males, with mean adult weights of 0.2199 g and 0.1414 g, respectively. These biometric and rearing data complement field observations on habitat requirements and ecological preferences, enhancing understanding of *E. catax* biology and ecology in Umbria (Italy) and providing evidence to guide conservation and habitat-management measures.

Bigger, better hedgerows – assessing hedge structure and landscape context for lepidoptera

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Abstract

Hedgerows are an important semi-natural habitat occurring over much of the farmed landscape in the UK. What plant species they are made up of, the area they cover and how they are managed can be crucial in determining how useful they are to insects in providing habitat, shelter and food. Invertebrates in turn provide ecosystem services such as pollination and pest control and act as food for birds, bats, amphibians and small mammals.

The 2007 countryside survey records that less than 50% of hedgerows were considered to be in good condition and less than 10% of managed hedgerows on arable land have good structural condition and well managed margins. Alongside this decline in suitable habitat, insect populations have been adversely affected by a warming climate and exposure to pesticides.

Hedgerows are particularly important habitats for native Lepidoptera (butterflies and moths) whose overall abundance has declined in the UK due to a combination of loss of suitable habitat, a warming climate, light pollution and exposure to pesticides and herbicides. Lepidoptera provide services as pollinators and play a crucial role in food chains as a prey resource for many bird and bat species. It's important we understand how different aspects of hedges such as height, width, age and connectivity affect their use by Lepidoptera. The UK government have proposed to create or restore 30,000 miles of hedgerows by 2037, and 45,000 miles of hedgerows by 2050, under the new Environmental Improvement Plan 2023. For these new hedgerows to be successful we urgently need to collate data and further investigate where pollinating insects are currently found and which elements of hedges are most useful to them.

Elevational diversity and turnover of Neotropical leaf beetles (Chrysomelidae) across the Ecuadorian Andes

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Abstract

Documenting species diversity patterns is a central goal in ecological research and an essential step toward understanding the mechanisms that shape communities. Phytophagous beetles are highly diverse and ecologically important, yet their diversity patterns remain poorly characterized in tropical regions such as Ecuador. In this study, we assessed diversity patterns of Neotropical leaf beetles (Chrysomelidae) in tropical montane forests along two transects spanning both sides of the Ecuadorian Andes. Specifically, we examined elevational trends in taxonomic diversity using Hill numbers and quantified species turnover patterns across spatial scales. Leaf beetles were sampled through canopy fogging in 42 plots distributed across three elevational levels in two transects established near Cajas and Sangay National Parks, with morphospecies delimitation based on morphological and molecular data.

Our results show that Chrysomelidae diversity declines with elevation at both sides of the Andes, and that diversity at equivalent elevations is lower in Cajas than in Sangay. Eumolpinae and Galerucinae were the most species-rich and abundant subfamilies, exhibiting consistent patterns across transects. Species turnover within the same altitudinal belt was medium to high, increasing rapidly with elevational distance, and turnover between similar belts across transects was also high.

This study provides one of the first comprehensive assessments of leaf beetle diversity across Andean elevational gradients using an integrative approach. The findings underscore the strong influence of elevation in shaping diversity and turnover, offering valuable baseline knowledge for understanding how montane phytophagous communities may respond to environmental change in one of the world's most biodiverse regions.

Woody encroachment effects on insect communities in mountain grasslands

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Abstract

Woody encroachment, driven by climate change and socio-economic factors, represents a major challenge for the management of mountain pastures. While previous studies suggest that moderate encroachment can enhance plant diversity by creating more heterogeneous habitats, its effects on insect communities remain poorly understood. To address this knowledge gap, this study investigates how woody encroachment influences insect species richness and abundance, as well as insect–plant interactions. In the summer of 2024, eight mountain pastures on calcareous substrate, at elevations between 650 and 1650 m a.s.l. were investigated in Berchtesgaden National Park (Bavarian Alps, Germany). We sampled insects using suction sampling in nine plots with and nine plots without woody encroachment, each measuring 1 m². Specimens were counted for major taxonomic groups and subsequently analyzed via metabarcoding to determine species-level richness. The effects of woody encroachment on insect diversity were assessed using Generalized Linear Mixed Models (GLMMs). Preliminary results indicate a higher insect species richness in plots with encroachment. Implications of woody encroachment for insect diversity under different management regimes are discussed.

Insect Responses to Early-Stage Riparian Restoration in Oil Palm Landscapes

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Abstract

Rapid agricultural expansion across the tropics has transformed natural ecosystems at unprecedented scales, leading to losses in biodiversity, ecological function, and climate-buffering capacity. As these landscapes continue to intensify, there is a growing need for tractable restoration approaches that can reinstate habitat complexity and support the recovery of key ecological communities. The Riparian Ecosystem Restoration in Tropical Agriculture Project (RERTA) is a large-scale Before–After Control–Impact experiment conducted within oil palm plantations in Riau, Indonesia. We compared passive restoration (natural regeneration) with active restoration (enrichment planting with six native tree species) to evaluate early changes in vegetation structure, microclimate, and insect assemblages. Active restoration, particularly in areas with remnant palms, enhanced vegetation complexity and improved thermal buffering, but did not produce distinct shifts in insect community composition. This pattern may reflect limited connectivity between restored riparian habitats and remaining natural forest, highlighting the importance of landscape-scale linkages in supporting ecological recovery. Climate projections for 2045 and 2085 indicate that restoration-driven habitat complexity will promote insect persistence and functional stability under future warming. Overall, our early results indicate active restoration may be the most tractable restoration approach in agricultural landscapes. If we get the treatments correct, then we could improve the area within the tropics = and determine the impact it could have.

Pheromone communication and nestmate recognition in the clonal raider ant.

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Abstract

Social insects, such as ants, rely on complex chemical communication to regulate a wide range of social behaviors, including nestmate recognition, division of labor, and collective coordination. Communication in ants primarily occurs through the production and detection of pheromones, volatile chemicals that are produced by exocrine glands and mediate behaviors such as trail following, recruitment, mating, and alarm-defense. Despite the central role of exocrine glands in insect communication, there are still large gaps in our knowledge of their function in any context in ants, and it remains unknown how particular pheromones produced by specific glands initiate distinct social behaviors in social insects.

Additionally, ants use cuticular hydrocarbons (CHCs), low-volatility chemicals found on the cuticle, to discriminate between nestmates from non-nestmates. Each colony has a unique CHC profile that varies across colonies of the same species. Recognition is thought to involve comparing others' chemical cues to an internal colony odor template: close matches lead to acceptance, while mismatches trigger aggression. This process may rely on both central template matching and peripheral sensory adaptation, whereby olfactory neurons become less responsive to familiar cues, enhancing the detection of unfamiliar ones. However, the formation and plasticity of these recognition systems remain poorly understood, in part because genetic and environmental effects on CHCs are difficult to disentangle.

Using the clonal raider ant *Ooceraea biroi*, which combines the rich social biology of ants with exceptional experimental tractability, I investigate (1) the functions of various exocrine glands and the sensory coding of their pheromones, by generating transgenic ants with genetically ablated glands, and (2) the neural and sensory mechanisms underlying nestmate recognition. Together, my work aims to advance our understanding of the chemical and neural bases of social communication in ants and how these processes enable the coordination and cohesion of insect societies.

Olfactory sensitivity and division of labor in the honey bee *Apis mellifera*

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Julia MARIETTE, Jean-Christophe SANDOZ, Julie CARCAUD

Abstract

Division of labor is found in many animal societies, with individuals specializing in specific tasks, and thereby enhancing the efficiency of the group. Task specialization is especially present in honey bees (*Apis mellifera*), in which it depends on the animal's age, but remains also flexible as it is influenced by the social context and the particular needs of the colony. Various models have attempted to explain division of labor, with the widely accepted response threshold model, which postulates that individuals differ in their response threshold to task-associated stimuli.

Division of labor in honey bees relies on an efficient communication system among colony members, with the use of many pheromones involved in almost all aspects of their life, making olfaction a crucial sensory modality for these species. Even if the response threshold model has been extensively studied in the honey bees, especially on the gustatory modality, the role of olfactory sensitivity has remained greatly overlooked.

We are thus testing the hypothesis that differences in olfactory perception, especially to pheromones, lead to task specialization in the honey bee colony. Behavioral assessments using an olfactometer as well as associative appetitive conditioning will allow to determine olfactory response thresholds to a diversity of olfactory stimuli, including social pheromone compounds, in different worker task groups. Complementary neurophysiological recordings using electroantennogram will allow to determine olfactory detection thresholds to the same olfactory stimuli.

Using both behavioral and neurophysiological approaches, we expect to identify a variation of olfactory detection specific to each worker task groups, in particular to social pheromones, and use these patterns to predict which task a worker will perform in the colony.

Social behaviour of *Lasioglossum marginatum* and their nestmate recognition

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Anna ŽALMANOVÁ

Abstract

Lasioglossum marginatum is a halictid bee whose extended five- to six-year colony cycle and delayed reproductive phases offer a distinctive system for studying social organisation and individual roles within long-lived nests. Colonies are founded by a single overwintered female and develop underground, eventually reaching sizes larger than those documented for any other species within the subfamily Halictinae.

In *L. marginatum*, ovarian enlargement in the foundress appears to begin only after all brood cells have been provisioned and the nest has been closed. Larval development is unusually slow, and males emerge only in the final year of the colony cycle. Workers likely contribute to laying unfertilised male eggs, and the potential presence of reproductive intruders adds further complexity to colony dynamics.

To better understand the biology of *L. marginatum*, we combine behavioural assays, chemical analyses, nest excavations, individual marking, and field observations of colony entrances and foraging activity. These complementary approaches allow us to examine colony-specific odour profiles, their variation among nests, and their reliability in mediating social recognition, while excavations and long-term monitoring provide insight into colony age structure, the presence of foreign females, and how reproductive potential shapes social interactions within the nest.

Development and individual experience combine to shape defensive behavior during worker-to-soldier differentiation in termites

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Abstract

Defense behavior is crucial for survival, especially in group-living animals that can attract many predators. Individuals can improve their defensive behavior in the course of their lives, allowing them to respond more efficiently to threatening situations. This behavioral flexibility might be accompanied by brain changes at the structural and functional levels, including activity of serotonin, a key molecule related to aggression. Here, we take advantage of termite soldier differentiation (worker-presoldier-soldier) in *Hodotermopsis sjostedti* to evaluate how development and individual experience shape defensive behavior and neuroplasticity, especially with respect to serotonergic activity. We combine worker-to-presoldier differentiation induced by a juvenile hormone analogue, aggressive encounter training with ants, and brain immunohistochemistry. Our results indicate that defense experience has a strong impact on presoldiers' aggressiveness, with a higher number of attack positions and bites than their inexperienced counterparts of the same age. This suggests that individual experience is important in shaping defensive response. Other behaviors, such as drumming and evading, increased over the training period but did not differ between experienced and inexperienced groups, suggesting that development alone might trigger such an increase. Presoldier brain scans and 3D reconstructions revealed eight groups of serotonin-like immunoreactive neurons in the brain and six in the suboesophageal zone (SEZ), an important brain region controlling mandibular movements. Volume comparisons of the SEZ and its serotonergic neurons between experienced and inexperienced presoldiers will reveal if higher aggression levels are linked to structural and functional neuroplasticity. Our data suggest that development and individual experience combine to shape aggressive behavior in termites, an assumption hitherto unexplored for these social insects.

Plasticity on multiple levels – mapping the adaptive capacity of the ant *Temnothorax crassispinus*

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Abstract

Ecosystems in our rapidly changing world have to face more frequently occurring stochastic events, mainly due to human-driven phenomena such as global climate change or habitat fragmentation. This raises the question of how fast and effectively organisms can adapt to changing environmental conditions. To predict how well organisms respond to such changes, it is essential to understand the mechanisms underlying their adaptive capacity. Heterogeneous landscapes provide suitable model systems for investigating these questions, as they expose organisms to markedly different environmental conditions over relatively small spatial scales. In this study, we investigated colonies of a cavity-dwelling ant species (*Temnothorax crassispinus*) in a Central European wood-pasture. This species occurs across all three woody habitat types of this landscape (i.e., solitary tree, forest edge, forest), therefore its colonies experience very different biotic and abiotic conditions. We examined colony structure in 92 collected colonies by enumerating the number of larvae, pupae, workers, queens, virgin queens, and males. In addition, we also extracted the CHC-profiles of workers originating from each habitat type. Although worker and larval number did not differ significantly among habitat types, allocation to reproductive individuals varied: colonies from solitary trees allocating significantly more in sexuals compared to forest and forest edge. Moreover, sex ratios differed among habitat types with colonies from solitary trees allocating significantly less into males compared to colonies collected from forest edge. We also observed habitat-specific variation in worker CHC-profiles. Our findings indicate that plasticity at both the molecular level and in colony composition contributes to the adaptive capacity of this ant species. Similar qualities may be critically important under future anthropogenic disturbances and ongoing global climate change.

Mixed forests can mitigate adverse effects of major disturbances on trophic interactions: Spruce dieback affecting wood ant foraging behaviour..

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Timo DOMISCH

Abstract

Natural disturbances, like spruce bark beetle outbreaks, become more abundant with climate change. Wood ants rely in their foraging for honeydew, one of their major food sources, highly on spruce. Thus, the main objective of this research was to assess the effects of a major spruce dieback in the Białowieża Forest (Eastern Poland) due to a bark beetle outbreak, on the ants' foraging behaviour and their host tree choice. When dead spruce proportions increased, the ants intensified their visits to the remaining living spruce trees, but also started to visit other tree species, like hornbeam and oak. When spruce proportions were inherently low, the ants used almost entirely spruce and, when available, also birch. The results show that when the proportion of spruce decreases abruptly due to a forest disturbance, the wood ants can switch their foraging to other tree species available in the forest. Therefore, mixed forests appear to buffer the effects of bark beetle outbreaks, in case not all spruce trees are affected. Consequently, forest management aiming to increase the proportion of mixed forests, ensuring their resilience, is of benefit also for wood ants in case of disturbance. Overall, our results demonstrate the importance of forest diversity in managed forests for mitigating adverse effects of major disturbances and for increasing the stability of trophic interactions.

Social control of queen specialization in ants

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Abstract

Insect societies show a division of labor between queens that monopolize egg production and workers that perform all the other tasks necessary to maintain the colony. Such reproductive division of labor between the queen and worker castes is central to the functioning, ecological success and evolution of social insects. It is generally accepted that queens are intrinsically specialized in egg production once they reach the adult stage, and that this constitutive specialization is independent of environmental conditions. We recently reported that this is not the case in two ant species, where the presence of workers both initiates and maintains the queen specialization. To investigate whether such social control of queen specialization is common across the ant phylogeny, we quantified the effect of the presence of workers on the brood care behavior of >400 queens from >35 ant species. While our behavioral analyses indicated that the social control of queen specialization could be found in multiple ant species, they also revealed interspecific variation in the flexibility of queen specialization, from queens that never express brood care (even in absence of workers) to queens that always do (even in presence of workers). We are in the process of mapping the behavioral data on the ant phylogeny to identify the factors and species-specific life-history traits that underlie variation among species in the flexibility of queen specialization. In addition to shedding light on reproductive division of labor in ants, our findings overturn the longstanding notion of social insect queens as intrinsically specialized egg-laying machines.

Challenges of desert ants while foraging: avoiding predators and rescuing nestmates

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Adi BAR

Abstract

Desert ants (*Cataglyphis* spp.) inhabit open habitats and forage individually over large areas for scattered prey. They are a classic model for studying arthropod navigation and have also been shown to possess advanced spatial learning abilities. While foraging, these ants face various challenges, including predation. Sit-and-wait predators such as antlions and spiders, some of which construct traps, frequently ambush foraging ants. Using a series of laboratory experiments, we show that desert ants learn to avoid pitfall traps simulating ambush predators, and that the spatial arrangement of traps strongly affects both capture and escape probabilities. We further show that desert ants rescue trapped nestmates, prioritizing pupae over adults, yet invest considerably more time in foraging and feeding than in rescuing. Only a minority of individuals engage in rescue behavior, while most foragers focus on searching for food. Rescuers exhibit several distinct rescue behaviors, and the “rescue behavioral profile” used depends on the type of victim (e.g., pupa vs. adult nestmate). We also demonstrate that the spatial arrangement of stimuli, i.e., prey, trapped nestmate, and pitfall traps, and their position relative to the nest entrance, influence both arrival at, and investment in each. Finally, we document a neglected cost of rescue behavior: Rescuers delay their arrival at food resources, a meaningful cost when prey is scattered. Previous studies have typically assumed such costs without directly quantifying them. In sum, desert ants face multiple trade-offs while foraging, improve their performance with experience, and must balance conflicting ecological demands.

Dealing with sanitary risks: corpse management in ant societies

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Quentin AVANZI

Abstract

Insect societies, which are at a high risk of disease outbreaks, have evolved sanitary strategies that contribute to their social immunity. Here, we have investigated in the red ant *Myrmica rubra*, how the removal of nestmate cadavers (i.e. necrophoresis) is socially organized, whether a functional group is specialized in corpse management and to what extent the social organisation of this task is modulated by the pathogenicity of waste items. First, a follow-up of tagged ant individuals allowed us to assign half of the colony members to functional groups (foragers, intermittent foragers, domestics, nurses, and inactive workers). Then, in response to the introduction of uninfected or sporulating corpses into the nest, we found that intermittent foragers were the most involved in necrophoresis, as they touched, moved, and discarded more cadavers. Interestingly, sporulating corpses induced a more generalized response involving workers from all functional groups, thereby accelerating the rejection of cadavers from the nest. The individuals in contact with corpses were also prophylactically engaged in more grooming behavior, suggesting the existence of hygienist workers within ant colonies. These findings raise questions about sanitary trade-offs in group-living insects, which may either concentrate health risks on a few workers who are highly specialized in waste management or expose a larger population of groupmates who cooperate to accelerate the sanitization of their environment.

Reference: Avanzi Q., Lisart L., Detrain C. 2024. Social organization of necrophoresis : insights into disease risk management in ant societies. Royal Society Open Science, 11(12). <https://dx.doi.org/10.1098/rsos.240764>

Corpse removal in ant societies: a social response to pathogen vulnerability?

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Claire DETRAIN

Abstract

Prophylactic sanitary behaviors, such as the removal of dead individuals (necrophoresis), play a major role in limiting disease transmission in insect societies. Colonies may differ in the efficiency of this waste management depending on their intrinsic susceptibility to pathogens. We hypothesized that more vulnerable colonies could compensate for weaker physiological immunity by investing more in collective sanitary behaviors. This prediction was tested in 17 colonies of the yellow meadow ant *Lasius flavus*. Worker survival after exposure to the entomopathogenic fungus *Beauveria bassiana* was used as a proxy for colony-level pathogen susceptibility, while sanitary performance was assessed through corpse removal dynamics. We found that worker mortality following pathogen exposure varied strongly among colonies but was highly consistent within colonies, likely reflecting shared genetic and physiological characteristics among nestmates. Colonies also differed markedly in their responses to introduced corpses. Interestingly, more vulnerable colonies initiated corpse removal significantly faster than more resistant ones during the first hour, but this relationship disappeared by the end of the four-hour observation period. This faster corpse removal may reflect a short-term behavioral response to compensate for higher pathogen susceptibility and may arise from variation in colony age structure: colonies with a higher proportion of older workers may be both more susceptible to infection due to immunosenescence and more efficient at corpse removal due to the presence of individuals specialized in necrophoresis. Together, these results suggest that collective sanitary behaviors can temporarily offset physiological vulnerability, highlighting that pathogen resistance emerges from both individual susceptibility and colony-level organization in social insects.

Changes in gene expression linked to foraging choices in self-medicating *Lasius platythorax* ants

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Hahn CHIRSTOPH, Heikki HELANTERÄ, Dalial FREITAK

Abstract

The ability of animals to alter their diet to include various medicinal compounds in response to pathogen infections is widely reported, but little is known about the internal mechanisms that drives this change in behaviour. We used a combined approach of behavioural and physiological methods to study self-medication in *Lasius platythorax*. By giving colonies a diet choice between a standard food and a food supplemented with 4% H₂O₂, we show that colonies exposed to the entomopathogenic fungus *Beauveria bassiana* increase in their foraging on the H₂O₂ supplemented food compared to sham-treated control colonies during the progression of disease. The dynamic shift in foraging choices of exposed colonies improved the survival against the pathogen infection, confirming self-medication in *L. platythorax* for the first time. In addition, RNA sequencing showed that there was significant gene regulation during the progression of infection with different genes being regulated at different times. Interestingly, ants showed a significant upregulation of the gene *Malvolio* during infection, showing an overlapping temporal pattern to the foraging on H₂O₂ food. *Malvolio* has been shown to play a part in immune responses and the modulation of dietary preferences in other insects, making it a specifically interesting gene to study further in a self-medication context. Our results confirm self-medication in a new species of ants, and gives the first insight into how infection may change the activity of genes which might influence self-medication behaviours in ants.

Task performance and queen presence influence the brain transcriptome in a bumble bee with a flexible division of labor system

Guy BLOCH (The Hebrew University of Jerusalem, Guy.bloch@mail.huji.ac.il)

Abstract

Division of labor in reproduction and in task performance are two hallmarks of insect societies. Bumble bees and honey bees are both eusocial but differ in the social organization of their colonies. Bumble bees exhibit size-related division of labor among adult workers that is not influenced by juvenile hormone (JH), whereas honey bees exhibit age-related division of labor among same size bees that is influenced by JH. We hypothesized that despite these differences, some common molecular pathways for social organization are shared between the two species. We addressed this hypothesis by analyzing brain transcriptomes of bumble bee foragers and nurses from queenright colonies, as well as of queenless workers, using RNA sequencing, followed by qPCR validation of selected genes. The brain transcriptome of nurses, foragers and queenless bees was different, with little overlap. The set of genes influenced by JH treatment overlaps with the genes influenced by the queen presences but not with those associated with the division of labor. These results support and extend the evidence that in bumble bees JH regulates reproduction but not the division of labor among workers. We found significant overlaps between genes differentially expressed among workers performing different tasks or as a function of the queen presence in the current study with bumble bees and previous studies with the honey bee *Apis mellifera*. These findings support the hypothesis that a common “toolkit” of genes is involved in the regulation of division of labor in reproduction and in task performance in honey bees and bumble bees.

The reversible specialization of ant queens allows them to start a new colony again

Hugo LE LAY (IRBI, Hugo.lelay@univ-tours.fr)

Romain LIBBRECHT, Léa DROESBEKE-FUENTE

Abstract

In eusocial insect colonies, the only function of queens is to produce eggs. This specialization is typically considered as being independent of environmental conditions. However, a recent study demonstrated that the queen specialization is regulated by the social environment. First, founding queens that express non-reproductive behaviors (e.g., brood care) to establish their colony become specialized when in presence of workers. Second, established queens experimentally isolated from their workers lose their specialization and revert to expressing brood care. Our objective is to understand why established queens retain this ability to express brood care. We propose that it would be beneficial in situations where queens lose all their workers and must start a new colony again. This hypothesis makes two predictions that we test using young *Lasius niger* colonies. First, we predict that some environmental perturbations may lead to the loss of all the workers. In the first months after the foundation, ant colonies may be exposed to various types of stress. If queens and workers differ in resistance to such stress, this could produce situations where all workers die but the queen survives. We are in the process of subjecting 190 young colonies to multiple stress to monitor the survival of queens and workers. The second prediction is that once isolated, queens would care for the brood to ensure the production of new workers. To test it, we isolated 82 queens either with 5 young larvae or completely alone. We found that within 5 months, 84% of the queens isolated with larvae would succeed in producing a new worker, while 53% of the fully isolated queens managed to do so. This demonstrates that the behavioral flexibility of ant queens enables them to start a new colony again, which will help us understand queen specialization and division of labor in ants.

#12526

EVOLUTIONARY GENETICS: Eco-evolutionary dynamics of sexual selection 2

30/06/2026 at 14:00, Montlouis

How animals beat the heat: sexual selection increases population fitness under thermal stress

Natalie PILAKOUTA (University of St Andrews, Npila1@gmail.com)

Abstract

Due to global climate change, animal populations are experiencing rapid environmental changes, which impose novel selection pressures on organisms and increase the risk of population extinction. There is thus a pressing need to understand what affects the capacity of populations to respond and adapt to thermal stress. In recent years, there has been increasing interest in how sexual selection may influence a population's ability to cope with thermal stress. For example, it has been suggested that stronger mating preferences for "good genes" could lead to higher quality offspring that are more likely to survive. Indeed, there is some experimental evidence that strong sexual selection can increase population resilience and reduce the risk of extinction. Sexual selection could therefore improve a population's ability to cope with climate change. Yet, temperature changes may also alter the strength or direction of sexual selection, thereby leading to complex interactions and eco-evolutionary feedback loops between climate change and sexual selection. In this talk, I will discuss the findings of two meta-analyses and an experimental study examining the complex relationship between sexual selection and population fitness.

#11185

EVOLUTIONARY GENETICS: Eco-evolutionary dynamics of sexual selection 2

30/06/2026 at 14:30, Montlouis

Sexual Selection and Adaptive Potential - Lessons from Seed Beetles

David BERGER (Department of Ecology and Genetics, Uppsala University, Sweden, David.berger@ebc.uu.se)

Abstract

Ever since Charles Darwin's own attempts at coming to grips with sexual selection, researchers have debated its influence on adaptation. More recently, particular attention has been devoted to understanding the impact of sexual selection on adaptive potential and extinction risk in populations facing rapid environmental change. A central issue underlying current controversies in this debate is the many opposing effects that sexual selection can have on reproduction and survival of individuals and populations. In this talk, using our own studies on the seed beetle, *Callosobruchus maculatus*, as a backdrop, I illustrate that these effects all occur simultaneously within single populations. I further show that their impact on population demography and adaptive potential is likely to be strongly dependent on the environmental conditions at which they play out. I finish by discussing results from a recent experiment testing theoretical predictions on the role of sexual selection in evolutionary rescue. The result from this experiment suggests that moving away from simple laboratory environments to study dynamics under more natural settings is likely to shift views on the net effect of sexual selection on population viability. Future research should aim to identify general mechanisms by which environmental variation influences mating systems and mating interactions to determine the long-term fates of natural populations.

Sexual selection favours the evolution of thermal stress tolerance in *Drosophila melanogaster*

Justine ARMENGAUD (Centre d'Ecologie Evolutive et Fonctionnelle, CNRS, Montpellier, Armengaudjustine@gmail.com)

Alexandra IDIER, Solène LIÉGEOIS, Vincent FORAY, Lucas MARIE-ORLEACH

Abstract

Will populations evolve rapidly enough to cope with global warming? As ectotherms, insect populations are particularly vulnerable to the rise of unusual temperature conditions and, while thermal adaptation is usually studied through the sole lens of natural selection, sexual selection can also play a crucial role. Here, we asked whether sexual selection promotes or hampers thermal adaptation. To address this question, we quantified genetic variances and covariances using a quantitative genetics framework in a natural population of *Drosophila melanogaster*. We estimated the narrow-sense heritability of heat and cold stress tolerance in both sexes, together with male competitive siring success as a proxy for sexual selection. Preliminary results showed weak heritability values for heat and cold stress tolerance in both sexes, and for male competitive siring success. Importantly, however, these results revealed a positive genetic covariance between male competitive siring success and (i) male cold stress tolerance, and (ii) female heat stress tolerance ; suggesting that genotypes favoured by sexual selection also are more tolerant to cold and heat stress. Thus, our findings overall reveal genetic correlations between thermal stress tolerance and components of sexual selection, documenting how eco-evolutionary dynamics between natural and sexual selection can shape thermal adaptation.

Plastic and evolutionary consequences of heat exposure on mating behaviour and fertility in a monandrous species

Leonor RODRIGUES (CE3C - Centre for Ecology, Evolution and Environmental Changes, Alrodrigues@fc.ul.pt)

Afonso GRANDELA, Marta ANTUNES, Marta SANTOS, Margarida MATOS, Pedro SIMÕES

Abstract

Rising temperatures have a detrimental effect on reproduction and, consequently, on population persistence in many organisms. In many taxa, the toll on fertility is due to males becoming sterile. Yet, the same temperatures that render males sterile do not affect females as much, meaning they can buffer the negative effect on male fertility, for instance, by mating multiple times. However, this rescue of fertility by females should be conditional on populations' mating system and sexes' mating behaviour. Unfortunately, most work on this subject has been done on polyandrous species, remaining unclear if and how will monandrous species respond. To fill this gap, we studied the real-time evolution of two bio-geographical distinct populations of a monandrous fly — *Drosophila subobscura* — subjected to a warming regime. We assessed the impact of high temperatures on male mating behaviour and fertility, as well as the impact of reduced male fertility on female mating behaviour and fertility. We found that the toll in mating behaviour due to heat can be recovered whereas that in reproductive success cannot. We also saw that monandrous females exposed to heat-stressed males accept to remate, an advantageous behaviour that leads to the recovery of their reproductive success. Interestingly, there was no relevant effect of population history nor of adaptation to warming on any of these traits, indicating these responses are mostly plastic. Ultimately, we bring new insights into the effects of high temperatures on monandrous species and provide a model to study how a shift from monandry to polyandry affects species' ability to respond to climate change.

Revisiting the age-old debate on fluctuating asymmetry and sexual selection

Roshan Kumar VIJENDRAVARMA (IRBI- CNRS, Roshan.vijendravarma@univ-tours.fr)

Abstract

The developmental instability-sexual selection hypothesis postulates fluctuating asymmetry (FA) in individuals as a readout of their developmental instability, and that it is thus a reliable cue to assess the genetic quality of potential mates and competitors. Innumerable studies across the taxa have tested this hypothesis over the last four decades, but the experimental data is heterogeneous and largely inconclusive. The hypothesis remained a highly controversial topic in biology with several criticisms levied against it, including allegations of fraud. The observed heterogeneity in the vast amount of empirical data, is biologically relevant and needs to be understood. By revisiting this empirical data, I propose a new theory that re-establishes the idea that FA is indeed a target for sexual selection; explains satisfactorily the heterogeneity in data so far; and addresses the criticisms levied against some postulates of the original hypothesis. Using *Drosophila melanogaster*, a species wherein females identify symmetric males through their song and preferentially mate with them, I empirically validate this new theory.

#10984

EVOLUTIONARY GENETICS: Eco-evolutionary dynamics of sexual selection 2

30/06/2026 at 15:30, Montlouis

Integrating thermal limits of fertility and field microclimates to understand ectotherm responses to heatwaves

Graziella IOSSA (University of Lincoln, Giossa@lincoln.ac.uk)

Luke CROSBY, Sylvain PINCEBOURDE

Abstract

Heatwaves, and other climate extremes, impact ectotherm survival. Critical thermal limits are established viability thresholds when studying the impact of climate change on natural populations. Thermal fertility limits of species have been proposed alongside critical thermal limits, to better assess the sublethal effects of rising temperatures on species persistence. However, mounting evidence shows that extreme temperatures produce variable effects on reproductive traits depending on species and context. To explain this variation, and understand how sublethal effects affect ectotherms, we need to integrate physiology, ecology and evolution to be able to predict future species persistence under climate change. Here, we point towards the key role of microclimate ecology in driving this variability. Temperature extremes may affect fertility in nature interacting with microclimates, sexual selection and conflict in insects and, in turn, affecting population growth and persistence.

#10578

EVOLUTIONARY GENETICS: Eco-evolutionary dynamics of sexual selection 2

30/06/2026 at 15:45, Montlouis

Confirming the identity of genes evolving under sexual selection in *Drosophila pseudoobscura*

Michael RITCHIE (University of St Andrews, Mgr@st-andrews.ac.uk)

Stewart LEIGH, Rhonda SNOOK

Abstract

Identifying genes responsible for adaptation remains challenging, especially for genes involved in behaviours such as sexual selection. We carried out experimental evolution of *Drosophila pseudoobscura* under altered sexual selection regimes and replicate lines diverged for a range of appropriate behaviours. Genetic analyses of the lines have identified several regions of the genome showing evidence of divergence. But how do we confirm individual genes in a species lacking the genetic resources of *D. melanogaster*? Here we have knocked out several candidate genes within the divergent genomic regions, including accessory gland proteins and genes involved in sensory perception. Most mutants showed changes in relevant behaviours, and some showed sexually antagonistic effects. Pleiotropy was common. Our approach has therefore successfully identified genes evolving under sexual selection.

The plasticity and evolution of sexual conflict in response to temperature

Carazo PAU (Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, Pau.carazo@uv.es)

Abstract

Sexual selection helps purge the genome of deleterious mutations, protecting populations against extinction and allowing them to adapt faster in response to environmental changes. However, strong sexual selection can also lead to scenarios where male and female evolutionary interests do not coincide, which we call sexual conflict. Increasingly recognized as a fundamental process in evolution, a particularly striking consequence of sexual conflict is male harm, whereby males increase their reproductive success at the expense of harming females and, consequently, decreasing population productivity. Despite being a widespread occurrence across the tree of life, we still know little about what ecological factors modulate the evolution of male harm. Here, I will talk about recent work examining how temperature mediates sexual conflict in wild *Drosophila melanogaster*. Temperature is a particularly salient abiotic ecological factor that exhibits substantial temporal variation (e.g. daily, seasonally and inter-seasonally), and hence for most species in the wild sexual selection will regularly unfold in a dynamic thermal environment. Our work combines behavioural experiments, fitness assays, experimental evolution, genomics and proteomics to show that pre- and post-copulatory male harm exhibits marked phenotypic plasticity in response to normal temperature fluctuations, even within the optimal range of temperatures to which populations have adapted. Such phenotypic plasticity largely buffers the negative fitness effects of male harm to females and populations, and seems to contribute to the maintenance of substantial genetic variation in sexually selected traits via strong GxE interactions. Lastly, we show evidence of rapid divergent evolution of sexual conflict traits in populations subject to different temperature regimes. Altogether, our results suggest that temperature fluctuations might be a key driver of past and future evolution of sexual conflict.

Individual condition mediates the costs of sexual conflict through both male harm and female resistance

Miguel GOMEZ (Karlstad University, Migurl.gomez@kau.se)

Abstract

Sexual conflict arises when the reproductive interests of males and females diverge, leading to decreased female fitness due to male-induced harm. Theory predicts that individuals in good condition invest more in costly traits associated with male harm and female resistance. Moreover, local adaptation should increase the costs of sexual conflict by improving individual condition. Here, I test these predictions by manipulating individual condition in males and females of the red flour beetle (*Tribolium castaneum*) and quantifying female fecundity under high and low sexual conflict. I show that the individual condition mediates the costs of sexual conflict, and this effect is driven by both condition-dependent male harm and female resistance. Furthermore, using populations selected in a poor-resource environment, I show that although female condition shows evidence of local adaptation, male condition does not, limiting the increase of the costs of sexual conflict. I propose that sex-differences in local adaptation, being faster in females than in males, are responsible for these results. Together, my findings demonstrate clear evidence of individual condition modulating the costs of sexual conflict due to its effect in both male harm and female resistance. Further research studying sex-differences in local adaptation and the mechanistic underpinnings of male harm and female resistance would be needed to better understand the evolution of condition-dependent sexual conflict.

Do males matter for offspring recruitment?

Anneli BRÄNDÉN (Karlstad university, Anneli.branden@kau.se)

Miguel GOMEZ, Stephen DE LISLE

Abstract

The male role in population demography is unclear and overlooked, furthermore, most ecological studies on the effects of density have used a sex-ratio of 50%. We used experimental population demography to study how males affect fecundity and recruitment in *Drosophila melanogaster* by manipulating sex-ratio and adult density in three different nutritional environments reflecting male and female nutritional optima. We measured offspring recruitment, egg production (fecundity) and per capita recruitment from each vial and then fitted demographic birth functions as a complement to our analyses. Unsurprisingly, female density was (mostly) positively correlated to offspring recruitment and negatively correlated to per capita recruitment. However, we also found male density and the nutritional environment to matter for offspring recruitment, although male density dependence was far weaker than female density dependence. Our experiment places sexual conflict in an explicit demographic context and shows how males play an important role in population demography, and increasing female density is not necessary the most efficient way of maximizing recruitment to the next generation since female density dependence is far stronger than sexual conflict.

Ecological variables predict patterns of molecular evolution in seminal fluid proteins

Bahar PATLAR (Institute of Biology, Martin Luther University Halle-Wittenberg, Bahar.patlar@zoologie.uni-halle.de)

Axel R. WIBERG, Claudia FRICKE

Abstract

Ecological variation, especially climate, is increasingly recognised as a driver of sexual selection and sexual conflict, but the molecular targets of that eco-evolutionary feedback are still being mapped. Here, we use whole-genome Pool-seq data from 144 *Drosophila melanogaster* populations spanning four continents (DEST 2.0) to test whether ecological gradients predict patterns of molecular evolution in seminal fluid proteins (SFPs), key mediators of sperm competition and intersexual conflict. Across a curated core set of >350 SFPs, we find consistently elevated nucleotide diversity, higher π_N/π_S , and more positive Tajima's D relative to the genomic background, indicating abundant standing genetic variation. Strikingly, population differentiation (population-specific F_{ST}) is not elevated and is often reduced when flanking regions are included, suggesting that gene flow and genotype-by-environment interactions can maintain polymorphism without strong local fixation. Linking molecular variation to the environment reveals that moisture-related variables, which are relative humidity and precipitation, dominate in explaining selection signals across dozens of SFPs, while SNP-level differentiation among populations shows broad associations with geography and climate. Focusing on Sex Peptide, we identify a specific SNP strongly linked to gene expression that shows clinal shifts in allele frequency and a pattern consistent with balancing selection at a functional nonsynonymous site associated with precipitation. Together, our results reveal that ecological conditions, especially atmospheric water, shape the evolution of male ejaculate proteins central to sexual selection and sexual conflict, providing a mechanistic foothold for understanding how the environment may alter reproductive dynamics, fertility limits, and the potential for reproductive isolation.

Facultative parthenogenesis and sexual conflict in *Drosophila mercatorum*

Ellie SMITH (University of St Andrews, Ebws1@st-andrews.ac.uk)

David SHUKER

Abstract

The paradox of sex has long fascinated evolutionary biologists, yet much of this debate assumes that sexual and asexual reproduction are mutually exclusive strategies. However, reproductive mode is not binary: some organisms can reproduce both sexually and asexually, a strategy known as facultative parthenogenesis. Facultative parthenogenesis complicates the paradox of sex, as in theory it is the optimal reproductive strategy allowing organisms to gain the benefits of both sexual and asexual reproduction. Yet facultative parthenogenesis is rare in animals. Therefore, the true paradox of sex may be why so many organisms are exclusively sexual. One hypothesis proposes that sexual conflict over mating shapes the evolution of facultative parthenogenesis. Theory predicts, for example, that if females are unable to effectively resist males, or that the costs of resistance are too large, then male coercion could constrain the evolution of parthenogenesis. Whilst there has been extensive modelling of these ideas, empirical studies exploring the costs of mating for sexual and asexual females remain limited. Here I will report a series of experiments exploring costs of mating in the facultatively parthenogenetic fruit fly *Drosophila mercatorum*. *D. mercatorum* is capable of low levels of parthenogenesis in natural populations and exclusively parthenogenetic female lines have been established and maintained in the lab for many years. By manipulating both the number of males and the duration of exposure to males for sexual and asexual females, I will quantify the fitness consequences of male-female interactions and how they differ for sexual and asexual females. The results of these experiments will allow me to begin to parameterise existing models and provide a more quantitative test of the role of sexual conflict in the evolution of facultative parthenogenesis.

The very short sperm of *Cotesia congregata* and the tiny spermatheca: a chicken-and-egg type evolution?

Christophe BRESSAC (IRBI University of Tours, Christophe.bressac@univ-tours.fr)

Abstract

By comparing insects in their reproductive systems, anatomy and physiology, it is possible to relate the morphological diversity of spermatozoa to the female storage organs. As an example, in the *Drosophila* group, some species have very long sperm, longer than the body of the male, which are stored in a so long spermatheca, keeping only longer spermatozoa and giving no chance to shorter ones. At the opposite, in other insects as parasitic wasps, tiny spermatozoa could have a flagellum shorter than the nucleus, resulting in an extreme miniaturization. It would be surprising if such reduction in gametes length resulted from an evolutionary process that was the reverse of the gigantism of spermatozoa.

The spermatozoon of the parasitoid wasp *Cotesia congregata* is an extremely short gamete measuring less than 7 μm , that is 12500 times shorter than the longest in animals. The small female spermatheca stored ~1000 sperm, resulting in a huge sperm concentration. Females produced up to 370 diploid daughters, corresponding to the effective use of 34% of the average sperm stock. Haploid males made up a greater proportion of broods in later parasitisms in this insect where females only mate once. This has evident consequences on the success of parasitism in this insect reared for biocontrol, and deserves to be investigated at the light of sexual selection.

Sperm miniaturization may be an adaptation to transfer increased quantities of sperm for the entire reproductive life of females in the absence of sperm competition but in the reduced space offered by the spermatheca. The question of the coevolution between sperm length and spermathecal volume reaches this of the chicken and egg...

One mother for two species: obligate cross-species cloning in ants

Jonathan ROMIGUIER (ISEM - CNRS - Université de Montpellier , Jonathan.romiguier@umontpellier.fr)

Abstract

Living organisms are assumed to produce same-species offspring^{1,2}. Here, we report a shift from this norm in *Messor ibericus*, an ant that lays individuals from two distinct species. In this life cycle, females must clone males of another species because they require their sperm to produce the worker caste. As a result, males from the same mother exhibit distinct genomes and morphologies, as they belong to species that diverged over 5 million years ago. The evolutionary history of this system appears as sexual parasitism³ that evolved into a natural case of cross-species cloning^{4,5}, resulting in the maintenance of a male-only lineage cloned through distinct species' ova. We term females exhibiting this reproductive mode as xenoparous, meaning they give birth to other species as part of their life cycle.

Laser remote sensing of foraging insect fluxes in the landscape.

Mikkel BRYDEGAARD (Lund University, Mikkel.brydegaard@fysik.lth.se)

Abstract

Insect flight direction close over ground can differ between anything from hitchhiking with the wind, plume searching perpendicular to the wind, host seeking flying upwind, ascending after hatching or descending invasion of pests. New photonic remote sensing schemes of insect in situ not only offer specific of discerning hundreds of groups, the concepts can also be used to assess insect dispersal and fluxes in the landscape in relation to topography and winds. We revise methods both for laser profiling of fluorescent tagged insects and unlabeled insects in situ. In the future we foresee how multiple time asymmetries in entomological lidar signals can simultaneously provide massive observation numbers, decent species specificity and three-dimensional flux assessment.

Flight Behaviour of Bees and Moths Revealed by Harmonic Radar

Jacqueline DEGEN (University of Oldenburg, Jacqueline.degen@uol.de)

Abstract

Understanding insect flight behaviour in natural environments requires tracking tools that combine sufficient spatial range with minimal disturbance to the animal. Harmonic radar provides such a framework by allowing the continuous recording of flight trajectories of small insects, while using extremely lightweight transponders that preserve natural behaviour. We employed such a harmonic radar system to track individually marked flying insects in the field, with positional updates every three seconds and a detection range of up to one kilometre. Using this system, we recorded the flight paths of honeybees during orientation and foraging flights. Radar tracking revealed that bees explore distinct sectors of the surrounding landscape during their initial orientation flights. These exploratory movements were not predictive of later foraging directions but supported the acquisition of visual landmark information that enabled efficient navigation and reliable return to the hive. Applying the same technique to nocturnal insects, we investigated the flight behaviour of moths navigating complex lightscapes. Radar recordings showed that celestial cues, particularly the moon, play an important role in orientation. Artificial light sources such as streetlights significantly altered flight trajectories, yet only a small fraction of individuals terminated their flights at the light source. Many moths passed streetlights without entering the light cone, suggesting that attraction to artificial light depends on flight altitude rather than simple phototaxis. Together, these studies illustrate how harmonic radar serves as a powerful, unifying tool to reveal key principles of insect flight behaviour across diurnal and nocturnal species.

Tracking the flights of moths to pheromone lures under natural bat predation pressure using event-based sensors

Yuval COHEN (Northern R&D, MIGAL - Galilee Research Institute, Department of Evolutionary and Environmental Biology and Institute of Evolution, Faculty of Natural Science, University of Haifa, Uvicohen@gmail.com)

Omri Yehuda SHERMAN, Arjan BOONMAN, Yossi YOVEL, Nir SAPIR, Liora SHALTIEL-HARPAZ

Abstract

Despite being essential for ecological and applied research, tracking insects in flight remains difficult due to their small size and rapid movements. Conventional frame-based cameras are poorly suited to this task because they cannot reliably trigger on insect motion and capture frames regardless of target presence, generating large amounts of unnecessary data. Event-based sensors (EBS) offer a promising alternative by recording only changes in pixel intensity at high temporal resolution, with high dynamic range and low energy consumption, thereby improving the signal-to-noise ratio. Despite several proof-of-concept demonstrations, EBS have not been applied to address insect ecological questions in natural field settings. We used EBS to track cotton bollworm moth flights over tomato fields with synthetic pheromone lures arranged in clustered, evenly spaced, or no-pheromone control treatments, while simultaneously recording bat activity with acoustic detectors to assess predation pressure. We hypothesized that moths would aggregate around clustered lures and modify their movement in response to pheromones, and that high bat activity would reduce moth activity and elicit more vigilant movement patterns. Using a spatter-tracking algorithm, we tracked 1,700 individual moth flights and extracted movement properties from six hours of recording spread across nine nights. Five hundred flights were classified as pheromone-attracted based on distinct movement properties, 71% of which occurred in the clustered-lure treatment. Moths in the clustered treatment displayed activity hotspots around the lures and flew longer, slower, and less straight flights than those in the other treatments. Although cotton bollworms can detect bat echolocation using their tympanic organs, we found no significant effect of bat activity on their flight behaviour. This may be because the dominant bat species recorded during the study primarily target smaller insect prey. We demonstrate that EBS can be used to study the flight responses of moths to multiple sensory cues under natural field conditions.

AnimalTA: A simple yet flexible tool for video tracking and manual corrections

Violette CHIARA (Museum and Institute of Zoology, PAS, Violette.chiara@gmail.com)

Alexis BUATOIS, Sin-Yeon KIM

Abstract

Recent advances in artificial intelligence, together with increased computing power, have led to the development of highly effective video-tracking programs. These tools enable the collection of extremely detailed data, previously unattainable. However, for simple tracking tasks, such programs are often unnecessarily complex. At the same time, there is a lack of accessible tools dedicated to simpler tracking needs, with most existing programs struggling to address the practical challenges researchers face in daily work.

AnimalTA was developed with the primary aim of facilitating the tracking process by keeping it user-friendly, and highly flexible. The program allows users to work with multiple videos simultaneously and to streamline most tasks, with the goal of minimizing the time investment required. AnimalTA is not powered by artificial intelligence and is therefore more limited than AI-based solutions. Nevertheless, because no training phase is required and thanks to a straightforward algorithm, the software is faster and easier to use, and therefore well-suited for simple tracking tasks in controlled environments.

We recently developed a new version of AnimalTA that also addresses a gap in the current video-tracking ecosystem. Although AI-based tracking tools generate increasingly large and detailed datasets, their outputs are still imperfect, and we observe a lack of tools allowing users to verify and correct tracking errors. The new version of AnimalTA enables the import of tracking data generated by other video-tracking programs. Once imported, the improved correction and analysis tools allow users to retain the benefits of high-quality automated tracking while gaining direct visual feedback and the ability to manually correct errors.

We believe that AnimalTA offers both a simple alternative to complex AI-based tracking programs for researchers who do not require highly detailed data, and a valuable complement to such programs by providing intuitive tools for data visualization, correction, and analysis.

Insect monitoring using automated traps and unmanned aerial vehicles

Julien SAGUEZ (CÉROM, Julien.saguez@cerom.qc.ca)

Simon CHAUSSÉ, Hazhir BAHRAMI, Karem CHOKMANI

Abstract

Monitoring insect pests is a key step in Integrated Pest Management programs. Monitoring in large-scale field crops requires tools that provide rapid and accurate data on the occurrence and the abundance of the pest. The development of new technologies such as unmanned aerial vehicles (UAVs) and automated insect traps offers new opportunities to enhance pest surveillance and support timely decision-making. UAVs equipped with high-resolution sensors allow the detection of early crop stress potentially associated with insect activity and damage. In parallel, automated traps, using optical sensors, cameras, the internet of things and machine-learning-based classification, provide continuous, real-time data on insect presence, abundance, and flight dynamics.

These technologies significantly reduce dependence on manual field scouting and increase the precision of monitoring programs for several key pests affecting crops, including wireworms, cutworms and other moth species. Furthermore, combining aerial imagery with automated trap data can facilitate the development of spatial models linking pest pressure to crop condition, ultimately improving risk assessment and supporting integrated pest management.

This talk will present an overview of current applications, and preliminary results obtained in the agricultural context in Quebec.

Visual conditioning in mosquito larvae and nymphs *Aedes aegypti*

Fernando GUERRIERI (Université de Tours, Fernando.guerrieri@univ-tours.fr)

Lucas STEBLESKI

Abstract

We studied visual conditioning in all the pre-imaginal stages of *Aedes aegypti* mosquito. Mosquito larvae live in water. They exhibit a stereotyped escape response to vibrations as a strategy to avoid potential dangers, such as predators. Our aim was to assess the ability of larvae and pupae to associate a neutral visual stimulus with vibration. Larvae or pupae were placed individually in Petri dishes that could be illuminated from below, revealing a shadow (the neutral visual stimulus), which was then followed by a vibration that elicited the escape response (the unconditioned stimulus). Over the course of ten presentations of the paired stimuli, larvae from stages L3 and L4 responded to the visual stimulus, which had become a conditioned stimulus. In contrast, larvae from stages L1 and L2, as well as pupae, did not respond to the visual stimulus at the end of training. Having an experimental protocol for studying associative learning in mosquito larvae and pupae will allow to apply different learning paradigms, to compare performances among different species and to assess the impact of environmental conditions on cognitive abilities.

High-resolution data on small arthropods: an in situ scanner to provide unprecedented information on their ecology

Cécile ALBERT (CNRS, Aix Marseille Univ, IMBE, Cecile.albert@imbe.fr)

François HAMONIC, Benoit GESLIN, Virgile CALVERT, Olivier BLIGHT

Abstract

Technological advances in animal tracking have provided unprecedented opportunities to address long-standing questions about individual animal movement. However, technical constraints still limit the acquisition of high-resolution in situ data to large species, leaving small arthropods largely overlooked. We developed an in situ RFID-based scanner capable of collecting high-resolution spatial and temporal data on small arthropods. Here, we introduce this new tool, demonstrate its efficiency and explore the types of species it can track. We used it to investigate the impact of habitat quality on the movement and habitat selection of a common beetle (*Asida sericea*). We showed that *A. sericea* is a nomadic species whose movement paths and the time individuals spend in different areas are influenced by stone cover. Our scanner enables us to address questions regarding the activity rhythm, navigation, space use, habitat selection and behaviour of small arthropods, opening up new avenues for understanding their ecology.

#11956

ECOLOGY & BEHAVIOR: Imaging sensing and tracking tools 2

30/06/2026 at 14:00, Villandry

Cracking a circuit for value-based memory in the larval brain

Claire ESCHBACH (Universite Paris-Saclay / CNRS, Claire.eschbach@cnr.fr)

Abstract

Efficient adaptation to stochastic environments relies on forming and updating associative memories that predict appetitive or aversive outcomes from sensory experience. How neural circuits generate such value-based predictions is a central question in our research.

We study the larva of *Drosophila melanogaster*, which offers unique experimental advantages, including a compact nervous system, powerful genetic tools, robust learning paradigms, and a synapse-resolution brain connectome.

In this talk, I will present the neurogenetic, imaging, and behavioral approaches we use and develop to dissect the circuits underlying value-based memory formation in the larval brain. Our goal is to derive general principles of memory circuitry that extend beyond *Drosophila*, to other insects and, more broadly, across animal species.

Using an optical sensor to measure the ground reaction forces of insects during locomotion

Vincent FOURCASSIÉ (Centre de Recherches sur la Cognition Animale - CBI, Vfourc@gmail.com)

Vincent FOURCASSIÉ, Elliot PEREZ, Pierre MORETTO, Vincent MANSARD

Abstract

Measuring the forces generated by the six legs of insects during locomotion, and the opposite forces exerted by the ground on them, i.e., the Ground Reaction Forces (GRFs), is essential for understanding the role of each leg in decelerating and accelerating their center of mass. However, measuring these GRFs is a difficult task due to the small size of insects and the weak intensity of the forces involved. Few systems have been designed to date to accomplish this task and those that do exist either are costly to manufacture or can measure the GRFs of only one or a few legs at a time. We designed a low-cost and versatile innovative system that is able to measure the planar components of the GRFs generated by insects and can be adapted to investigate the locomotion of insects with a large range of body sizes. The system is based on an array of flexible micropillars on which the insect is walking and whose deformation can be tracked by image analysis. It has a large observation field and can cover several times an insect's body length, allowing to measure simultaneously the GRFs of all legs in contact with the substrate on several locomotor cycles. We illustrate the use of our system with the measure of the GRFs produced by ants during turning maneuvers. Contrary to what happens in straight-line locomotion, in which the two alternate tripods have similar dynamics, we found that legs have slightly different roles during turning maneuvers, depending on whether they lie on the inside or the outside of the curve that the insect is following.

Kinematic reconstruction and dynamical analysis of microinsect flight: modelling

Dmitry KOLOMENSKIY (Skolkovo Institute of Science and Technology, D.kolomenskiy@skoltech.ru)

Sergey FARISENKOV, Nadezhda LAPINA, Egor ZHIRKOV, Aigul MUKHUTDINOVA, Victor KIREEV, Alexey POLILOV

Abstract

Insect flight research is an inherently interdisciplinary field that integrates a wide range of engineering tools and techniques within entomological investigations. It has become common practice to employ computational fluid dynamics simulations based on detailed morphological and kinematical models to evaluate the aerodynamic performance of insect species. Our presentation focuses on the application of such methods to microinsects with body lengths below 0.5 millimeters. To reconstruct flapping wing motions, we use data from synchronized high-speed camera systems equipped with macro lenses, providing a sufficient number of viewing angles for three-dimensional tracking. Geometric three-dimensional wing models are then constructed from data obtained through light and scanning electron microscopy. These models serve as inputs to a computational fluid dynamics solver, which produces a complete description of the surrounding airflow and the distribution of aerodynamic loads. We will demonstrate the use of these techniques in analyzing the aerodynamic performance of various thrips species. This study was supported by the Russian Science Foundation (Project No. 25-64-00002).

Evaluating the impact of bruchid beetle (*Bruchus rufimanus* Boh.) on faba bean (*Vicia faba* L.) seeds using 3D tomography analysis

Antoine PICHON (Teagasc & South East Technological University, Antoine.pichon@teagasc.ie)

Sherif HAMDY, Laurence LE CORRE, Louise MCNAMARA, Eamon NOLAN, Sheila ALVES

Abstract

The present study introduces, for the first time, the use of microtomography with optimized acquisition parameters to analyse the damage caused by *Bruchus rufimanus* in faba bean seeds. Seeds of faba bean, variety LYNX, from three seasons (total seed number = $500+1200+1200=2900$) were separated in (i) healthy seeds, (ii) seeds damaged by a bruchid larvae that died before completing its development, (iii) seeds damaged by a bruchid that successfully completed its life cycle, and (iv) seeds parasitized by a natural enemy and analysed by X-ray computed tomography, and 3D imagery was performed using software efX-CT and Avizo 9.0. From the 3D reconstructions, a wide range of morphological and structural descriptors were measured, including seed volume, surface area, diameter, flatness, surface rugosity and sphericity. In addition, damage-related traits were quantified, such as damaged volume, number of holes, location of damage, and the presence or absence of insect remains.

The results indicate a non-negligible season effect on seed morphology for healthy seed. Therefore, season was added as a random intercept in all subsequent mixed models and used as a stratification factor in multivariate analyses. Bruchid beetle infestation significantly impacted total seed volume, with smaller volumes associated with seeds damaged by a bruchid that successfully completed its life cycle, which may suggest the deployment of a specific plant mechanism upon successful seed infestation. The volume of damage varied from 0.02 to 50.7%, with a mean and median of 6.0% and 4.8%, respectively. The presence of bruchid beetle significantly increased rugosity and decreased sphericity of the seed. The characteristics of the seeds damaged by a bruchid larvae that died before completing its development and the seeds parasitized by a natural enemy fell between healthy seeds and seeds damaged by a bruchid that successfully completed its life cycle.

A new standardised method for high-throughput insect weight estimation from images

Melika BAGHOOEE (Center for Quantitative Genetics and Genomics, Aarhus University, Denmark, Melika@qgg.au.dk)

Robert THALHEIM, Fevziye HASAN, Quentin GEISSMANN

Abstract

Computer vision and AI are now widely used for automated insect classification, but their potential for estimating other traits, such as biomass, is not yet fully explored. Insect biomass is a key measure of ecosystem function, informing pollination, decomposition, food webs, and responses to environmental change. It is commonly used to track insect trends and declines and to estimate the carbon content of insect communities. Most monitoring programs measure wet bulk biomass because it is fast and practical. However, this method masks variation between specimens and limits our ability to understand how biomass changes within and between species across treatments or environmental gradients. Obtaining individual-level biomass is more challenging as each specimen must be dried and weighed. This labour-intensive process limits throughput and the use of individual biomass in monitoring. A standardized imaging setup combined with a computer vision model can estimate biomass rapidly and with greater resolution, enabling more scalable and informative monitoring.

“EntoScan” is a low-cost, standardized imaging system using a modified flatbed scanner to acquire high-resolution images of insect samples. The setup supports both Petri dish and multi-well plate formats, enabling efficient processing of large sample volumes or imaging individual insects with minimal handling. After image acquisition, we define a biomass factor based on the relationship between the insect size and measured biomass to train a convolutional neural network to estimate this factor directly from the images. The model’s predicted biomasses are validated against manually weighed specimens.

Our results show that our image-based approach provides very accurate ($R^2=0.9$) dry mass estimates while reducing effort and processing time. Because it is affordable, scalable, and easy to use, this method could serve as a standardized tool for monitoring insect biomass. By streamlining biomass estimation, it supports broader ecological assessments and the integration of biomass data into research, conservation, and agricultural management.

Functional morphology of the water strider tarsus: unique adaptations and evolution of the surface gliding specialisations

Jordan DRAPIN (IRBI (UMR 7261), CNRS/Université de Tours, Jordan.drapin@live.fr)

Rolf BEUTEL, Arnaud BADIANE, Mirjam URB, Mathieu VENIN, Jérôme CASAS, Abderrahman KHILA

Abstract

The acquisition of a new trait is a major factor in adaptation that can lead to species diversification. Due to the constraints of living between air and liquid, the diversification of Gerridae has been possible thanks to the diversification of their appendages in the middle leg and modes of locomotion. A good knowledge has been acquired on Gerridae and the association between the external morphology of the legs, gait variation performance and habitat. By contrast, there is a lack of information on the functional use of key tarsal structures such as the claws, and the more specialized one such as the fan present in certain species. We sought to understand how the structures into the last tarsomere of the middle leg varies between four species of Gerridae from the claw to the fan-shaped claws. Using X-ray microtomography and 3D geometric morphometrics, we sought to determine whether these structures are integrated and modular, and propose a full description of the movement of those structures.

Comparative study of forewing surface ultrastructure in Eneopterinae crickets, with possible implication on male song frequency (Gryllidae, Eneopterinae)

Louna ROYER (Biological Science, National University of Singapore & Institut de Systématique, Evolution, Biodiversité, MNHN, Paris, France, Lounaroyer@gmail.com)

Teddy GAIDDON, Ming Kai TAN, Antonia MONTEIRO, Tony ROBILLARD

Abstract

Acoustic signals play a key role in animal communication and are shaped by both sexual and natural selection. In crickets, males produce sound using specialized forewing structures, leading to strong sexual dimorphism in forewing morphology and functioning. While the macroscopic structures of the forewings and sound-production mechanism are well understood, they have been little studied at the microscopic scale. Yet surface ultrastructure of the forewings' membrane likely plays a role in shaping its physical properties and vibratory behavior. In the subfamily Eneopterinae, species belonging to the tribe Lebinthini show remarkable high-frequency calling songs with dominant harmonics that could be partly explained by ultrastructural differences. In the present study, we used scanning electron microscopy to compare male and female forewing membrane ultrastructure of 33 species of Eneopterinae crickets, including species producing low-frequency and high-frequency calling songs. We highlighted a great diversity of ultrastructure within the subfamily. Our results show remarkable differences between males and females in the non-lebinthini species concerning hexagonal "cells" on the dorsal face of the forewings, and between the males of the different tribes. The presence of pronounced hexagonal cells in Lebinthini males (high-frequency singers), in contrast to the flattened harp membrane of non-Lebinthini species (low-frequency singers), added to the strong sexual dimorphism of the structures, suggest a link with sound production. We are now conducting a comparative study using PGLMM to test the significance of these ultrastructural differences in relation to acoustic properties of the males' calls. We test the effect of presence/absence of the hexagonal cells on dominant frequency value and nature of frequency (fundamental or harmonic), as well as the effect of the size of these structures. We also test the hypothesis that loss of sexual differentiation for these traits in Lebinthini males, or the reinforcement of females' traits, alters the membrane's, acoustic properties.

The importance of integration – how automated monitoring methods can support the long-term monitoring of insects.

Charlie OUTHWAITE (Institute of Zoology, Zoological Society of London, Charlotte.outhwaite@ioz.ac.uk)

Abstract

InsectAI is a COST Action project that aims to develop a common understanding of the opportunities and challenges for image-based insect AI technologies and to build a coordinated approach to our research, to the benefit of all involved. In this talk, I will introduce the Action, its aims, ongoing work, and opportunities for participation. I will also focus on the ongoing projects of Working Group 4 which focuses on data analysis and integration.

Automated vision-based monitoring of insects offers an opportunity to complement ongoing long-term insect monitoring that uses traditional data collection methods. Each approach has strengths and weaknesses, but integration offers an opportunity for complementarity. However, there are challenges to integrating methods, data, and inference from different sources to gain a more complete picture of insect biodiversity change. In a paper by Working Group 4 members, we present a roadmap to highlight important considerations for integration focusing on three main areas - integrating data collection methods including understanding what vision-based methods can offer for the questions being asked, integrating data types and metadata to ensure collected data are comparable, and the need for robust inference for integrating data sources using hierarchical models. I will present this roadmap as well as ongoing work to develop a toolbox for exploratory and statistical analysis. This toolbox aims to make data integration more accessible for those interested in combining data from different collection methods and to reduce the currently steep learning curve required. The Action is open to participants from across Europe so I will also highlight ways to get involved.

AI-supported mosquito species identification based on wing images

Felix SAUER (Bernhard Nocht Institute for Tropical Medicine, Felix.sauer@bnitm.de)

Kristopher NOLTE, Renke LÜHKEN

Abstract

In mosquito surveillance and monitoring programs, accurate species identification is crucial because different mosquito species vary distinctly in their medical relevance. Traditional identification methods rely on taxonomic keys based on morphological characteristics or on molecular assays. However, these approaches require specialized entomological expertise and access to well-equipped laboratories. Here, we present AI-supported approaches for mosquito species identification by means of wing images. In contrast to mosquito bodies, the two-dimensional wings simplify the standardization during the imaging process, and the wing vein patterns provide ideal targets to capture species-specific shape variations. We developed two pipelines for wing-based species classification. The first uses convolutional neural networks (CNN) trained on labelled images, which are preprocessed to eliminate undesired features associated with the different imaging devices (e.g., background or colour variations). For the second one, we developed a tool to automatically collect landmark coordinates on the wing veins, which are subsequently used for species classification by means of geometric morphometrics. Both pipelines were applied on our freely available database with currently more than 20,000 wing images of 72 mosquito taxa. The trained CNN models consistently achieved an accuracy exceeding 95% in distinguishing 21 mosquito taxa and an additional “other” class, summarizing all mosquito taxa with fewer than 80 specimens available. The species classification algorithm based on the landmark coordinates revealed an overall accuracy greater 95%, and even achieved a high accuracy (> 90%) to discriminate *Cx. p. pipiens*, *Cx. p. molestus*, and *Cx. torrentium*, which cannot be distinguished with classical taxonomic keys. A web-hosted application is available to provide access to the system for a wide range of users (<https://balrog.bnitm.de>). The results highlight the potential of AI to facilitate insect identification. Our system offers a valuable tool for mosquito surveillance and research, and suggest its applicability to the identification of other Dipteran insects.

AI Meets Entomology: Benchmarking Genus-Level Classification of European Bark Beetles

Intuon LERTRUSDACHAKUL (The Marie and Louis Pasteur University, Intuon.lertrusdachakul@univ-fcomte.fr)

Pierre-Emmanuel LENI, Camille TABARY, Coralie BERTHEAU-ROSSEL, Coralie BERTHEAU-ROSSEL

Abstract

As climate change causes more frequent extreme weather events, bark beetle (Scolytinae) outbreaks in temperate forests have emerged as a growing threat to both biodiversity and forest economy. Identifying these pests is crucial but challenging due to their small size, similar morphology, and the limited availability of high-quality reference images. To address this challenge, we developed an innovative tool that combines entomological expertise with artificial intelligence to improve forest health monitoring in the context of climate variability.

We created a classification benchmark for genus-level bark beetle using approximately 1,600 raw images across 13 genera. Several deep learning models were modified and tested, including AlexNet, SqueezeNet, VGG, and different ResNet architectures. ResNet-50 outperformed all other models, achieving 96% validation accuracy. These results highlight the effectiveness of our classification system, which closely matches real-world identifications. Additionally, the system showed 97% precision, 96% recall, and 96% F1-score, all of which confirm the robustness and reliability of the predictions. These results were further supported by multi-class confusion matrices, ensuring the high degree of accuracy.

Our automated system provides practical benefits by reducing the labor-intensive time required for taxonomic work especially in biology, ecology, and forestry. By enabling faster and more accurate identification, this application can help in conserving woodland, protecting biodiversity and maintaining ecosystem stability.

In addition to improving taxonomic workflows, the system provides a scalable solution for real-time pest monitoring, allowing researchers to track beetle inhabitants across regions and anticipate potential impact of pest infestation before they cause widespread damage. These valuable insights into pest population dynamics offer a proactive approach to forest health management and help enhancing the resilience of natural forests in the face of an increasingly unpredictable climate.

Identification of honey bee subspecies using wing images and artificial intelligence

Adam TOFILSKI (University of Agriculture in Krakow, Rotofils@cyf-kr.edu.pl)

Abstract

Within the natural distribution of the western honey bee (*Apis mellifera*), numerous subspecies have been recognized that differ in morphology and behavior. Several of these subspecies are currently threatened due to beekeeping practices and the importation of non-native bees. Therefore, accurate identification of these subspecies is essential for the conservation of honey bee genetic diversity. Traditionally, identification has relied on molecular markers or morphometric analyses. However, beekeepers and queen breeders favor wing morphometrics due to the high costs and long processing times associated with molecular methods. This approach is accessible and requires only wing imaging and manual landmark placement using specialized software. While measurements performed by experienced users are relatively fast and highly repeatable, results may vary among operators.

To overcome these limitations, artificial intelligence methods were applied to automate and accelerate the identification process while reducing dependence on user expertise. This study used honey bee wing images from Poland, Romania, Croatia, and Serbia that were obtained from open repositories. Subspecies recognition was based on analyzing entire wing images without manual landmark annotation. A deep learning model was implemented in PyTorch, trained on a labeled dataset, and used to classify unknown wing images according to their country of origin. The model achieved high classification accuracy, demonstrating the strong potential of deep learning-based approaches for practical applications in honey bee subspecies identification and conservation.

AphiDetect : open-by-design equipment and computer vision to characterize plant-aphid interactions in controlled conditions

Océane GOURDIN (INRAE IGEPP, Oceane.gourdin@inrae.fr)

Stéphane JUMEL, Marc GALLAND, Maïwenn LE FLOCH, Nicolas LABROCHE, Théo FABIEN, Nicolas PARISEY, Emmanuel DOUMARD, Gaëtan DENIS

Abstract

Aphids exemplify adaptive evolution in response to the strong anthropogenic pressures exerted by poorly diversified and chemically protected agroecosystems. On the one hand, more sustainable agriculture would benefit from integrated pest management practices, which require a deeper understanding of plant-aphid interactions. On the other, increased cultivation of legumes (*Fabaceae*) could help reduce greenhouse gas emissions and enhance biodiversity in agroecosystems. However, existing legume collections remain partially characterized, and traditional phenotyping methods are laborious, destructive, and prone to human error. To study the genetic and molecular determinants of plant-pest interactions and describe key traits such as plant growth and aphid fecundity, the AphiDetect system was developed.

Initially tested on faba bean (*Vicia faba*) inoculated with the pea aphid (*Acyrtosiphon pisum*) under controlled conditions, AphiDetect uses an open-by-design, reproducible, and low-cost phenotyping booth to count and classify aphids by developmental stage. For each inoculated plant, the system acquires a series of 360° images. The YOLO11 model, trained on single-view images, achieves a mean absolute error (MAE) of 0.61 and a relative root mean square error (rRMSE) of 0.09, with an F1-score of 0.96 for classifying larval and adult stages. An explainability analysis (XAI) using Grad-CAM suggests that the model employs morphological criteria similar to those used by experts for stage classification. The number of aphids in each image of the series, combined with mathematical estimators, provides an estimate of the total aphid count per plant.

As a modular and open system, AphiDetect is adaptable to other legumes and pests. Future integration with multi-omics data could refine our understanding of plant resistance mechanisms, paving the way for new data-driven breeding strategies and a renewed understanding of plant-aphid interactions.

Combining image database and deep learning to understand diversity of ant colors

SEBASTIEN OLLIER (1Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland, Sebastien.ollier@unil.ch)

Tristan KLAFTENBERGER, Cleo BERTELSMEIER

Abstract

Cuticle coloration may play a key adaptive role in shaping the interactions between ants and their environment. It can influence thermoregulation, camouflage, and even protection against pathogens. Yet, very few studies have explored the diversity of coloration in ants, and to date, no comprehensive overview exists for this hyperdiverse group of Hymenoptera.

To address this gap, we developed a computer vision pipeline that combines classical image analysis tools with AI-based recognition to extract detailed color profiles of ant cuticles. Using images from AntWeb – the world's largest online database of ant specimens – we processed over 30,000 images representing more than 10,000 species. Our approach provides an objective framework that surpasses traditional methods, which often rely on subjective qualitative descriptions where human observers assign colors based on reference charts. Furthermore, it improves upon previous quantitative techniques that typically focus on a single body part and reduce its coloration to one value, or one dimension of color (generally lightness).

Our color-profiling method offers a rigorous alternative to subjective categorization and captures the full spectrum of color diversity without collapsing it into a single dimension. We demonstrate the performance of this framework compared to existing approaches, revisiting the exploration of color diversity at a global scale, across the entire family of Formicidae. For the first time, we provide a quantitative synthesis of ant coloration and examine its links with phylogeny and environmental factors that have shaped the evolution of color in ants. We demonstrate how our framework can advance the understanding of macroecology and evolution of color in ants and discuss its applicability to other insect taxa.

From Zygote to Adult: A Comprehensive Single-Cell Multi-omics Atlas of Drosophila Development to train Deep Learning models

Hannah DICKMÄNKEN (VIB.AI / KU Leuven, Hannah.dickmaenken@kuleuven.be)

Valerie CHRISTIAENS, Katina I. SPANIER, Anton DE BRABANDERE, Marta WOJNO, Suresh POOVATHINGAL, Stein AERTS

Abstract

Single-cell transcriptomics and epigenomics have transformed our understanding of cellular identity, yet a continuous developmental time course for an entire animal has remained elusive due to technical limitations. Here, we present the first droplet-based single-nucleus multimodal (RNA-seq and ATAC-seq) atlas of full insect development. We cover the whole 10 days of *Drosophila melanogaster* development to train Deep Learning models for cell type specification. As both the experimental strategy and the models are species-agnostic, they offer a blueprint for building comparable developmental atlases in other insects and non-model organisms, or the Biodiversity Cell Atlas(1), to which we conducted the first trial, including spatial transcriptomics.

For snATAC, we combined commercial 10x Genomics chemistry with our high-sensitivity, low-cost HyDrop v2 protocol to profile over 4 million nuclei in consecutive time bins. This novel resource covers embryonic, larval, pupal, and adult stages, yielding a complete zygote-to-adult regulatory roadmap. Using these data, we trained sequence-to-function models to predict regulatory elements that drive cell type specification and identify key DNA-binding proteins, i.e., transcription factors, that bind cis-regulatory elements controlling cell states over time. To link chromatin accessibility to gene expression, we additionally profiled 2.5 million nuclei using scRNA-seq and integrated the epigenomic and transcriptomic atlases. On this joint resource, we trained Borzoi deep-learning models, i.e., neural networks reading DNA sequence, and learn which motifs and features control cell-type-specific gene activity.

Based on this new resource, we infer enhancer-driven gene regulatory networks and dissect transcription factor combinations and pathways underlying the emergence of cell-type identity. Together, our technical advances for large-scale single-cell profiling and our predictive models provide a comprehensive framework for studying gene regulation and cell fate across an organism's life cycle. These offer new possibilities for insect taxonomy, allowing for testing how conserved or divergent regulatory programs shape biodiversity.

(1) Sebé-Pedrós et al., Nature (2025)

#11780

EVOLUTIONARY GENETICS: Symbionts and insects as holobionts 3

30/06/2026 at 10:30, Vouvray

Diverse routes to male killing: symbionts, mechanisms, and evolution

Daisuke KAGEYAMA (National Agriculture and Food Research Organization (NARO), Kageyama000@gmail.com)

Abstract

Over the past few decades, a wide variety of symbionts, including bacteria, protists, and viruses, have been discovered living within insect cells. Intriguingly, some of these symbionts are capable of biasing the sex ratio of their host insects toward females. Such manipulation is evolutionarily advantageous for symbionts that are transmitted strictly through females and lack horizontal transmission. Although there are multiple ways to bias the sex ratio, male killing, developmental arrest of males during embryonic or early larval stages, represents the most widespread strategy and is employed by taxonomically diverse symbionts. Recent studies have begun to identify bacterial and viral genes responsible for male killing. Unexpectedly, these genes are remarkably diverse: even within a single bacterial or viral species, distinct male-killing genes and mechanisms may operate. In this talk, I will discuss recent findings on the spread of host nuclear suppressors against male killing and the emergence of male-killing symbionts that are unaffected by these suppressors. Such antagonistic coevolution may promote the recurrent emergence of novel male-killing symbionts and mechanisms, which may drive the evolution of sex-determining systems as well as other aspects of insect ecology and evolution.

Regulation of bacteriocyte-based symbiosis in aphids: integrative crosstalk between apoptosis, UPR, CLEAR pathways and the endomembrane system

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Abstract

Microbial symbionts enable insects to thrive on nutritionally unbalanced diets and to persist under adverse environmental conditions. These beneficial symbionts can reside extracellularly, or within specialized host cells, the bacteriocytes. However, bacteriocytes are more than a privileged niches to house symbionts: they represent key evolutionary innovations, pivotal to ensure the maintenance and vertical transmission of intracellular symbionts across host generations. Recent research has shown that both symbiont and bacteriocyte numbers appear to be dynamically regulated depending on the nutritional demand, environmental stressors, and host age. Such plasticity suggests the existence of regulatory mechanisms that operate throughout the insect life cycle to control the physiology and the fate of these unique cells. Yet, the molecular and cellular determinants orchestrating bacteriocyte-symbiont communication are poorly understood. Aphids, owing to their well characterized symbiotic metabolism with the obligate symbiont *Buchnera aphidicola*, together with the availability of high-quality genome assemblies and advanced imaging technologies, provide a powerful model for dissecting the gene regulatory program underlying bacteriocyte development and morphogenesis. By integrating physiological analyses, immunohistochemistry, and RNA-seq, we recently uncovered that evolutionarily conserved metazoan pathways have been co-opted and diversified to regulate this intimate symbiosis. Using machine-learning-approaches to infer gene regulatory networks, we identified key genes and regulatory hubs, demonstrating that three major pathways (apoptosis, the UPR, and the CLEAR pathways), interact with the endomembrane system to enable bacteriocytes to accommodate millions of bacteria throughout development and adjust symbiont numbers to the insect physiology. Taking a broader evolutionary perspective, multiple aphid genomes will be used to trace the history of these pathways and to explore how this regulatory architecture extends from the mono-symbiotic system including *B. aphidicola* to more complex multipartite symbioses.

Convergent genome evolution across repeated transitions to insect endosymbiosis

Matteo MONTAGNA (University of Naples Federico II, Matteo.montagna@unina.it)

Giobbe FORNI, Jacopo MARTELLOSSI, Benoit MOREL, Dario PISTONE, Claudio BANDI

Abstract

Endosymbiosis represents one of the major transitions in the history of life. In addition to the numerous evolutionary implications for both partners, this process has consistently led to the emergence of highly reduced genomes in prokaryotes. To date, the processes shaping gene content throughout endosymbiosis have not been investigated within a broad phylogenetic framework encompassing multiple independent lifestyle shifts. Using the Enterobacterales order of Gammaproteobacteria as a representative model, a complex phylogenomic framework was inferred across more than two hundred genomes, including inferences based on single-copy gene concatenation and gene families. This diverse clade is of particular interest due to the presence of multiple independent transitions to endosymbiosis, predominantly in association with insect hosts, where endosymbionts typically provide nutritional supplementation (e.g., for blood- and phloem- feeding insects).

Analysis of over 200 genomes revealed a remarkable consistency in patterns previously reported only from scattered observations. In particular, a massive spike in gene loss was consistently associated with the transition to endosymbiosis. Subsequent loss rates within endosymbionts did not consistently increase compared to free-living species. Despite variation among clades, the results point to a contribution of reduced gene acquisition mechanisms, such as horizontal transfer and duplication, to the genome erosion occurring after the transition to endosymbiosis. A significant correlation was detected in the frequencies of gene family loss across independent endosymbiotic clades. Genes with more conserved functions, such as those with core cellular functions, and stronger sequence-level evolutionary constraints were lost less frequently, and this correlation appears to be driven by different degrees of gene essentiality. Overall, the findings highlight the constraints shaping endosymbiont gene content and the role of gene essentiality in driving parallel evolutionary trajectories.

When new symbionts enter old systems: evolutionary patterns of symbioses in leafhoppers

Veronika ANDRIENKO (Doctoral School of Exact and Natural Sciences, Jagiellonian University, Krakow, Poland, Veronika.andrienko@doctoral.uj.edu.pl)

Diego C. FRANCO, Adam STROÍŃSKI, Piotr ŁUKASIK, Anna MICHALIK

Abstract

Nested symbioses represent some of the most complex and understudied forms of insect-microbe interactions. Auchenorrhyncha, sap-feeding insects such as leafhoppers, planthoppers, spittlebugs, and cicadas, depend on two ancient bacterial partners, *Sulcia* and a betaproteobacterial symbiont (*Nasuia*, *Vidania*, or *Zinderia*). These associations persisted for ~300 million years and form one of the most stable symbioses known in animals. These associations are characterized by extreme symbionts' genome reduction, metabolic complementarity, and strict vertical transmission, enabling exploitation of a nutritionally imbalanced sap diet and promoting host diversification. Despite this long-term stability, some Auchenorrhyncha lineages have acquired additional microbial partners. Here, we show that leafhoppers of the genus *Aphrodes* host the gammaproteobacterial symbiont *Sodalis*, which, as confirmed by fluorescence in situ hybridization (FISH), resides inside *Sulcia* cells, forming a rare nested symbiosis. To investigate the evolutionary dynamics of these systems, we combined light and electron microscopy with amplicon sequencing and short- and long-read metagenomics across multiple *Aphrodes* species from European populations. Microscopy revealed transovarial transmission of *Sodalis* during oogenesis, with exclusive localization within *Sulcia* cells. Unlike the ancient obligate symbionts, which are present in all individuals and closely track host phylogeny, *Sodalis* shows a patchy distribution, frequent strain coexistence, and strong phylogenetic incongruence with host lineages. Long-read sequencing enabled recovery of nearly complete *Sodalis* genomes, and genome-based reconstructions indicate complementary retention of essential amino acid biosynthesis pathways between *Sulcia* and *Nasuia*, whereas *Sodalis* retains broader inferred metabolic potential. Similar patterns were observed in the leafhopper *Cicadella viridis*, which has lost *Nasuia* and its later replacement (*Baumannia*), retaining only *Sulcia*, highlighting the importance of dynamic *Sodalis* associations. Together, these findings reveal how ancient and newly acquired symbionts coexist within evolutionarily complex leafhopper symbioses, providing insight into the dynamics and potential evolution of nested microbial partnerships. Project funded by the National Science Centre, grant No. 2021/41/B/NZ8/04526.

The collaboration between *Anomala corpulenta* and its gut symbionts in degrading corn straw

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Jun-Bo LUAN

Abstract

Insects and their gut symbionts play vital roles in plant biomass utilization, yet the underlying mechanisms remain unclear. This study is the first to evaluate the ability of *Anomala corpulenta*, a scarab beetle, to degrade corn straw. Our results demonstrate that *A. corpulenta* can effectively degrade corn straw, and that its degradation capacity is significantly reduced following antibiotic treatment. High-throughput sequencing revealed that both *A. corpulenta* and its gut microbiota encode diverse carbohydrate-active enzymes (CAZymes), with the microbial enzymatic system compensating for the host's limited capacity to produce biomass-degrading enzymes, highlighting the crucial role of the gut microbiota in assisting the host's degradation processes. Amplicon sequencing was used to characterize the composition of the gut microbiota, and the core microbiota of *A. corpulenta* was identified by comparing individuals across different geographic populations, developmental stages, and dietary treatments. Using culture-dependent methods, more than 50 bacterial genera and nearly 10 fungal genera were successfully isolated, several of which exhibited strong straw-degrading abilities. This study provides new insights into the functional potential and application prospects of the *A. corpulenta* gut microbiota and establishes a solid foundation for further investigations into the mechanisms underlying plant biomass degradation by insects and their symbiotic microbial communities.

Identifying novel amino acid transporters in *Acyrtosiphon pisum* endosymbiosis

Catriona ANDERSON (School of Natural and Environmental Sciences, Newcastle University, UK, Catriona.anderson@ncl.ac.uk)

George PARSONS, Veronika PAVLASOVA, Alex WILSON, David THWAITES

Abstract

Acyrtosiphon pisum, like other sap-feeding Hemiptera, are dependent on close symbiotic relationships with particular microbes. In aphids, *Buchnera aphidicola* is housed in specific bacteriocyte cells and each is surrounded by a host-derived symbiotic membrane. These bacteria provide the host insect with many essential nutrients including amino acids. Complete nutrition, for both host and endosymbiont, is only achieved by their combined metabolic capacities. For this relationship to be sustained, specific transport of various nutrients (such as essential amino acids) and intermediates across the symbiotic and bacteriocyte plasma membranes must be achieved. To date, only two amino acid transporters (ApGLNT1, ApNEAAT1) have been characterised, both from the SLC36-related gene family, which is expanded in many insects. Using protein structure homology modelling and comparison to mammalian orthologues of known function we identified candidate genes for transport of specific amino acids. Empirical functional assays (heterologous expression in *Xenopus laevis* oocytes, radiotracer flux and electrophysiology) have identified and characterised the function of novel H⁺-coupled amino acid transporter proteins from *A. pisum*.

Loss of *Wolbachia*-mediated cytoplasmic incompatibility in agricultural pests

Nick WYBOUW (Ghent University, Nicky.wybouw@ugent.be)

Emma VAN REEMPTS, Godefroi GIGNOUX, Yuta OHATA, Felipe KAUAI

Abstract

Maternally transmitted *Wolbachia* symbionts induce cytoplasmic incompatibility (CI) to spread through arthropod populations. *Wolbachia*-based pest control programs rely on strong CI to suppress or replace harmful pest populations. However, CI is often weak, constraining *Wolbachia* spread and the efficacy of *Wolbachia*-based pest control. Here, we study the underpinning molecular-genetic mechanisms that shape CI strength from the perspective of both *Wolbachia* and host. Using *Liriomyza* and *Tetranychus* as pest models, *Wolbachia* transinfection and introgression uncover host genotypes that suppress CI. Effects of host genetics and development on CI strength and infection density are tracked to better understand the mechanisms of host suppression. Comparative genomics and transcriptomics provide further insights into the causal host genic factors. In parallel, we leverage circular *Wolbachia* genomes and exhaustive genome re-sequencing to track changes in the CI gene repertoires in these systems. We uncover a prominent role of several mobile genetic elements in the transfer and pseudogenization of CI genes, explaining variation in CI strength and directionality. Together, these findings inform future *Wolbachia*-based control programs and help elucidate the molecular mechanisms that underlie the widespread occurrence of maternally transmitted symbionts in arthropods.

An inordinate fondness for symbionts: Beneficial bacteria as sources of evolutionary innovations in beetles

Martin KALTENPOTH (Max Planck Institute for Chemical Ecology, Kaltenpoth@ice.mpg.de)

Abstract

Symbiotic associations with microbes are important driving forces of evolutionary innovation. The megadiverse insect order Coleoptera, the beetles, are associated with an astounding diversity of symbionts that provide a wide range of functional benefits to their hosts. Highlighting a few selected beetle-microbe associations, I will report on novel findings of symbiont-provided defense, microbe-enabled digestion of plant material, and symbiont-mediated adaptation to the abiotic environment. These examples are intended to show the impact of symbionts on niche expansion and diversification in beetles, but also provide insights into life-style switches from parasitism to mutualism in bacteria as well as the process of extreme genome reduction beyond the well-known intracellular symbioses. Furthermore, we managed to introduce a genetically tractable intracellular bacterium into one of our experimental model beetles that now allows us to study the molecular basis of symbiosis establishment as well as the interaction between the newly introduced bacterium and the ancient endosymbiont. The results provide interesting first insights into the molecular host-symbiont interplay as well as the evolutionary steps leading to the establishment of novel symbioses.

Experimental evolution reveals physiological and ecological costs of plant defence suppression in herbivores

Sara MAGALHÃES (Ce3c- Centre for ecology, evolution and environmental changes, Faculdade de Ciências da Universidade de Lisboa, Snmagalhaes@fc.ul.pt)

Mariya KOZAK, Sofia COSTA, Ines FRAGATA, Alison DUNCAN, Leonor RODRIGUES

Abstract

Herbivores have evolved a plethora of strategies to cope with plant defences. The maintenance of such diversity may result from associated physiological costs, a hypothesis lacking empirical validation. Defence suppression is a particularly enthralling counter-defence strategy, as resources made available by suppressors can be exploited by competitors, suggesting that ecological costs may also explain why this strategy is not pervasive. Here, we empirically test the existence of such costs by carrying out 26 generations of experimental evolution exposing *Tetranychus evansi*, a herbivorous mite that suppresses plant defences, to regimes where suppression does not yield a clear benefit: on tomato plants with impaired induced defences, or on tomato plants with intact induced defences in the presence of competitors. We show that suppression was counter-selected in both regimes, as compared to a regime where mites evolved on plants with intact defences and no competitors, thus clearly demonstrating the existence of physiological and ecological costs of defence suppression. As compared to the control, fecundity on plants with intact defences decreased, but only in populations evolving with competitors, suggesting distinct mechanisms underlie physiological and ecological costs. This was confirmed by different transcriptomic signatures of plants exposed to mite populations from the different regimes. Such a fast evolutionary response reveals the existence of variability in defence suppression in the ancestral mite population and lends support to the hypothesis that ecological and physiological costs are key ingredients in the maintenance of the diversity in strategies to cope with plant defences within and among herbivore species.

Leaf penetration by endophytic *Metarhizium brunneum* enables infection of *Phthorimaea absoluta* in tomato mines while inducing the crop defense system

Esther AGUILERA CUENCA (Agricultural Entomology Area, Department of Agronomy, University of Cordoba , G62agcue@uco.es)

María José GARCÍA DEL ROSAL, Fabián GARCÍA ESPINOZA, Enrique QUESADA MORAGA, Irene Magdalena RODRÍGUEZ GÓMEZ, Meelad YOUSEF YOUSEF

Abstract

The endophytic entomopathogenic fungus *Metarhizium brunneum* Petch EAMa 01/58-Su shows strong potential for managing *Phthorimaea absoluta*, a major tomato pest. We evaluated this strain at the threshold-recommended application time on heterogeneous populations, covering pre- and post-mining stages and individuals arriving after treatment to assess its protective effect against subsequent infestations.

Pre-mine sprays caused up to 40% total mortality and significantly reduced larval survival, gallery formation and adult emergence. Post-mine sprays reached 78.12% mortality, shortened pupal duration, reduced adult emergence and resulted in post-mortem sporulation. At 9 days post inoculation (DPI), histology revealed intercellular colonisation of tomato leaves and systemic infection of *P. absoluta* larvae within mines. In plants sprayed prior to infestation, females showed a slight preference for treated plants and minor larval penetration at 2 DPI. Despite this early behavioural response, long-term effects were evident, total mortality reached 28.6% at 2 DPI and 31.3% at 14 DPI, indicating induced systemic resistance (ISR) activation supported by marked induction of ethylene/jasmonic acid-related genes (*SIACO1*, *SIACS6*, *SIERF1*, *SIAOS2*, *SIOPR3*, and *SIWRKY70*), despite only trace fungal DNA in distal tissues.

These results underscore the fungal strain biocontrol potential not only towards *P. absoluta* pre-mine stages, but more importantly, a previously unreported leaf penetration behaviour enabling larval infection in the mines. Moreover, the fungal-related induction of tomato ISR can extend the impact of the treatment to new reinfestations of the lepidopteran pest, highlighting the potential of this *M. brunneum* strain to be incorporated into *P. absoluta* IPM programs.

Local adaptation in herbivorous insects: a meta-analysis

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Abstract

Local adaptation, wherein populations are well adapted to local biotic and abiotic conditions, is a common outcome of natural selection and a driver of diversification. Previous theory identified two criteria to detect local adaptation: 1) the home-away criterion compares the fitness of a population in their home environment to their fitness in a different environment, and 2) the local-foreign criterion examines differences in fitness between a local and a foreign population when experiencing the local environment. We conducted a meta-analysis synthesizing empirical evidence of insect herbivores' local adaptation to their host plants using both criteria to assess how diet breadth, geographic distance among populations, and herbivore taxonomic affiliation, impact the likelihood of detecting local adaptation. Overall, we found evidence for herbivore local adaptation using both the home-away and local-foreign criteria. Notably, contrary to theory about factors that should promote local adaptation, herbivore diet breadth, taxonomic affiliation, and geographic distance between herbivore populations did not affect the likelihood of finding local adaptation. However, the likelihood of finding evidence for local adaptation varied with herbivore clonality, the herbivore response variable measured, taxonomic distance among host plants, and features of the study design. Our results allow us to understand how local adaptation functions in the most diverse group of multicellular life on Earth, herbivorous insects.

Trichoderma harzianum enhances indirect plant defenses induced by the stink bug *Nezara viridula*

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Abstract

Plant growth-promoting fungi (PGPFs) of the genus *Trichoderma* are well known for their ability to enhance plant defenses against biotic stressors. While the effects of *Trichoderma* spp. on plant defences against phytopathogens are well documented, less is known on insect pests, particularly in terms of indirect defenses mediated by herbivore-induced plant volatiles (HIPVs). Recent studies show that *Trichoderma* species can modulate HIPV emissions that attract natural enemies of herbivores; however, information on their role in influencing plant signals involved in stink bug–egg parasitoid interactions is still limited. In particular, little is known about how *Trichoderma* spp. affect parasitoid attraction to plants induced by stink bug oviposition, and even less regarding responses triggered solely by stink bug feeding. To address this gap, we used a multitrophic system involving tomato (*Solanum lycopersicum*), the southern green stink bug (*Nezara viridula*), its egg parasitoid *Trissolcus basalis*, and *Trichoderma harzianum* T22. We carried out olfactory bioassays under controlled laboratory conditions to investigate whether root inoculation of tomato plants with *T. harzianum* T22 enhances the response of the egg parasitoid *T. basalis* to HIPVs induced by *N. viridula*. Specifically, we tested whether indirect plant responses to stink bug feeding depend on the interaction between the herbivore's sex/physiological state and root colonization by beneficial soil microbes. We also used gas chromatography-mass spectrometry (GC-MS) to assess how root inoculation with *T. harzianum* T22 influences the chemical composition of induced plant volatiles. These findings are discussed in the context of plant-insect-microbe interactions and their potential application in biological pest control.

KEY WORDS: plant growth-promoting fungi, multitrophic interaction, egg parasitoid, olfactometer experiments.

Influence of Global Change-Driven Host Tree Stress Physiology on the Bark Beetle-Associated Microbiome Composition

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Abstract

Climate-induced drought in conifer-dominated forests is often accompanied by bark beetle outbreaks. Although drought events can alter host tree physiology and defense chemistry, the mechanisms behind host tree stress and the success of bark beetle establishment remain incompletely understood. Increasing evidence highlights the bark beetle microbiome as a key mediator of nutrition, detoxification, communication, and colony establishment. We hypothesize that the microbial assemblage of the bark beetle holobiont shifts in response to feeding on drought-stressed host trees. We investigate how three years of experimentally induced drought alter the physiology and biochemistry of Norway spruce (*Picea abies*), and how host-level changes shape the microbial assemblage within the Eurasian spruce bark beetle (*Ips typographus*). Continuous physiological monitoring and biochemical analyses of host trees were combined with microbial profiling of beetle samples through metabarcoding of bacterial 16S rRNA and fungal ITS1 regions, after controlled pheromone-induced bark beetle attack. Our results demonstrate drought-associated changes in host phloem chemistry and their relationship to shifts in bark beetle-associated microbial communities, pointing towards the role of environmental stress in this multitrophic host tree-bark beetle-microbiome system.

Unveiling the factors shaping ecosystem stability under global change: phytochemistry and multitrophic interactions

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Abstract

Maintaining the stability of multitrophic interactions is at the core of agroecology. Plant chemistry is a key mediator of such interactions, however few studies have addressed the impacts of global change on phytochemicals in a holistic manner. Our project aims to investigate whether and how global change factors affect chemical profiles of plants and, in turn, plant natural defences. To address this question, we studied anthropic perturbations (tilling, warming, fragmentation) in twelve connected pairs of enclosures located in a natural grassland. We focused on two plant species: *Cardamine pratensis* (Brassicaceae) and *Pulicaria dysenterica* (Asteraceae), both families being of agronomic relevance. We measured leaf metabolites (LC-MS and NMR) at two time points, and recorded herbivores and plant performance parameters throughout the plant's life cycle. Regardless of the species, we found that soil perturbation was associated with an increase in chewing percentage, which was mitigated by warming. Moreover, undamaged cages connected to perturbed cages experienced more herbivory than cages connected to undisturbed cages. A similar pattern was observed for the size of the plants and the number of leaves and inflorescences, as well as the reproductive success of *C. pratensis*, whereas *P. dysenterica* seemed to produce more leaves and inflorescences in a warmer environment. We are currently analysing the composition of invertebrate herbivore communities' composition and structure, as well as annotating metabolomes. We expect that the results will connect the effect of global change on phytochemicals to the disruption of specific plant-herbivore interactions, and will link plant functional traits to community dynamics and stability. It will inform which chemical classes and compounds are most affected by global change, and which factors are the strongest drivers of variation in leaf chemistry. Eventually, this project may provide key insights into chemical changes that could be useful to inform adaptation measures in crop production systems.

Genetic diversity and outbreaks of the gall midge *Schizomyia castanopsisae* (Diptera: Cecidomyiidae) in Japan

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Abstract

Outbreaks of herbivorous insects can cause severe ecological and economic impacts by disrupting host plant reproduction. The gall midge *Schizomyia castanopsisae* induces inflorescence galls on *Castanopsis sieboldii* (Fagaceae), leading to drastic reductions in acorn production. Since the early 2000s, large-scale outbreaks have been recorded in the southern Izu Islands, Japan, where acorn crops have nearly failed for decades. On Miyakejima Island, larval populations were estimated at approximately 158 billion in 2017 and 36 billion in 2018. Recent surveys revealed that the species has expanded its range northward to other parts of the Izu Islands and Honshu, raising concerns about further spread and forest ecosystem impacts.

To elucidate the invasion history and genetic structure of *S. castanopsisae*, we compared mitochondrial haplotypes from populations distributed across Japan and Korea. Our results revealed two major genetic groups: (1) Kyushu, Korea, and the Yaeyama Islands, located in the southwestern part of the Ryukyu Islands, and (2) other parts of the Ryukyu Islands, the Izu Islands, and Honshu. Multiple haplotypes were detected in Kyushu and the Ryukyu Islands, whereas the Izu Islands and Honshu populations shared only two haplotypes, both common in the Ryukyu Islands. These findings suggest that outbreaks in the Izu Islands originated from recent invasions from the Ryukyu Islands, facilitated by the absence of natural enemies such as parasitoid wasps. The recent detection of *S. castanopsisae* in Korea further raises questions about its historical distribution and potential recent introductions. In addition, isolated distributions of haplotypes similar to Kyushu and Korea in the Yaeyama Islands populations suggest the possibility that allied haplotypes may be found in Taiwan and the Chinese continent.

Hidden diversity of gall midges (Diptera: Cecidomyiidae) associated with flower buds

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Abstract

Insect decline threatens ecosystem structure and function, yet insect diversity remains vastly underexplored and largely undescribed. Recent biodiversity surveys have highlighted gall midges (Diptera: Cecidomyiidae) as the most species-rich insect lineage, with global estimates exceeding one million species. However, fewer than 7000 species are currently described, indicating the presence of substantial hidden diversity. Most known species are herbivores that induce remarkable species-specific abnormal plant growth termed “galls”, while other species are phytophagous without gall-induction, predators or mycophages. Our recent surveys have revealed several gall midge species inhabiting flower buds of various plant taxa without inducing conspicuous galls, and some of these species function as pollinators. This group of flower-bud associated gall midges has never been comprehensively surveyed and has rarely been the focus of taxonomic studies. In this study, we surveyed gall midges associated with flowers and flower buds across various angiosperm families in Japan. The gall midge individuals collected were categorized into operational taxonomic units (OTUs) based on a fragment of the COI mitochondrial gene to infer species diversity. Using OTU richness, we estimated the potential number of gall midge species developing in angiosperm flowers and flower buds in Japan, using richness estimators and rarefaction/extrapolation.

Insect sentinel species exploring and monitoring agroecosystem viruses

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Abstract

Despite being the most abundant biological entities on Earth, viruses remain remarkably underexplored in terms of their diversity and ecological roles. Although considerable efforts have been made to bridge this knowledge gap, effective sampling is still limited by inaccessible regions, elusive host species, and regulatory constraints. An emerging alternative involves the use of sentinel species—organisms that respond rapidly and measurably to environmental changes—as biological samplers of viral diversity. Building on previous metagenomic work that revealed an unexpectedly high diversity of viral sequences in army ants (*Dorylus* sp.), we propose to use these ants as sentinels to explore viral diversity and for plant virus surveillance in agroecosystems in the Republic of the Congo. Specifically, we aim to investigate how accurately the army ant virome (i.e., the overall collection of viral sequences) reflects the viral diversity present in surrounding cultivated plant communities. To achieve this, we apply the virion-associated nucleic acid (VANA) metagenomics approach—which isolates and sequences viral particles without prior knowledge—to both cultivated plant leaves and army ants found in agricultural plots. We will develop metrics and analytical tools to estimate the representativeness of the army ant phytovirome, using the phytovirome of the hosting agroecosystem as a reference (e.g., fraction of plant viruses detected, percentage of reads covering plant viruses). We will further assess putative associations between army ants, cultivated plants and viruses. Finally, we will investigate possible routes of viral acquisition through dietary analyses using metabarcoding and metaproteomics. Our study aims to enable effective sentinel-based viral exploration and surveillance systems.

Friend, Foe or Freeloader: Commensalisms in Generalist Predators

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Abstract

Non-trophic interactions contribute significantly to ecosystem functioning and may be positive, neutral or negative for either of the interacting parties. Commensalisms are interactions in which one party, the commensal, is benefiting from the interaction, and the other party, the host, is neutrally affected. Despite significantly impacting ecosystem functioning and service provision, commensalisms are scarcely incorporated into wider studies of ecological networks. Flower crab spiders (*Misumena vatia*) use flower heads as platforms from which to predate flower visitors attracted by the rewards offered by the flower. We can predict the outcome to the flower visitor, but how does this impact the flower, if at all?

Using a combination of spider dietary metabarcoding to detect trophic interactions, surface eDNA from flowers to detect recent visitors and nectar macronutrient analysis to determine nutrient provision, ecological and nutritional networks will be constructed. Alongside community science data and public records of spider-flower-prey interactions, we are investigating the nature, diversity and drivers of the potentially commensal interactions between flower crab spiders and their flowers, and the implications of and for their prey. Using this model system, we will determine the ecological outcomes of commensalisms, approaches for their integration into wider ecological networks and their implications for ecosystem service provision.

Flower-derived arthropod eDNA reveals community diversity, species abundances and ecological interactions – A case study in bee pollinators

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Abstract

Environmental DNA metabarcoding has revolutionized our ability to monitor biological communities. The method has two important advantages over traditional arthropod monitoring approaches. First, eDNA analysis is entirely non-invasive. And second, the approach holds the potential to exhaustively recover true biotic interactions between arthropods and plants. But despite its undeniable promise as a non-invasive tool to study arthropod community and interaction diversity, eDNA metabarcoding from plants has several limitations. One problem of eDNA metabarcoding is its limited capabilities to quantitatively survey organisms and sampling is often performed by collecting plant materials which is invasive for plants. To address these problems, we focus on wildbees in an agricultural landscape and compare data from traditional monitoring methods against eDNA data. We show that the arthropod communities recovered by the invasive and non-invasive sampling methods are similar, but especially for monitoring bee species the invasive approach gives a more complete picture as it recovers more species. In addition, we can also make statements about arthropod-plant interactions as we have recovered the arthropod community of different plant species. Here we can show the specificity of different insect species or, conversely, identify species that are not associated with a particular plant species. The overlap of bee species found by the eDNA method and the traditional methods is high, indicating that eDNA can be used as a monitoring tool for wild bees. We were also able to semi-quantify the bees detected by eDNA. This is a major step forward in the use of eDNA as a monitoring tool. We can also make statements about the flower-bee interaction of the bees using eDNA, as we know which flower species they were found on. It is therefore possible to identify oligolectic and polylectic bee species. Our results highlight eDNA as a tool for monitoring arthropods and studying arthropod-plant interactions.

Host ecology and phylogeny shape the temporal dynamics of social bee viromes

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Abstract

Virome composition is often dependent on a combination of eco-evolutionary factors such as host trait and ecological niche. To identify the drivers shaping bee viromes, we sampled honeybee and co-foraging bumblebees, and sequenced their RNA across three time points during one year: in spring when colonies emerged, in early summer, at the peak of colony productivity, and in late summer, when colonies produce sexuals. We identified more than 100 viral species, one third being plant viruses. We used host genetic and ecological distances (measured from plant-pollinator networks) to explore the virus spatio-temporal dynamics. We found that insect viruses were mainly host specific, with honeybees showing a distinct and more diverse virome than bumblebees. Using small RNA sequencing, we also found a very small proportion of viruses that can infect both bumblebees and honeybees, whilst bumblebees share more viruses within the clade. In contrast, the presence of plant viruses in bee samples was defined by the bee's ecological niche and time of year, reflecting the dynamics of plant-pollinator interactions. This work demonstrates the respective role of host phylogeny and host ecology on the composition of pollinator viromes (Doublet et al. 2025 Nat. Commun). In addition, our results highlight the vectoring capacity of social bees for plant viral diseases, and illustrate further our concern of potential pathogen spill-over from commercial bumblebees into natural ecosystems.

Integrating ecological and macroevolutionary perspectives on host-use dynamics in seed Beetles (Coleoptera: Chrysomelidae: Bruchinae)

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Abstract

In the 1970s, Daniel Janzen's pioneering work highlighted the role of highly specialised phytophagous insects in maintaining tropical forest diversity. Focusing on seed beetles (Coleoptera, Chrysomelidae, Bruchinae), he showed how their strict host-plant specialisation and seed-eating larvae made them ideal models to study plant-insect interactions and their impact on plant fitness. Despite the crucial ecological importance of such highly specialised interaction networks, few studies have focused on the processes that led to their creation.

Here, we wish to demonstrate the benefits of considering these dynamics within an integrative framework, taking into account both ecological dimensions (structure of interaction networks) and macroevolutionary dimensions (links between host shift, plants and diversification). Our study focuses on bruchines, Janzen's original model group, comprising over 1,700 species of seed-predating beetles worldwide. Though their evolutionary history is marked by a close association with Fabaceae, it has not prevented bruchines from colonising more than 30 botanical families. Here, we identify and measure the frequency of host gains and losses in these dynamics, and how host-plant diversity influences the diversification of specialised insects.

We employ a hybrid phylogenomic approach combining genomic data and legacy markers to reconstruct the first comprehensive Bruchinae phylogeny, covering ca. 700 species and all major lineages. A thorough literature review, supplemented with unpublished data, yielded a database covering host-plant associations for 650 beetle species involving over 1,100 plant species.

Using dated phylogenies and interaction networks, we analyse the parallel evolutionary history of Bruchids and their host plants. This new integrative method provides ecological justification and ensures the evolutionary consistency of analyses estimating ancestral host repertoires. Our findings reveal a complex history of host associations, where patterns of phylogenetic niche conservatism coexist with frequent reversals and dramatic host shifts to phylogenetically distant plants.

Tree-specific associations, not canopy flora, explain the composition of canopy leaf beetle communities in tropical forests of Ecuador

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Abstract

Tropical studies of herbivorous insect associations rely mainly on canopy fogging, which infers host use from the fogged tree but also captures species dependent on epiphytes and vines, or on crane-based hand- or net-collecting, which assumes physical presence of an insect on tree tissues or canopy flora to reflect true ecological associations. These studies have produced contrasting conclusions about the role of tree-species specificity in shaping herbivorous insect communities. Targeted canopy crane-collections, for example, indicate that up to half of the phytophagous beetle species may feed on lianas rather than on the tree itself, whereas more accessible fogging generally obscures host identity and specificity. Regardless of sampling approach, accurately determining host specificity in such systems is essential for food-web analyses and for modelling reliable biodiversity estimates. In this study, we advocate for molecular ecology approaches to investigate the diet of fogged communities in the tropics as a cost-effective method to refine this critical understanding of their structure. Specifically, we sampled by fogging insect communities in two elevation forest gradients in the Pacific and Amazon slopes of the Andes in Ecuador, selecting leaf beetles as study case and inferring their diet using cpDNA sequences as plant species barcodes. Focusing on a sample of the highly diverse subfamily Eumolpinae, represented by 87 species in the study sites, we established that more than 75% of inferred trophic associations were with tree species above or in the vicinity of the fogging site. About 40% of host-tree associations were with Fabaceae, particularly *Inga* spp., but the diversity of tree hosts was high, involving some 20-30 families. Less than 15 and 5% of associations were on vines (e.g., *Muehlenbeckia* or *Solanum*) and epiphytes (e.g., *Macleania* or *Sphyrospermum*), respectively. This unprecedented knowledge of plant-herbivore interactions provides stronger foundations for biodiversity modelling in these tropical forest ecosystems.

Towards an integrated framework of thermal damage and repair dynamics in ectotherms

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Abstract

Increasing temperatures combined with larger seasonal and diurnal temperature variation cause more frequent extreme heat events for many ectothermic organisms. The severity of such heat stress depends on the intensity and duration of exposure but also the organisms' ability to recover from thermal injury when the stress is alleviated. Traditional measures of thermal limits (CT_{max}) are generally inadequate to analyze responses of periodic heat stress. The recently (re)introduced Thermal Death Time (TDT) model has resolved many of these issues. Importantly, the TDT model can be understood through the analysis of competing rates of repair and injury across temperatures. Here we outline the recent conceptual basis of TDT analysis and use experimental data we support the hypothesis that injury-repair dynamics can be accurately predicted considering antagonistic rates of homeostatic repair and perturbation. We show that the premise of TDT modeling applies not only to heat mortality, but also to sublethal thermal limits, including loss of reproduction. Based on these experimentally validated ideas we discuss how the TDT framework can improve mechanistic models of heat stress exposure for ectotherms in general. We also consider current conceptual limitations of the model and ways to overcome these limitations.

Separating good from bad – finding the critical temperature that separates stressful and permissive temperature ranges for ectothermic organisms

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Abstract

Temperature strongly influences the lifespan and biological processes of ectothermic organisms, shaping not only how they perform in their environment at permissive temperatures but also their rate of mortality if temperatures exceed their thermal limits and become stressful. Together these two facets of thermal biology (performance and tolerance) play a central role in shaping species distributions around the globe. Most measurements in thermal biology can be considered correlates of either thermal performance or thermal tolerance. At the same time, it is evident that the critical temperature (T_c) that separates permissive and stressful temperatures, and thus performance and thermal tolerance measures, is central for understanding thermal biology. Surprisingly, no assays that we are aware of are designed specifically to characterise this transition temperature (or temperature zone) that is so central for understanding and modelling the ectothermic responses to thermal fluctuation. Using the aquatic plant (*Lemna gibba*) and a terrestrial insect (*Drosophila suzukii*), we evaluate four experimental approaches for estimating T_c : thermal performance assays, constant temperature assays, ramping assays, and alternating constant temperature assays. Across both species, three of the four methods converged on comparable T_c estimates, whereas ramping assays proved impractical and yielded unreliable results. In both organisms, T_c coincided with the temperature at which performance-based measures declined to zero or became net negative and where mortality rates increased sharply, indicating a common physiological transition between sustained function and net damage accumulation. Finally, we introduce a non-parametric thermal death time framework that can be used to identify T_c by quantifying how temperatures contribute to damage accumulation or repair across any thermal regime including fluctuating temperatures.

Crossing thermal boundaries: Quantifying the developmental impact and energetic cost of sublethal heat stress in black soldier fly (*Hermetia illucens*)

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Mads DAM THEM, Mattias SCHOW-MADSEN

Abstract

Thermal fluctuations in a warming world increasingly expose ectothermic animals to conditions oscillating between permissive temperatures that support fitness and stressful temperatures that induce physiological injury. While thermal performance curves (TPC) and thermal death time (TDT) models are well established for these respective ranges, the biological and ecological consequences of crossing the boundary between them remain poorly quantified.

To address this gap, we conducted experiments to quantify the costs of sublethal heat stress by measuring performance after the organisms returned to benign conditions. Using black soldier fly larvae as a model ectotherm, we applied controlled “doses” of sublethal heat stress (e.g., 10%, 20%, or 30% of the lethal dose) and assessed how stress magnitude subsequently constrains growth and elevates energetic costs of development.

Our results show that sublethal heat injury reduces subsequent performance in direct proportion to stress dose, demonstrating that thermal stress imposes measurable and proportional costs even when mortality is avoided. These costs are additive across different stress intensities and stress durations and the costs manifest over multiple timescales: immediate reductions in growth, longer-term developmental delays, and ultimately increased energetic costs, as indicated by higher oxygen consumption per gram of bio-mass assimilated.

By quantifying stress costs through post-exposure limitations under permissive conditions, our framework provides a robust method for evaluating the consequences of sublethal and periodic heat stress. This approach has broad relevance for predicting ecological responses to climate warming and also for managing applied ectotherm systems - such as aquaculture or insect production - where brief thermal excursions can have lasting energetic, developmental, and fitness consequences.

Metabolomic profiling of dose-dependent heat stress response in *Drosophila suzukii*

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Abstract

With the recent reintroduction of the Thermal Death Time (TDT) model, it has become possible to characterize the thermal tolerance landscape of ectotherms much more exactly and predictably than using traditional methods. As ectotherms are exposed to stressful temperatures, they will begin accumulating stress in an exponential and highly predictable manner, allowing the calculation of the exact 'dose' of thermal damage the animal has accrued even at fluctuating temperatures. This then begs the question of whether the accumulation of heat damage is driven by the same metabolic mechanism from healthy animals to highly stressed animals at extremely stressful and mildly stressful temperatures respectively. To determine whether this is the case, we exposed a cohort of the invasive horticultural pest *Drosophila suzukii*, to an identical range of 'doses' of thermal damage, at three different stressful temperatures spanning the stressful range, namely 35, 37 and 39 °C. By utilizing GCMS to perform a targeted and quantitative metabolomics analysis we have been able to characterize the metabolomic profile for each of these treatments and preliminary results show a marked difference between metabolic responses at the highest (39 °C) vs the mildest (35 °C) stressful temperatures. This is likely indicative of an acute thermal stress response at the highest level of heat stress (LT50 (39 °C) < 20min) and a more chronic stress response with the employment of adaptive responses at milder heat stress (LT50 (35 °C) ≈ 4.5h). This highlights the complex interplay between ectotherms and their environment and the importance of well characterized thermal tolerance landscapes.

Linking respiratory structures to heat and desiccation tolerance in terrestrial isopods

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Abstract

Climate change is raising average temperatures and decreasing local precipitation, increasing the number and intensity of heatwaves and droughts. Temperature and humidity are crucial for the survival of organisms, especially ectotherms. Among these ectotherms, terrestrial isopods (Oniscidea), commonly known as woodlice, are detritivorous and the only Crustacean suborder to have fully colonized dry land. A key adaptation to terrestrial life in these arthropods is the diversity of their aerial respiratory system, which includes a primitive gill-like structure, and pseudotracheae (2 or 5 pairs of pleopodal lungs depending on species), providing enhanced respiratory performance and better tolerance to desiccation. However, as crustaceans and ectotherms, their tolerance to heat and desiccation remains unclear. We quantified these tolerances in five species differing in pseudotracheae number (0-5) to evaluate whether a higher number confers higher physiological limits. Heat tolerance was assessed using the Thermal Death Time (TDT) framework, and desiccation tolerance was tested at 34°C under three relative humidity levels. Species with pseudotracheae showed higher tolerance to both stresses, supporting their role in thermal and desiccation tolerance. Yet, under low humidity, the five-pair species was more sensitive than the two-pair species, suggesting that other morpho-behavioral traits, such as volvation also shape desiccation tolerance. In a context of climate change, these results highlight the role of morpho-anatomical traits in modulating stress tolerance which has led to terrestrial isopod diversity.

Does the timing of heat events matter for the evolution of life-stage- and sex-specific thermal tolerance?

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Loke von SCHMALENSEE, David BERGER

Abstract

Climate change is increasing the frequency of extreme heat events, posing growing risks to biodiversity and ecosystem stability. For insects, vulnerability to heat stress depends not only on temperature intensity but also on when heat events occur, because individuals in natural populations experience thermal extremes at different developmental stages. Although many studies quantify immediate survival or short-term reproductive impairment, population persistence ultimately depends on whether heat exposure causes lasting fitness consequences expressed later in life during the reproductive phase. We know very little about insects' ability to adapt to extreme heat events and if adaptation to chronic temperatures in one part of the life-cycle affects heat tolerance to other forms of heat stress experienced by other life-stages. Here, we examined how the timing of both long-term (chronic) and short-term (acute) heat stress shapes survival and reproduction males and females of a cosmopolitan insect pest - the seed beetle *Callosobruchus maculatus*. Using an outbred reference population, we show that juvenile survival was largely maintained across immature stages at moderate temperatures, while is drastically decreased at extreme heat exposure, revealing a sharp upper thermal limit. Lifetime reproductive performance remained stable following moderate heat exposure but declined markedly after extreme heat, particularly when stress occurred during male late development. We used our results to formulate predictions for how adaptation to chronic heat during development should affect tolerance to acute temperature stress at later developmental stage and test these predictions in long-term experimental evolution lines, evolving for more than 120 generations at hot and cold temperature. Together, our findings show that the ecological impact of heat events depends critically on their timing within the life-cycle and on whether heat exposure produces short-term mortality or enduring reproductive costs. Incorporating life-stage and sex-specific thermal sensitivity is therefore essential for predicting insect resilience under increasingly frequent heat extremes.

Local adaptation of diapause induction has strong timing-dependent fitness effects but does not limit the range expansion of a temperate butterfly.

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Mats ITTONEN, Martina BOVALENTA

Abstract

Climate change affects species distributions and is pushing many insect species polewards. As a consequence, species encounter novel abiotic conditions, such as new daylength variation and season lengths, leading to altered selection on life cycle timing. Local adaptation in photoperiodism for seasonal timing evolves predictably across latitudinally distinct populations. Still, fitness consequences of variation in photoperiodism and voltinism during rapid range expansions are not well understood. We performed a common garden field-experiment at the northern range margin of the range expanding Wall brown butterfly (*Lasiommata megera*) and demonstrate rapid evolution of photoperiodism for diapause induction during the northern range expansion. By experimentally manipulating the start of the last annual generation of both southern “core” populations and northern “range margin” populations, we show that, as expected, northern populations enter diapause earlier in the season compared to southern populations. However, this difference was only present in the earliest developing larvae of this last annual generation, and only the early eggs of the southern populations were likely to produce an additional generation that was clearly maladaptive. The effect of oviposition timing largely overshadowed the genetic difference between populations. Consequently, although it was almost exclusively southern, maladapted populations that produced an additional “lost generation”, the effect of oviposition timing allowed most individuals also of these populations to avoid this maladaptive “developmental trap”. Once in diapause the southern animals survived winter equally well as populations adapted to the northern range margin. Our field experiment simulated the expansion of southern, photoperiodically maladapted, genotypes to a more northern location and suggest that despite this maladaptation they could potentially colonize this region. In conclusion, our field experiment indicates that even though latitudinal differences in daylength regimes exert strong selection that may lead to rapid adaptation, they are unlikely to restrict climate change-driven range expansions.

Life in the Arctic: Seasonal Pressure Shapes Physiology, Phenology, and Microclimate Use in Ants

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Košťál VLADIMÍR, Alice DENNIS, Overgaard JOHANNES

Abstract

Insects living in high-latitude environments must contend with extreme seasonality, short growing periods, and prolonged cold exposure. These constraints impose powerful selective pressures that operate simultaneously on species' physiology, phenology, and habitat use. In this presentation, we'll explore how ants integrate metabolomic adjustments, metabolic compensation, obligate diapause, and microclimate exploitation to persist in environments where thermal opportunities are narrow and unpredictable. Comparative data from temperate, Scandinavian, and Arctic species show that northern ants exhibit metabolic adjustments consistent with life in colder environments. These physiological shifts are partly synchronized by endogenous annual timers that enforce wintering in colonies even under permissive environmental conditions. This ensures the timely acquisition of cold tolerance and modulates acclimation potential, resulting in cold-tolerant phenotypes shaped both by endogenous colonial clocks and by environmental exposure. At finer spatial scales, Arctic ants selectively exploit warmer microclimates to sustain brood development and foraging, retaining striking thermal conservatism in their microhabitat use and upper thermal limits despite inhabiting some of the coldest climates at the regional scale. Together, these findings illustrate how survival in northern and shifting environments is shaped by a coordinated suite of physiological, phenological, and microclimatic strategies, where the timing of life-history events can be as critical as the thermal limits that constrain them.

Physiological mechanisms of cold tolerance plasticity and its role in the recent poleward expansion of the invasive vector mosquito *Aedes albopictus*

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Abstract

Knowledge of the molecular processes underlying thermal tolerance and how thermal tolerance responds to selection are both crucial to anticipating insect responses to novel climatic conditions. Cold tolerance is a key determinant of insect distributions and phenology. In insects, lower thermal limits are often very plastic through either diapause entry (a pre-programmed response to a token cue such as photoperiod), cold acclimation (a response to recent temperature conditions), or a combination of the two. However, few studies have disentangled these two forms of phenotypic plasticity at the physiological level or explored their relative roles in the evolution of greater cold tolerance. We used the invasive vector mosquito *Aedes albopictus* to investigate how the cold tolerance of eggs (the overwintering stage) is influenced by diapause, cold acclimation, and their interactions. First, we assessed whether these two plastic responses share physiological mechanisms at the metabolomic and lipidomic levels. We then compared the effects of diapause and cold acclimation on egg cold tolerance in six range-edge and six range-core *Ae. albopictus* populations to determine how these two forms of plasticity may have contributed to climatic adaptation during this species' recent invasion and poleward expansion in the eastern United states. This research has important implications not just for our understanding of the regulation and evolvability of cold tolerance in insects, but also for the role of phenotypic plasticity in adaptation more generally.

Overwinter life stage is a key determinant of diapause metabolic plasticity

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Philipp LEHMANN

Abstract

In seasonal environments, winters are dominated by stressful abiotic conditions and limited available resources. To cope with the challenging conditions associated with winter, organisms often enter dormancy. For insects, this comes in the form of diapause, a programmed dormancy, associated with arrested development and suppressed metabolic rate. During diapause, most insects operate on a fixed energetic budget, making the management of stored resources important for survival and investment of remaining energy into post-winter processes. Across insect taxa, there is substantial variation in the life stage that a species overwinters as. Energetic demands both during, and after emergence from dormancy vary substantially between life stages, making overwintering life stage a potential key life history trait that can influence vulnerability to warming winters. In this study, we measured metabolic rate-temperature curves for eleven species of butterflies that overwinter as either adults, pupae, or larvae, during diapause and after termination of diapause. We then added diapause metabolic rate data from twelve other published species to examine the relationship between mass and metabolic rate between overwintering life stage across holometabolous insects. Using this data, we found that mass scaling of diapause metabolic rate across two orders of magnitude is isometric regardless of life stage. Overall, pupae had lower diapause metabolic rates per unit mass than larvae and adults, but thermal sensitivity is similar in all life stages. When integrated across an entire winter, the higher overall metabolic rates in larvae and adults can lead to substantial impacts in winter energetic costs, particularly in warm winters. Together this data highlights a potential fundamental diapause energetic property, which could have large impacts on species abundances, occurrence patterns, and implications in predicting the energetic impacts of climate change in winter.

Unique winter diapause strategies in aphids in the face of climate change

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Martyna MATEROWSKA, Tomasz DURAK

Abstract

Diapause in aphids exhibits several unique features that distinguish it from the survival strategies employed by most other insects. This specificity is evident in both the transgenerational induction mechanisms and the progression of embryonic development during winter. Winter diapause in aphids takes the form of a facultative embryonic diapause occurring in the egg stage. Based on our analysis of various species, two distinct models of this process have been identified: a strategy of slow, continuous embryonic development and a strategy of complete developmental arrest.

Studies on species from the *Cinara* genus (*C. cupressi*, *C. juniperi*), as well as *Brachycorynella asparagi* and *Maculolachnus submacula*, revealed the absence of a typical "resting stage" and uninterrupted embryonic growth throughout the winter. Continuous mitotic activity was observed across the entire embryo body, resulting in progressive increases in body length and leg proportions. Cell divisions were detected using immunocytochemical staining with Anti-phospho (Ser10)-acetyl (Lys14)-Histone H3 antibodies, while biometric analyses were performed using confocal microscopy and scanning electron microscopy. In contrast, *Appendiseta robiniae* exhibits a complete absence of cell divisions and arrested embryonic development until diapause termination. The selection of a specific diapause strategy is likely correlated with host plant phenology, enabling synchronization of fundatrix hatching with food availability.

Ambient temperature plays a decisive role in modulating embryonic development, particularly during the final diapause phases. Elevated winter temperatures markedly accelerate morphogenesis in species exhibiting continuous development, as demonstrated in *M. submacula*. However, this phenomenon carries a risk of developmental anomalies, such as disproportionate limb lengths or general body malformations. Global warming may therefore lead to the desynchronization of aphid life cycles and their host plants, significantly impacting the abundance of spring populations.

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Range shift and thermal tolerance in the seaweed flies *Coelopa pilipes* and *C. frigida*

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Abstract

Over the last few decades, the impact of global change on species distributions has been major. Notably, the increase of temperature has affected species' ranges, resulting in reductions, expansions or shifts in their distribution. An increase of temperature often leads to shifts of species distribution towards higher latitudes and altitudes, usually through the modification of available habitats or suitable living conditions. Strong relationships between thermal (cold) tolerance and insect biogeography have been reported for several insect groups and meta-analyses have confirmed this trend on a global scale. Due to the direct effects of temperature on their metabolism, insects are good indicators to understand the influence of temperature on current and future distributions through the study of thermal limits. Using GBIF data, I established that the range of *Coelopa pilipes* (Diptera, Arthropoda) has moved northwards over the last decades, making it a good model to study the role of temperature on distributional shifts. Measuring a large set of traits to assess the thermal performances of *Coelopa frigida* and *Coelopa pilipes* from Roscoff (France) and Steninge (Sweden), I investigated the role of temperature on the distribution of both species. My experiments showed that the two species displayed different thermal performances for both survival and fertility, with *Coelopa frigida* having a higher tolerance to cold and heat than *Coelopa pilipes*, a better fertility at 4°C and 12°C, and a better recovery time after a chill coma. Cold tolerance alone is not the unique determinant of the species' current or future distribution, which may also be constrained by other abiotic or biotic factors. Low temperatures could influence range expansion via degree-day requirements, highlighting the importance of characterizing developmental reaction norms in ongoing study.

Thermoregulation and adaptations to climatic variations in mountain butterflies

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Abstract

Global warming is causing long-term destabilization of ecosystems and is one of the key drivers of biodiversity loss. Despite the urgent need to document this phenomenon, little is known about how species assemblages respond to changing environmental conditions. Mountain environments provide a particularly relevant natural laboratory: their steep ecological gradients lead to rapid shifts in climatic conditions with altitude, offering an ideal setting for analyzing species adaptation along environmental, and especially climatic gradients.

As ectotherms, insects are highly sensitive to climatic variation: their activity depends on specific thermal requirements, and their survival is constrained by their thermal tolerances. Among insects, butterflies offer many advantages for studying adaptation to climatic conditions. The microstructure of their wings is a membrane covered with scales, and their pigments have a role in temperature regulation, allowing heat dissipation during overheating or, conversely, increase absorption of solar energy under cold conditions. In ectotherms, where activity depends on maintaining a sufficiently high body temperature, individuals and species living in colder environments tend to be darker (the thermal melanism hypothesis), which increases the absorption of solar radiation and facilitates heat accumulation. Moreover, coloration and physiology are not the only traits contributing to optimal thermoregulation. We also find different behaviors depending on the species assemblages present in this altitudinal gradient, such as basking posture and movement among microhabitats.

These findings contribute to know how butterfly species adapt to climatic conditions along temperate altitudinal gradients (Alps), using experimental biology approaches and comparative analyses. The goal is to better understand the effects of climatic variation on the evolution of optical, physiological, and behavioral traits in alpine butterflies.

Life cycle simplification in aphids drives changes in evolutionary rates and selection regimes

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Abstract

Transitions toward simplified life cycles can reshape evolutionary trajectories, yet their impact on the rate of molecular evolution remains poorly understood. In aphids, host alternation (heteroecy) entails obligate seasonal migration between highly distinct plant hosts - typically woody and herbaceous species - and has been repeatedly lost, giving rise to monoecious species with simplified life cycles. Using comparative genomics across 46 aphid species, we tested whether transitions from heteroecy to monoecy alter evolutionary dynamics at the gene level. We identified 9,304 orthologs and estimated evolutionary rates (dN/dS) and shifts in selection regimes in the diverse Aphidinae subfamily. We found that 715 orthologs evolved faster in monoecious species, primarily due to relaxed selection, while heteroecious species showed signatures of intensified selection. Genes under relaxed selection in monoecious species were enriched for functions related to environmental sensing, signaling, nutritional adjustments, morph determination and migration related - traits likely central for host alternation. These results suggest that the loss of a complex life cycle leads to reduced selective constraints as a consequence of ecological simplification. This study provides a robust evolutionary framework for understanding how life cycle transitions shape molecular evolution and drive gene decay following trait loss.

When and how inversion polymorphisms bias demographic and selection inference - a case study in the spruce bark beetle (*Ips typographus*)

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Abstract

Genomes often harbor extensive within-species structural variation and are far less collinear than traditionally assumed. As an increasing number of inversion-rich genomes are documented, a key question emerges: are our classical inference methods, such as demographic and selection inference, robust to the presence of polymorphic inversions in genomic data? Addressing this question is essential for studying adaptation, particularly because many known inversions underlie local adaptation and can facilitate rapid evolutionary responses to changing climates or biological invasions.

Here, we take advantage of a recently discovered inversion-rich genome in the spruce bark beetle (*Ips typographus*) to test how a complex landscape of inversion polymorphisms influences evolutionary inference. We find that while demographic inference is only mildly affected by the presence of inversions, selection inference and the identification of loci under selection can be substantially biased. Our results not only provide new insights into the demographic history and selection landscape of this important forest pest, but also offer practical guidance for analyzing inversion-rich genomes more broadly.

Drosophila glue: biomechanics, genome evolution and ecology

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Abstract

Drosophila glue is a fascinating proteinaceous material produced by Drosophila larvae at the end of the larval stage that allows the animal to adhere strongly to a substrate for several days during metamorphosis. We aim to use the powerful genetic tools of the model organism *Drosophila melanogaster* to explore the molecular basis of both bioadhesion and adaptation. We want to identify genes involved in glue adhesion and understand how they changed during evolution so that different glues can stick to various substrates in diverse environments. We developed a new assay to quantify Drosophila glue adhesiveness and compared adhesion between different *Drosophila melanogaster* populations and *Drosophila* species in order to identify the most adhesive fly glues. Furthermore, we also explore natural environments (rotten fruits, soil, microorganisms, ants, etc.) to understand how Drosophila glue participate in interactions between species. Our ultimate goal is not only to better understand adaptation but also to develop new bioadhesives inspired from Drosophila glue.

Hidden Battles Within: Gene Expression Landscapes Underlying Emamectin Resistance in *Trichogramma chilonis*

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Abstract

Hidden Battles Within: Gene Expression Landscapes Underlying Emamectin Resistance in *Trichogramma chilonis*

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Trichogramma chilonis is widely used in biological control, but continuous insecticide exposure may select for resistance. We developed an emamectin benzoate-resistant strain and conducted comparative transcriptome profiling to investigate molecular responses linked to resistance. De novo RNA sequencing generated a robust assembly of 41,691 transcripts (GC ~41%, N50: 2,585 bp), with 94.9% completeness (insecta_odb10). Functional annotation identified 15,283 NR-matched proteins, 12,797 EggNOG assignments, and extensive domain characterization through InterProScan. Gene ontology categorized transcripts across Biological Process, Molecular Function, and Cellular Component terms.

Differential expression analysis revealed 5,321 significantly altered transcripts between resistant and susceptible populations, of which 559 met stringent criteria ($\log_2FC \geq |2|$): 260 upregulated and 299 downregulated. Enriched functional categories included detoxification processes, gene regulation, protein homeostasis, and signalling pathways. Detoxification genes spanned biotransformation, transport, and catabolic components, while regulatory changes involved transcription, RNA processing, and protein modification. Alterations in proteostasis-associated genes and shifts in kinase/phosphatase expression suggest broad cellular remodelling during resistance development.

This study provides the first transcriptomic insight into emamectin resistance in *T. chilonis*, highlighting coordinated responses across metabolic, regulatory, and signalling networks. This knowledge enhances understanding of adaptive responses in biological control agents and offers molecular targets to monitor resistance evolution and safeguard the efficacy of *T. chilonis*-based pest management strategies.

Keywords: *Trichogramma chilonis*; emamectin benzoate resistance; transcriptomics; differential gene expression; detoxification pathways

Dynamics of Aphid Speciation and Genome-Based Outbreak Prediction

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Seunghwan LEE

Abstract

Understanding the dynamics of aphid speciation is essential for predicting pest emergence and outbreak risk under rapidly changing environments. In this study, we systematically reestablish the aphid group Pterocommatinae Wilson, 1910 (Hemiptera: Aphididae), which had previously been synonymized, and investigate its evolutionary diversification in relation to habitat and host-plant shifts. We analyzed complete mitochondrial genomes from 151 terminal taxa representing major lineages of Aphididae, using maximum likelihood phylogenetic inference with strong nodal support.

Our results robustly recover Pterocommatinae as a monophyletic lineage, supporting its phylogenetic revival at the subfamily level. Integrating taxonomic classification with host-plant association and ecological data, we demonstrate that transitions in habitat and host use have been key drivers of speciation and lineage richness within this group. These evolutionary shifts are accompanied by detectable changes in morphological adaptation, suggesting coordinated responses of genome, phenotype, and ecology during diversification.

Importantly, the observed coupling between habitat change, speciation dynamics, and lineage richness provides a predictive framework for understanding aphid outbreak potential. Genome-scale phylogenetic resolution enables the identification of rapidly diversifying lineages associated with specific ecological niches, which may be prone to population expansion under environmental change. Our findings highlight how evolutionary genomics can inform genome-based outbreak prediction and contribute to anticipatory pest management strategies in agroecosystems.

Mastering a novel behaviour: how flies evolved eye movements

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Abstract

Many animals are capable of eye movements. Insects, however, have been traditionally viewed as being incapable of moving their eyes independently of the head. Yet, one group of insects – true flies (Diptera) – has been shown to possess muscles that shift the retina underneath the stationary lenses of the compound eye. Retinal movements have been functionally characterized recently in the fly model *Drosophila melanogaster*, and remarkably, these flies exhibit active visual strategies that are reminiscent of vertebrate eye movements.

Our goal was to survey retinal muscles (based on anatomical evidence) and retinal movements (based on behavioural evidence) across insects to better understand the evolutionary trajectory and to establish any potential links to visual ecology.

Our anatomical evidence for retinal muscles covers 27 out of 29 extant insect orders as well as 3 non-insect Hexapod orders, 39 Diptera families (out of ~150), and 14 Drosophilid species. For most of these taxa, we have collected anatomical evidence from multiple individuals and of both sexes. Our behavioural evidence for retinal movements covers 10 insect orders and 25 Diptera families.

These data suggest that specialized retinal muscles have evolved late and are only found in Diptera. Within Diptera there is a remarkable variation of retinal muscle presence, number and size. Together with behavioural data this forms a pattern of step-wise evolution of specialized retinal movements and muscles across Diptera.

Supported by phylogenetic analysis, our hypothesis is that the first retinal muscle to evolve was *Musculus orbito-scapalis* (MOS), which allowed some lower Brachycera to perform self-timed retinal movements, whatever function they might serve. Evolution of the optokinetic reflex (OKR) is then linked to the emergence of *Musculus orbito-tentoralis* (MOT) in Eumuscomorpha. This is further confirmed by the repeated loss of MOS but not MOT in families retaining the OKR.

From Plants to Insects: Horizontally Transferred Phenylpropanoid-Biosynthesis Genes and Stress Resilience in *Bemisia tabaci*

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Shai MORIN, Osnat MALKA

Abstract

Flavonoids play a critical role in plant survival and adaptation by attracting pollinators, mitigating oxidative damage, regulating developmental processes, and defending against stresses such as UV radiation, pathogens, drought, and heat. These compounds are synthesised via the phenylpropanoid pathway, initiated by the conversion of phenylalanine to cinnamic acid by phenylalanine ammonia-lyase (PAL). Another key enzyme, chalcone synthase (CHS), catalyses the formation of chalcones, the precursors of flavonoids. In animals, flavonoids are known for their beneficial health effects, including antioxidant, antimicrobial, and stress-reducing properties. However, these effects were previously attributed solely to dietary intake.

Here, we report the first evidence that an animal genome encodes core enzymes of the flavonoid biosynthesis pathway. We discovered that the phloem-feeding whitefly *Bemisia tabaci* acquired two PAL genes (*BtPALs*) and one CHS gene (*BtCHS4*) from plants via horizontal gene transfer (HGT). Transcriptomic analyses confirm that these genes are expressed throughout the insect's life cycle, supporting their functional integration. Consistent with this, metabolomic profiling detected flavonoid-related signatures compatible with endogenous production. Functionally, RNAi-mediated silencing of *BtCHS4* significantly increased adult susceptibility to UV-B radiation, indicating that this horizontally acquired pathway contributes to stress tolerance.

UV-B exposure is one of the many environmental challenges *B. tabaci* faces, particularly during its sessile nymphal stages. In addition, to cope with their sugar-rich yet nitrogen-poor diet, phloem-feeding insects must ingest large volumes of phloem sap and excrete excess sugar onto the leaf surface, creating a microhabitat prone to the rapid proliferation of numerous microorganisms, including various plant and insect pathogens. Our results indicate that the acquisition of *BtPALs* and *BtCHS4* enables a previously unrecognised chemical defence strategy in a phloem-feeding insect. This study redefines the known boundaries of animal metabolism and highlights the role of HGT in the coevolutionary arms race between plants and herbivores.

One Order, Many Strategies: Comparative Genomics of Hymenopteran Diversity

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Cintia OI, Yoann PELLEN, Seirian SUMNER, Eyal PRIVMAN, Gavin BROAD

Abstract

Hymenoptera is one of the most diverse and ecologically impactful insect orders, encompassing ants, bees, sawflies and wasps. These taxa provide essential ecosystem services such as pollination, biological control, and key contributions to trophic networks. Their ecological success is mirrored by striking variation in life-history strategies, ranging from solitary to eusocial systems and from phytophagy to predation and parasitism. While comparative genomic studies in some groups (particularly social insects such as ants and bees) have begun to reveal links between genotype and phenotype, the broader patterns shaping genome evolution across Hymenoptera remain insufficiently understood.

This study investigates the genomic foundations of hymenopteran diversity using 252 high-quality, chromosome-level genomes from initiatives such as the Darwin Tree of Life project. We employed an integrative comparative framework that combines phylogenomic reconstruction, molecular dating, genome-wide synteny analyses, gene family evolution, and inference of selection pressures (dN/dS). In addition, we incorporated ancestral trait reconstruction to explore how transitions in social organization, parasitic strategies, and dietary specialization may be associated with shifts in genome architecture.

Through this approach, we characterized chromosomal evolution across major hymenopteran lineages, identify lineage-specific genomic features and analysed evolutionary patterns in gene families critical notably for environmental perception - such as odorant receptors, which are established sensory mediators and likely contribute to various behavioural adaptations. Subsequently, we will determine whether convergent evolution of life-history traits corresponds to conserved genomic signatures. By synthesizing genomic, phylogenetic, and ecological data, this work aims to provide a clearer understanding of the evolutionary mechanisms that have contributed to the remarkable diversification and ecological success of Hymenoptera.

Reference genomes for all European Lepidoptera: The 10kLepGenomes COST Action

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COST Action 10KLEPGENOMES

Abstract

Genomic data has been at the center of a myriad of biological questions for the past two decades, being paramount to track and understand global biodiversity loss, crop pests and their control, and the effects of climate change on local populations. However, the continuous increase in sequenced specimens and chromosome-level reference genomes requires novel initiatives to advance on how to manage and utilise this data, as well as providing new insights into the biology of the sequenced species. The COST Action 10kLepGenomes aims to sequence, curate, and analyze all ~11,000 European Lepidoptera genomes. The 10kLepGenomes COST Action has five core working groups addressing subjects including understanding societal and stakeholder's needs, field collection, genomic and population analyses, and the usage of genomic data in applied fields. This presentation will highlight how collaborators from more than 28 European countries can be brought together to collect, produce and analyze chromosome level genomes of all European Lepidoptera. Many research institutions across Europe are mobilized to study Lepidoptera phylogenetics, conservation genomics, lepidoptera-cobiont interactions, and gene and chromosome evolution with currently more than 1,000 sequenced genomes. In the following years, 10kLepGenomes will continue to provide substantial genomic data and analytical tools for Lepidoptera research. Moreover, it will reinforce the importance of this clade as a model to study crucial biological questions to understand our fast-paced changing environment, and, more importantly, how to protect it.

A three body problem: primary sex determination signals in parasitoid wasps

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Abstract

During early embryo development, “primary sex-determination signals” initiate a pathway that directs differentiation toward either a male or female phenotype. Although the outcome and the terminal components of this pathway are highly conserved, the primary signals themselves vary widely, even among closely related species. Here, we show that in parasitoid wasps of the genus *Nasonia*, multiple gene-duplication events gave rise to a tripartite trigger for female sex determination.

Insights on the structure, organization and regulation of Tephritid sex chromosomes.

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Kostas MATHIOPOULOS

Abstract

Sex chromosomes and the mechanisms underlying their evolution across lineages represent a long-standing and intriguing field of study. Driven by sexual reproduction and the need for sex determination, sex chromosome systems have evolved independently in multiple organisms, yet often display convergent characteristics. In lineages where heteromorphic XY sex chromosomes exist, the Y chromosome is typically highly repetitive, degenerated, and gene poor, while the X-chromosome usually evolves dosage compensation mechanisms to balance the hemizygous X state in XY males.

Despite these shared characteristics, the gene repertoire and expression dynamics of sex chromosomes might vary among different lineages. In *Drosophila melanogaster*, the model species of Diptera, its typical morphology of heteromorphic XY chromosomes is mirrored in many Tephritidae species, like *Ceratitis capitata*. However, the sex chromosome-linked genes vary between these two lineages, with *D. melanogaster*'s X-linked genes appearing autosomal in *C. capitata* and vice versa. This divergence underscores the dynamic evolution of sex chromosomes and questions the suitability of *D. melanogaster* as a model for sex chromosome biology.

To elucidate this, we investigate the structure, organization and regulatory mechanisms of Tephritid sex chromosomes. We employ sexed single embryo RNA-seq to detect *C. capitata* early embryonic expression patterns, where we also observe signals of active dosage compensation on X-linked genes. We further extend the analysis to adult stages where we perform RNAi-mediated characterization of known dosage compensation mediators to assess their chromosome-wide regulatory impact. In parallel, we analyze the structure and organization of the poorly studied Tephritid Y chromosomes, to elucidate its origin, evolutionary relation and divergence across Tephritid species.

Stage-Dependent Antennal Proteomics in *Bombus terrestris* (L.): From Larva to Adult

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Mehmet Ali BALCI, Fatih DIKMEN, Vahap ELDEM

Abstract

Bumblebees (*Bombus* spp.) are vital pollinators with about 250 described species and among them *Bombus terrestris* (L.) is very important with its contributions to agricultural production. All this importance and interaction depends on their pivotal sensory organ, antenna. This sensory system mediates behaviors that are critical for survival and ecological fitness. Despite its importance, the molecular basis of chemosensory processes—especially protein-level changes during antennal development in holometabolous insects—remains largely unexplored.

Here, we report the first developmental antennal proteomics study in *B. terrestris*. Proteomic analyses were performed on the apical head region of larvae and on antennal tissues from early- and late-stage pupae and adults from commercially reared colonies. In total, 3,860 proteins were identified across developmental stages. GO and KEGG enrichment analyses ($p_{\text{adjust}} < 0.05$) revealed a marked developmental reorganization of the antennal proteome, with significant enrichment of pathways involved in signal transduction, cellular regulation, and sensory functions, including the mTOR signaling pathway, phosphatidylinositol signaling system and inositol phosphate metabolism, particularly in mature antennae. Correlation analyses further identified 188 proteins with progressively increasing and 105 proteins with progressively decreasing expression patterns, indicating a developmental transition from early proliferative and biosynthetic processes toward signal integration and sensory specialization during antennal maturation.

Together, these results map the proteomic trajectories that underlie antennal morphogenesis and sensory specialization in *B. terrestris*, providing candidate molecular effectors for experimental validation. This study advances understanding of sensory organ development in an ecologically and economically important pollinator and supplies a resource for comparative and functional studies, including targeted genome-editing of antennal genes.

Investigating the ongoing Invasion of a Transposable Element in European lepidoptera genomes.

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Abstract

The study of transposable element (TE) integration in genomes is mostly focused on ancient events.

We recently discovered a TE insertion shared by multiple European butterfly species. In at least five species (*Pararge aegeria*, *Polyommatus icarus*, *Anania crocealis*, *Pyrausta nigrata*, and *Pyrgus malvae*), these TE insertions display 100% pairwise identity with a homolog found in the genome of the parasitoid wasp *Cotesia vestalis*, which may represent the original donor sequence. This perfect sequence match suggests the TE has not yet undergone significant divergence through genetic drift, indicating a very recent integration event — and potentially an ongoing invasion.

Our objective is to characterize this invasion at multiple levels. First, by analyzing a Lepidoptera collection comprising over 1,000 species, we aim to assess the extent of this invasion across Lepidoptera biodiversity. In a second axis, we wish to investigate the geographic extent of this invasion and the suspected vector mediating it. Finally, to estimate the timing of the initial integration event, we examine a *P. icarus* collection containing historical specimens dating back to the early 20th century, housed in Swiss museum collections.

By combining broad taxonomic screening, geographic sampling, and historical data, we aim to unravel the dynamics of this TE integration event. Our findings will hopefully contribute to a better understanding of TE behavior and genome evolution in insects.

This talk provides an overview of my ongoing thesis project and presents the preliminary results obtained during this early stage of the work.

Repeated Horizontal Gene Transfer Enables Varying Levels of Cyanide Detoxification Across Herbivorous Clades of Arthropods

Lennert BEELE (Ghent University, Lennert.beele@ugent.be)

Siebe VAN WUNNIK, Godefroi GIGNOUX, Dries BONTE, Nicky WYBOUW

Abstract

Understanding how herbivores detoxify and overcome chemical plant defences and how these detoxification mechanisms evolve is central to plant-herbivore evolutionary ecology. Plant cyanogenesis is a widespread plant defence mechanism that releases cyanide, a potent toxin, upon herbivore feeding. Through horizontal gene transfer (HGT), *Tetranychus urticae*, a highly polyphagous arthropod herbivore, acquired a bacterial gene that encodes for a cyanide detoxification enzyme. The evolutionary history, functional divergence, and selective advantage of this HGT event for related herbivorous genera remains however poorly understood.

We investigated the complex evolutionary trajectory of this detoxification enzyme across the arthropod phylum, identifying multiple HGT events. We further combined exhaustive comparative genomics with phylogenetic analyses to resolve both the arthropod recipient and bacterial donor species. Our sequencing results indicate that this gene has a strong selective advantage for several herbivorous arthropods. To formally test this hypothesis, we performed phenotypical tests using a herbivore panel with varying host plant ranges and a panel of white clover genotypes. The cyanogenic potential of the clover panel was assessed using Feigl-Anger assays and functional genotyping. Plant-herbivore interactions were quantified by measuring several fitness components at high resolution. Our results revealed substantial differences in fitness among species and uncovered complex genotype-by-genotype interactions, with varying herbivore performance across clover genotypes.

Our integrative framework allowed us to detect lineage-specific patterns of molecular evolution following the HGT event. We also uncover how HGT has conferred selective advantages across polyphagous and monophagous arthropod herbivores. By integrating herbivore/plant genetics and phenotyping, our study advances our understanding of how co-evolution shapes natural populations.

Cognitive Neuroscience in Miniature Brains – Long-Term Memory and Higher-Order Learning in Honey Bees

Martin GIUREA (Center of Neurosciences - Sorbonne Université, Martin.giurfa@sorbonne-universite.fr)

Abstract

Despite possessing a brain of only $\sim 1 \text{ mm}^3$, honey bees exhibit a remarkably sophisticated behavioral repertoire. They are able to learn and memorize multiple sensory cues associated with flowers. Beyond serving as convenient models for the study of simple associative learning, bees have also emerged as powerful organisms for investigating higher-order forms of learning in both the visual and olfactory domains. Here, I focus on olfactory learning as studied through the conditioning of the proboscis extension response (PER). Contrary to conclusions drawn from decades of research, we show that protein synthesis–dependent long-term memories can be formed after a single conditioning trial and emerge as early as 4 h after training. To move beyond simple associative learning toward higher-order learning, we investigated non-linear discriminations, specifically negative patterning. We demonstrate that bees are capable of solving this complex learning problem and that intact mushroom bodies are required for successful performance. More specifically, we trace this capacity to a subset of GABAergic feedback neurons within the mushroom bodies, which prove to be essential for solving this type of discrimination. By presenting these findings, I aim to highlight key experimental challenges and outline future directions for investigating the neurobiology of higher-order learning in insects, with the broader goal of identifying fundamental neural architectures underlying cognitive processing.

Exploring the effect of temperature on insect sensory physiology and behaviour

Emily BAIRD (Stockholm University, Emily.baird@zoologi.su.se)

Abstract

Increasing global temperatures and, in particular, the increasing number of heatwaves, threaten important insect pollinator groups such as bees and butterflies. However, we still understand little about how temperature affects how insect pollinators sense and process information about their environment or how this affects their behaviour and interaction with plants. In this talk, I will present recent work that my lab has been doing to address this by investigating how exposure to elevated ambient temperatures affects physiology, sensing, cognition, foraging and pollination behaviour of insects. Our results suggest that the effects of heat on these aspects have significant implications for insect behaviour and pollination outcomes. This work highlights some important knowledge gaps in our understanding of how insect sensory, neural and behavioural systems will respond to increasing temperatures.

Pheromonal information processing in the honey bee brain

Julie CARCAUD (University Paris-Saclay, Julie.carcaud@universite-paris-saclay.fr)

Julia MARIETTE, Benjamin ANDREU, Jean-christophe SANDOZ, Gaëlle CLAISSE

Abstract

Sociality is considered as one of the major transitions in evolution, and the most advanced level of sociality is found in eusocial insect societies. The success of social insect colonies lies in the capacity of all members of the society to behave in a well-organized and context-dependent manner, thanks to elaborate communication among colony members. Honey bees, in particular, use a sophisticated chemical communication system based on the use of a high number of pheromones, most of which have already been identified. How does the social insect brain manage to encode such a plethora of highly-meaningful and ecologically-relevant signals? To what extent does olfactory sensitivity to pheromones influence division of labor and task specialization in social insects colonies? Our work tries to address these questions by using heterologous expression of honey bee olfactory receptors, electrophysiological recordings and in vivo optical imaging (using GCaMP-expressing bees) together with genome-editing approaches to investigate the peripheral and central circuits involved in pheromone processing in the honey bee brain.

Influence of social and ecological factors on the evolution of the olfactory system in Hymenoptera

Simon MARTY (Research Center on Animal Cognition, CNRS, Université de Toulouse, France, Simon.marty@utoulouse.fr)

Antoine COUTO, Patrizia D'ETTORRE, Stephen MONTGOMERY, Jean-Christophe SANDOZ

Abstract

Eusociality is a remarkable form of animal society featuring a reproductive division of labor where individuals (workers) forego their own reproduction to assist reproductive individuals (queens) and their progeny. Because the fitness benefit of this helping behavior is lost if directed toward non-relatives, the ability to discriminate kin from non-kin appears pivotal for the emergence of the eusociality. Hymenoptera display multiple emergences of eusociality, suggesting that some factors may have promoted evolution toward eusociality. The use of cuticular hydrocarbons (CHCs) in nestmate recognition has been described in many eusocial species, and in ants and hornets, a specialized olfactory subsystem likely dedicated to CHCs processing has been characterized. In the later, olfactory sensory neurons housed within basiconic sensilla, a specific type of sensory structures on the antenna, detect CHCs and project to a distinct region of the antennal lobe, the primary olfactory center. Interestingly, this region is characterized by a lack of serotonergic projections, which innervate the rest of the antennal lobe. Since ants and hornets independently acquired eusociality and are phylogenetically distant, we explored whether this subsystem evolved convergently in the eusocial lineages or represents a conserved feature predating them. To address this, we conducted a comparative neuroanatomical study to unveil the evolutionary origins of this trait across the phylogeny of Hymenoptera. We described this specialized subsystem in different solitary species, indicating that it predated the emergence of eusociality. In fact, we found that sociality has little influence on the olfactory system, whereas general diet appears to be a major factor driving its evolution. In addition, the lack of serotonergic projection in the antennal lobe subregion is not a ubiquitous feature of the subsystem but rather the result of a complex evolutionary pattern.

Connectome of a miniature wasp's antennal-head proprioceptors reveals drastic adaptations to miniaturization and potential for biomorphic network prototyping

Anna DIAKOVA (Lomonosov Moscow State University, Faculty of Biology, Department of Entomology, MicroInsectLab, Anndiakova@yandex.ru)

Elena Nikolaevna USTINOVA, Kazunori SHINOMIYA, Anastasia Alekseevna MAKAROVA, Pat GUNN, Song PANG, C. Shan XU, Harald F. HESS, Dmitri B. CHKLOVSKII, Alexey Alexeevich POLILOV

Abstract

Studying the limits of miniaturization in nervous and sensory systems helps to uncover fundamental principles of efficient, compact biological neural network organization. A striking example is the parasitoid wasp *Megaphragma viggianii* (~200 μm), which exhibits a remarkable adaptation: the lysis of nuclei in most adult neurons. While its nervous system retains sufficient complexity to perform essential functions, certain ultrastructural adaptations, such as the fate of sensillar accessory cells, have remained unexplored.

This work aims to describe the adaptations of the antennal-head joint proprioceptors to extreme miniaturization in *M. viggianii*, including the reconstruction of their connectome. We demonstrate that a key adaptation is the complete loss of accessory cells in proprioceptive sensilla during metamorphosis – a phenomenon not previously described in insects. Despite this significant structural simplification, the sensory neurons remain intact and form a fully functional, multi-layered network of ten proprioceptors.

Connectome reconstruction revealed both direct two-neuron reflex pathways to motor neurons and ascending connections to higher-order processing centers in the brain. Using this biological blueprint, we developed a biomorphic neural network to model proprioceptive signal processing. Simulations showed that increased network depth enhances activation selectivity, effectively integrating rapid reflexive responses with sophisticated information routing. Thus, our study identifies novel principles of neural optimization, offering a biological prototype for the design of compact and energy-efficient biomorphic artificial neural networks.

This work was supported by the Russian Science Foundation (project № 25-74-00012, <https://rscf.ru/project/25-74-00012/>)

A multi-scale investigation of olfaction in arthropods

Ryan PALMER (University of Bristol, Ryan.palmer@bristol.ac.uk)

Abstract

The sense of olfaction in honeybee's is enabled, in part, by sensory receptors along their antennae in the form of placodes and hairs. Placodes sit close to and densely cover the antennae's surface, whilst hairs protrude further from the surface with a range of configurations seen amongst different species. Each form of sensory receptor is covered by hundreds of innervated pores that capture olfactory particles.

We have experimentally and theoretically studied how these morphologies and their configurations impact an arthropod's ability to smell. Experimentally, we have categorised the shape, size and configuration of these sensors. Modelling has focussed on the flow of air around the antenna and how interactions with these sensors leads to increased or diminished volatile capture.

A Ca^{2+} -activated Cl^- channel shapes olfactory receptor neuron responses and modulates olfactory behaviors in *Drosophila melanogaster*

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Christelle MONSEMPES, Thomas CHERTEMPS, Philippe LUCAS

Abstract

Insects rely on highly sensitive olfactory systems to locate food, mates, and other essential resources through detection of volatile odorants. Chemical stimuli are converted into electrical signals in the outer dendrites of olfactory receptor neurons (ORN) via a complex transduction cascade. ORN output is then transmitted to the antennal lobe and higher olfactory centers, ultimately generating appropriate behavioral responses. Although Ca^{2+} signaling is a key component of insect olfactory transduction, the specific contribution of Ca^{2+} -dependent mechanisms remains incompletely understood. Here, we identified and characterized a Ca^{2+} -activated Cl^- channel (CaCC) that mediates the rapid termination of odorant-evoked responses in *Drosophila melanogaster* ORNs. This channel is essential for shaping the temporal dynamics of neuronal responses. Genetic manipulation of this channel revealed a direct link between channel activity and olfactory-guided behaviors, including pheromonal communication. These findings demonstrate that this CaCC is a critical regulator ensuring precise encoding and transmission of olfactory signals.

The behavioral and neural basis of the Monarch butterfly compass

Basil EL JUNDI (University of Oldenburg, Institute of Biology and Environmental Science, Basil.el.jundi@uni-oldenburg.de)

Abstract

Some insects can migrate over thousands of kilometres to reach highly specific locations at the end of their journey. For instance, the North American Monarch butterfly migrates more than 3,600 km from North America and Canada to its overwintering site in the mountain ranges of Central Mexico. But how can this insect master such a remarkable migration despite having a brain smaller than a grain of rice? To shed light on this, we are studying the Monarch butterfly compass using behavioural and neurophysiological techniques, such as multichannel tetrode recordings from tethered, flying butterflies in a flight simulator. These experiments have allowed us to discover that the butterfly navigation system contains head-direction, goal-direction, and steering neurons. Recently, we have succeeded in performing long-term neural recordings from migratory Monarch butterflies under the real sky to study how these neurons encode migration under ecologically relevant conditions. Remarkably, these experiments reveal that all neurons in the Monarch's navigation network are spatially tuned to the migratory direction, inherently informing the butterfly about the desired course. Many neurons were sensitive to the sun and encoded the migratory direction irrespective of the time of day, suggesting that they are part of a time-compensated sun compass. Taken together, Monarch butterflies offer a unique window into the core principles of animal migration – from sensory processing to neural control.

Scaling of the minute wasp brain under artificial selection

Anastasia MAKAROVA (MicroInsectLab, Department of Entomology, Faculty of Biology, Lomonosov Moscow State University, Moscow, Russia, Amkrva@gmail.com)

Maria FEDOROVA, Alexey POLILOV

Abstract

Understanding the principles of brain scaling is essential for comprehending its evolution. Haller's rule states that brain size scales allometrically with body size, such that smaller animals possess relatively larger brains. The neuropilar constant, on the contrary, demonstrates the conservatism of brain organization and reflects the unchanged ratio of neuropil size to cell body rind across insects.

We examined brain scaling within the natural range of body sizes, and under the influence of disruptive artificial selection based on body mass. Using a laboratory culture of *Trichogramma telengai* (Hymenoptera, Trichogrammatidae) we established three lines representing different size classes. The size of individuals was modulated via population density of parasitoids and number or size of the host eggs. Body mass of each individual was measured with Sartorius cubis II MCA2.7S ultra-microbalance (range of body weight from 2.4 to 40.1 μg). CLSM stacks were segmented using machine learning in Ilastik and used for 3D reconstructions of brains in VAST lite, for 60 individuals per line (5–10 generations). Allometric analyses were performed in smart R.

Comparative analysis showed that the brain changes allometrically within individual lines and across them. Brain volume ranges from about 2% of body volume in large individuals to 10% in small ones. The allometric coefficient for relative brain size is lower in small individuals than in medium or large ones. Thus, our results contradict earlier findings that reported isometric brain scaling in *Trichogramma* (Woude et al., 2018). We also performed, that artificial selection significantly shifts the neuropilar constant (Polilov, Makarova, 2020) from its typical range (decreasing markedly in smaller individuals).

Comparing the brain-scaling patterns with the results of behavioral experiments will help define the limits of brain miniaturization that can affect the cognitive abilities in minute insects.

This work was supported by the Russian Science Foundation (project no. 22-74-10008-P).

Sugar perception in phloem-feeders – from feeding-site allocation to regulation of sugar intake

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Ofer AIDLIN-HARARI, Esther YAKIR, Osnat MALKA, Jonathan BOHBOT

Abstract

Sweet taste sensation is crucial for feeding site allocation, diet assessment, and appetite regulation in insects. The ability to successfully conduct these three tasks is especially important for phloem-feeding insects, as their feeding site is deeply embedded inside the leaf and is highly rich in sugars (mainly sucrose) but poor in other nutrients, such as essential amino acids. The molecular mechanism of sweet taste perception is based on the activity of gustatory receptors. Previously, we expressed the five sugar gustatory receptors of the phloem-feeding whitefly *Bemisia tabaci* in *Xenopus laevis* frog oocytes, and recorded their responses to a panel of 17 potential sugar ligands, using the two-electrode voltage clamp system (TEVC). This work provided evidence that gustatory receptor 1 (BtabGR1) of *B. tabaci* is highly tuned to sucrose detection. Further on, we demonstrated, using artificial diet choice and gene silencing assays, that BtabGR1 plays a significant role in feeding-site allocation. In the current study, we present a broader research perspective that explored the possible involvement of BtabGR1 also in feeding site evaluation and diet ingestion regulation in *B. tabaci*. We found that BtabGR1 is not only a narrowly-tuned sucrose receptor but also accepts as a ligand the amino acid arginine. Moreover, our results indicated that arginine is acting as a pH-dependent modulator of BtabGR1 activation, enhancing the response of the receptor to sucrose in the context of the insects' gut pH, presumably playing a role in diet intake regulation. Besides being the first description of a dual-factor-dependent modulation of an insect gustatory receptor, our findings raise the possibility that phloem-feeding insects use the same gustatory receptor for identifying feeding sites that are rich in both sugars and essential amino-acids and modify their diet intake accordingly.

How does miniaturization shape sensory systems? Whole-body sensilla mapping in a miniature beetle *Scydosella musawasensis* (Coleoptera: Ptiliidae).

Kseniia ABUDIAK (Lomonosov Moscow State University, Faculty of Biology, Department of Entomology, MicroInsectLab, Kdiyak@gmail.com)

Alexey POLILOV, Anna DIAKOVA

Abstract

Sensory perception in insects relies on specialized cuticular structures called sensilla that detect mechanical, chemical and other stimuli, yet how the sensory systems are organized in the smallest insects remains poorly understood. In beetles, detailed descriptions of sensillar morphology and distribution have focused mainly on larger species, leaving a gap in our knowledge of how sensory equipment is reduced or reorganized during extreme miniaturization. Here we show the external sensillar anatomy of all body parts of the minute ptiliid beetle *Scydosella musawasensis* studied with scanning electron microscopy (SEM). We identified five major sensilla types — chaetoid, trichoid, campaniform, basiconic, and styloconic. The antennae exhibit the greatest diversity of sensilla (chaetoid, trichoid, basiconic, and styloconic), the mouthparts have trichoid and basiconic sensilla, while the rest of the body possesses only chaetoid, trichoid, and campaniform sensilla. This unevenness might indicate a leading role of the antennae in sensory perception in these beetles. Total sensillar counts in *S. musawasensis* (about 1400) are markedly lower than in larger staphylinoid beetles, which possess several thousand sensilla. Fixed distribution of sensilla among individuals also contrasts with the more variable distribution seen in non-miniature relatives. Unlike some larger beetles, sexual dimorphism in sensilla structure and distribution is negligible besides differences at the male and female pygidia. These findings indicate that miniaturization in insects reduces the number of sensory organs and makes their distribution more determined, while retaining a core set of sensillar types. Our results provide a reference point for understanding the minimal sensory complement necessary for effective environmental interaction in insects and confirm general principles governing the scaling of sensory structures with body size.

The study was supported by the Russian Science Foundation (project № 25-64-00002).

Neuroecology of Dipteran Halteres

Anna VERBE (Institut de Recherche sur la Biologie de l'Insecte, Anna.verbe@cnr.fr)

Abstract

Members of Diptera, known as true flies, are among the most agile flying animals. Their flight ability partly relies on the small halteres, club-shaped structures that evolved from the second pair of wings and that are essential for flight control. Halteres quickly sense rotational movements to help flies keep stable flight. They also send rhythmic signals to the wing-steering system, which the visual system can influence indirectly. Their multitasking nature is believed to depend on groups of mechanosensors called campaniform sensilla, located on the dorsal and ventral surfaces of the haltere. It is hypothesised that each sensor group provides different flight-related information and that they are functionally organised, experiencing varied cuticular forces during flight. However, we know little about how specific physiology, mechanistic and neural design are related to flight ability. Furthermore, given the diversity of three-dimensional flight capabilities and related haltere structures observed, we can wonder whether all species use halteres for the same purposes.

In Verbe et al. 2024, I use in vivo calcium imaging during tethered flight to obtain population-level recordings of haltere sensory afferents in specific sensilla fields. I found that haltere feedback from both dorsal fields is continuously active, modulated during closed-loop flight, and recruited during saccades to help flies actively manoeuvre. In this paper, we also found that the haltere's multifaceted role may arise from the haltere's steering muscles, which regulate haltere stroke amplitude to modulate campaniform activity. Taken together, our results underscore the crucial role of efferent control in regulating sensor activity and provide insight into how the sensory and motor systems of flies coevolved.

My work aims to investigate the neural control and processing of haltere-derived mechanosensory information, as well as the functional organisation of campaniform sensilla. It will contribute to our understanding of the evolution and diversification of flight neural circuitry.

Muscarinic Receptor–Mediated Control of Salivation in the Tick *Ixodes ricinus*

Ladislav SIMO (ANSES, INRAE, Ecole Nationale Vétérinaire d'Alfort, UMR BIPAR, Laboratoire de Santé Animale, France, Ladislav.simo@vet-alfort.fr)

Caina NING, Sabine RAKOTOBÉ, Khalid BOUSSAINE, Alison CARTEREAU, Emiliane TAILLEBOIS, Tereza KOZELKOVA, Filip DYCKA, Ondřej HAJDUSEK, Radek SIMA, Jan PERNER, Steeve THANY

Abstract

Ticks rely on sophisticated neural mechanisms to regulate saliva secretion, a process essential for counteracting host immune and haemostatic responses during their prolonged blood meals. Although pilocarpine, an exogenous muscarinic agonist, has long been used to experimentally induce salivation, the identity and physiological roles of the endogenous cholinergic receptors involved have remained largely unresolved. In this study, we identify and functionally characterize two muscarinic acetylcholine receptor subtypes (mAChRs) in *Ixodes ricinus*, the principal European vector of Lyme disease, designated type A and type B. Pharmacological profiling indicates that these receptors differ markedly in their responses to muscarinic ligands, with type B displaying a noncanonical pharmacological profile compared with vertebrate mAChRs. By integrating neuroanatomical mapping, *in vivo* pharmacological assays, and saliva proteomics, we demonstrate that distinct populations of central neurons selectively innervate specific classes of salivary gland acini. These neuronal pathways engage different mAChR subtypes and operate, in part, through neuropeptide-mediated signalling cascades to coordinate the secretion of fluid and bioactive proteins. Together, our findings reveal a previously unrecognised layer of muscarinic regulation in tick salivation. This work provides new insight into the neurochemical control of a key physiological process that underpins tick feeding and pathogen transmission, and identifies receptor-based molecular targets for potential anti-tick interventions.

Environmental control of oviposition preference in *Drosophila melanogaster*

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Manraj SALL, Penny FORD, Herman WIJNEN

Abstract

Oviposition represents a crucial step in the insect life cycle that is influenced by environmental factors including diet, mating behaviors, temperature, and photoperiod. Moreover, oviposition is a key target for pest management strategies. To investigate how environmental determinants regulate oviposition preference, we employ behavioural genetics using the fruit fly *Drosophila melanogaster* as a model organism. *Drosophila melanogaster* shows preference for ovipositing both on substrates pre-exposed to conspecific males or mated females. We found that this oviposition aggregation response persisted in flies with mutant genotypes strongly affecting vision, taste or olfaction and even in virgin flies that were genetically manipulated to uncouple oviposition from mating. Moreover, the signals triggering aggregation of oviposition were not disrupted by antibiotic treatment of the pre-exposure flies. In contrast, mutant genotypes specifically impacting olfactory detection of dietary acids exhibited defects in oviposition preference. We found that dietary acids themselves directly induced oviposition preferences in a context-dependent manner. Finally, we examined the role of the monoamine neurotransmitters Octopamine (OA) and Tyramine (TA) on the oviposition aggregation response. Flies deficient in OA due to loss-of-function mutation in the Tyramine beta hydroxylase (Tbh) and those deficient in OA and TA due to loss-of-function mutation in Tyrosine decarboxylase-2 (Tdc-2) do not ovulate and accumulate mature eggs in their ovaries. This phenotype can be partially reversed by feeding OA. However, oviposition preference was rescued by OA feeding in Tbh mutant, but not in Tdc-2 mutant flies suggesting potential involvement of the OA precursor TA in the oviposition aggregation response. We will discuss our results and their wider implications.

DNA Repair Pathways in the Two-Spotted Spider Mite *Tetranychus urticae*: Enhancing Homology-Directed Repair

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Wannes DERMAUW, Thomas VAN LEEUWEN

Abstract

The two-spotted spider mite, *Tetranychus urticae*, is both a significant global agricultural pest and an increasingly important chelicerate model organism for functional genomics. Its rapid life cycle, high fecundity, and compact genome have positioned it as a promising system for dissecting mite biology. Genome-editing breakthroughs - particularly the recently developed SYNCAS method which enables maternal delivery of CRISPR-Cas9 ribonucleoprotein complexes - have opened the door to precise gene knock-outs (KO) and knock-ins (KI) in species that previously were difficult to modify genetically.

Despite these advances, knock-in efficiencies can be much lower than the high KO efficiencies that are achieved through the SYNCAS method. An important factor that can influence KI efficiencies is the competition among endogenous DNA double-strand break (DSB) repair pathways, which determine whether Cas9-induced breaks are resolved through end joining or homology-directed repair. Although these pathways are well described in some mammalian and arthropod models, very little is known DNA repair in Chelicerata.

This work presents the first functional investigation into DSB repair mechanisms in a chelicerate species. By dissecting the roles of key repair factors and examining how their disruption alters the balance between competing pathways, new insights are provided into the molecular determinants that govern genome-editing outcomes in *T. urticae*. These insights offer opportunities to improve precise genome engineering in this and potentially many other hard-to-transform arthropods.

Alternative strategies based on transgenic *Drosophila melanogaster* for the functional characterization of insect Ionotropic Receptors

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Cristina Maria CRAVA, William B. III WALKER

Abstract

Background: Insect Ionotropic Receptors (IRs) are a relatively uncharted territory. Some studies have documented IR activation by recording neuronal activity *in situ*, others by their heterologous expression in *Xenopus oocytes* or misexpressing IRs from *Drosophila melanogaster* or from the related *D. sechellia* into the *D. melanogaster* “ionotropic receptor decoder” neuron, which lacks the endogenous tuning receptor subunit but expresses IR-coreceptors.

Results: In this study, we first made use of *Drosophila* olfactory sensory neurons (OSNs) different from the “ionotropic receptor decoder”, demonstrating that by replacing or introducing IRs alongside the native *D. melanogaster* ones, functional heteromeric complexes can be formed. IR41a1 from the lepidopteran *Cydia pomonella* exhibits binding to polyamines and the IR75d from the dipteran *Drosophila suzukii* binds hexanoic acid. Structural modeling analysis identifies key amino acids features explaining the binding of hexanoic acid by IR75d. Finally, alternative methods to express IRs in Human Embryonic Kidney cells report a correct expression of these receptors but without achieving their successful deorphanization.

Conclusions: Our findings highlight the potential use of *Drosophila* OSNs as a valuable tool for the functional characterization of IRs from different insect species. For the first time, we have provided evidence of IR-functionalities within alternative OSNs from the *Drosophila*’s “ionotropic receptor decoder” neuron to functionally characterize and deorphanize IRs from lineages that are evolutionarily distant from the *D. melanogaster* subgroup, contributing to the understanding of chemosensory modalities in *D. suzukii* and *C. pomonella*, two globally significant agricultural pests.

Perspectives: Results from this investigation represent the first step towards a more ambitious approach: in the frame of the ongoing project at the C3A-center of the University of Trento, we claim to isolate neurons from transgenic *D. melanogaster* to transit *in vitro* the functional investigation of the heterologous IRs from several pests of agriculture and forestry, and from other invasive or commercial arthropods.

Present state of the insect decline debate

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Abstract

It is now well established that insect biomass and abundance of terrestrial insects have declined drastically over the past decades. In 2020, we synthesized global evidence for changes in insect biodiversity, and could show that declines are common for terrestrial insects, despite local variation. We found that Declines occur in both protected and unprotected areas. Freshwater fauna, on the other hand were found to increase, most probably due to an improvement in water quality in the parts of the world from where data was available.

In 2024, we delved deeper into our dataset, and found that these declines are mostly driven by disproportionate declines of the species that used to be abundant in the past, but that no other species have risen to take their places. At the same time, local insect species richness is declining at a lower rate.

Although these characterizations are robust, they do not really help understanding the drivers of declines, or why the formerly abundant species show particularly strong declines. Several overview papers of potential drivers of declines have been published, but actual evidence of the comparative strength of these drivers remains elusive.

In this talk, I will give an overview of the evidence for insect declines and its drivers, and I will present new results, using an extended and updated version of our global database of insect time series, to give the newest estimated rates of global insect biodiversity change. I will finalize with some potential mitigation measures that have emerged from my older work.

Cinderella biodiversity: capturing long-term abundance and phenology trends in undervalued, forgotten and often sparsely recorded insects and spiders.

James R. BELL (Keele University, J.r.bell@keele.ac.uk)

Yoann BOURHIS, Bill KUNIN, Matt HAMPSON, Dan BLUMGART, Chris SHORTALL, Alice MILNE

Abstract

Arthropod declines have been reported widely, and yet the spotlight has fallen on relatively large, colourful insects, rarely considering the abundant, small-sized, yet charismatic flying insects and ballooning spiders we class as neglected and undervalued 'Cinderella species'. This diverse set of arthropods contribute important ecosystem services, such as decomposition, pollination, pest regulation and nutrient cycling. We sampled a 30-year long archived arthropod collection, preserved in ethanol from the daily 12.2 m suction-trap catches at four sites in the UK, to provide new data on more than 600,000 previously unidentified insects and spiders. Group or family-level trends for the Coleoptera (beetles), Diptera (true flies), Hemiptera (true bugs) and Hymenoptera (bees, ants and wasps) as well as trends for seemingly less well known orders including the Psocoptera (barkflies), Dermaptera (earwigs) and Araneae (spiders) are provided. Our aim is to produce 30-year trends (1990–2020) in abundance and phenology for 71 Cinderella arthropod groups, assessing those by taxonomic group, trophic guild and habitat use during the immature stage. We trained random forest models to predict log abundance and phenology (day of 5% catch) using a set of landscape and weather-related drivers. We show that the majority of arthropod taxa, all trophic groups and nearly all habitat use groups, report increasing abundances and earlier phenologies. We also found that across taxa, earlier phenologies tended to lead to a rise in the abundance of those taxa. These trends are strongly driven by weather, with increases in diurnal, daily, seasonal and average temperature drivers, for example, and landscape drivers, the strongest of which is the proportion of arable land. A total of 32 drivers were modelled which differ in slope direction and strength. Our research highlights robust trends in undervalued, forgotten and often sparsely recorded insects and spiders.

Genomics of *Bombus veteranus*, an endangered bumblebee in restored floodplains in the Netherlands

Bart PANNEBAKKER (Wageningen University & Research - Laboratory of Genetics, Bart.pannebakker@wur.nl)

Dominic DIJKSHOORN, Joost VAN DEN HEUVEL, Frank BECKER

Abstract

The critically endangered bumble bee *Bombus veteranus*—once widespread across western Europe—has since the 1980s seen its populations in the Netherlands collapse to just two isolated areas: the Haringvliet former tidal inlet system and the Biesbosch floodplains. Following large-scale nature restoration on the island of Tiengemeten and in the Biesbosch, *B. veteranus* populations have rebounded, earning it the nickname “the Panda of the Dutch Delta.” However, despite its establishment in the Biesbosch since 2004, the species has yet to expand further, raising questions about the long-term viability of these populations.

To assess their resilience and connectivity, we employed a genomics-based approach. We collected tarsi samples for whole-genome resequencing, mapping reads to a *de novo* assembled *B. veteranus* genome generated using Oxford Nanopore long-read sequencing. Our analysis focused on key genomic indicators for conservation: population structure, genomic diversity, and inbreeding. Given the vulnerability of bumble bees to inbreeding due to complementary sex determination—which can result in sterile diploid males under inbreeding—we also screened for their presence.

Our findings provide the first insights into the genetic health of these populations and lay the foundation for a long-term genomic monitoring program. This work will inform conservation strategies aimed at restoring and protecting *B. veteranus* and other endangered pollinators in the Netherlands.

Archived natural eDNA samplers reveal four decades of biodiversity change in terrestrial and aquatic arthropod communities

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Isabelle JUNK, Julian HANS, Manuel STOTHUT

Abstract

Alarming and dramatic declines of arthropod biomass have been reported across the globe. However, comparatively few standardized historical time series datasets are available to identify the causes and patterns of the observed declines. Novel sources of data for analyzing biodiversity change across time and space are thus urgently needed. By metabarcoding highly standardized biota samples from a long-term pollution monitoring archive in Germany, we here analyze community diversity for thousands of arthropod species from terrestrial marine and limnic environments across four decades of. The archived samples—tree leaves, marine macroalgae, and marine and limnic mussels—represent natural community environmental DNA (eDNA) samplers. They preserve a taxonomically diverse imprint of their associated arthropod biodiversity at the time of collection. Tree leaves and macroalgae preserve eDNA traces of arthropods, which interacted with the plant's tissue, for example from bite marks or leaf mines. The mussel's digestive tract contains an imprint of the eDNA, which they filtered out of the water column. By metabarcoding these eDNA sampler organisms, we enrich the DNA traces of arthropods and reconstruct patterns of community diversity over four decades. Our results show no patterns of universal biodiversity decline at individual sites. Instead, a gradual taxonomic turnover emerges as universal pattern of temporal biodiversity change in Germany's terrestrial and aquatic arthropod communities. Through the immigration of novel widespread taxa and the loss of many site-specific ones, this turnover results in biotic homogenization throughout ecosystems. Germany's ecosystems hence harbor less, but more widespread arthropod species.

Assessing the in natura effects of pesticide use on a wide range of flower visitors in France

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Colin FONTAINE, Emmanuelle PORCHER, Mathieu DE FLORES, Nicolas BECH, Nicolas DEGUINES

Abstract

Intensification of agricultural practices (e.g., landscape simplification, increases in quantity and diversity of pesticides) has been impacting biodiversity for several decades. Although pesticides antagonistic effects have been demonstrated under lab conditions for a few flower-visitors species (mainly bees), studies are lacking regarding in natura effects, often encountered at sublethal doses and in cocktails. Here, we aim at analysing responses of a broad range of flower-visitors to pesticides use on a national scale.

We used data from a monitoring scheme of flower visitors across France based on citizen science (Sipoll) and related occurrences to pesticides indicators derived from the French database on pesticide purchases: i) active substance quantities, and ii) the diversity of pesticides purchased locally. We also account for covariables describing the potential resources and pressures from surrounding landscape (such as landscape heterogeneity or urban areas proportion), and covariables describing observations conditions (e.g. weather, time). Using generalized linear mixed models, we assessed responses to pesticides for ca. 40 separate species from major flower visitors' guilds (bumblebees, solitary bees, hoverflies, butterflies, and beetles).

Results highlight diverse responses at species level to pesticides (both the quantity of active substance and substances diversity). Multiple interaction between pesticide and resources variables (i.e., linear length of hedges, diversity of crops, heterogeneity of composition) were observed, leading to the conclusion that the latter help to offset the negative effects of pesticides. We also observed interactions between the quantity and diversity of pesticides, most often negatively impacting the probability of species presence.

Perspectives for these results are i) to understand which species functional traits explain the various responses to pesticides we observed, and ii) to add a temporal dimension to understand if the reduction or even ban of specific pesticide families is followed by changes in flower insect communities.

#12116

BIODIVERSITY: Insect decline and conservation biology 1

01/07/2026 at 12:00, Loches

Resurveying Swiss Agricultural Landscapes: Changes in Ground Beetle Abundance and Biodiversity Over Three Decades

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Natacha BODENHAUSEN

Abstract

Environmental shifts in agricultural landscapes are profoundly altering insect communities overtime, threatening vital ecosystem services such as pollination, natural pest control, and herbivory. Despite the urgency, long-term data on insect population trends remain scarce, particularly in Switzerland. Identifying the drivers of this loss is critical for developing effective conservation measures. Since intensive agriculture is a primary driver of biodiversity loss, this study evaluates how insect communities differ across organic, integrated, and conventional farming systems. By replicating studies from the 1990s using standardized methods, this research compares contemporary data with historical baselines to quantify long-term changes in the biodiversity and abundance of ground beetles. The analysis considers their functional ecology and the status of endangered species relative to cultivation intensity.

Historical baseline to track long term insect decline using museum specimens

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Inés CARRASQUER, Camille PITTELOUD, Enolà LE BASLE, Marylène BACAICOA, Aristide PARISOD, Nathan CORNIDE, Hélène MOTTAZ, Julia BILAT, Jérôme GOUDET, Nadir ALVAREZ, Jérémy GAUTHIER

Abstract

The large-scale decline of insects in the past decades is increasingly evident and widely documented. However, the trend and the causes of this decline are still widely debated. One reason could be the lack of a reliable baseline because the studies are based on recent trends - since the 1970s. Moreover, these studies generally rely on biomass estimations that do not fully reflect the state of populations. Yet an ample set of samples is available to undertake a large-scale study, both spatially and temporally. Most museum collections comprise insects collected over this period, forming genuine time series. Thanks to recent developments in museomics, it is now possible to access the genetic information carried by these samples and thus to study the evolution of genetic diversity over time. Following thorough databasing in the five main Swiss museums, we selected seven insect species among Ephemeroptera, Orthoptera and Lepidoptera. We then achieved a comprehensive sampling of insect tissues from museum specimens, yielding a total of nearly 1,462 historical samples spanning the entire 20th century, and covering a large number of localities in Switzerland. In addition, historical localities have been resampled in 2021-2022, resulting in 919 fresh specimens. A cutting-edge genomic tool, hybridization RAD, was applied to recover genetic information from historical samples. This innovative museomics approach recovered thousands of nuclear loci, enabling the estimation of various population genetic indices to assess population dynamics. Initial findings indicate a widespread erosion of genetic diversity of approximately 40% in the species studied. In some populations, genetic diversity began to decline prior to 1950, with results revealing widespread and, in some cases, drastic losses. These findings highlight the genetic consequences of anthropogenic pressures experienced over the last century. Beyond these results, this study reveals the importance and richness of museum collections for investigating crucial evolutionary questions.

Shifts in baselines: Long-term changes of insect communities

Eva KNOP (University of Regensburg / University of Zürich, Eva.knop@ieu.uzh.ch)

Abstract

Insect communities have changed over the past decades. Yet, baselines and the main drivers of those changes are still poorly understood, partially due to a lack of long-term data coupled with information on the drivers. Based on datasets spanning large parts of the 20th century, I will focus on long-term changes of various characteristics of insect communities and relate them to the changes of two main drivers, namely land-use intensity and climate warming. I will show how baselines have shifted over time and that it is key to account for this when setting restoration goals and priorities. Also, I will show that land-use intensity and climate warming explain many of the observed community changes, but that their relative importance changes over time, with climate warming becoming more and more of a dominant driver for selected insect groups.

Hoverfly biodiversity, size and diet as potential indicators for agroecological transformation in the agricultural landscape

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Adrian JAICH, Juliet Daniela ARANIBAR LUNA, Maximilian PINK, Johannes UHLER

Abstract

Hoverfly species are important ecosystem service providers (especially pollination and pest control). Their populations are threatened by a variety of stress factors and are in sharp decline in several European regions. Since 2019, our research has focused on developing methods for monitoring hoverflies (MonViA project – nationwide monitoring of biodiversity in agricultural landscapes, <https://www.agrarmonitoring-monvia.de/en/monvia-the-nationwide-monitoring-of-biodiversity-in-agricultural-landscapes>) and also on boosting the effects of agricultural transformation on their populations (FInAL project (Promotion of Insects in Agricultural Landscapes, <https://www.final-project.de/en/>). Through regular monitoring with various trap systems (pan traps, Malaise traps, prototypes of AI camera traps), we report here on data on species richness and abundance of hoverflies at several locations in the agricultural landscape of Germany over a period of five years. Different size patterns in certain species over the years could also be described as an indicator of their fitness. A well-known measure to promote hoverflies is to increase flower resources through flower strips or specific flowering plants. To assess whether these introduced flower resources were used, we examined the pollen profile in the intestines of the captured hoverflies by isolating the pollen and identifying the plant species using metabarcoding. The results showed that the hoverflies did indeed use the floral resources that had been introduced into the respective agricultural landscapes.

A landscape-scale experiment shows that the effects of habitat loss outweigh those of fragmentation on ground-dwelling arthropods

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Romain MONASSIER, Naïs PÉNAGÉ, Benoit GESLIN, Cécile ALBERT

Abstract

Habitat loss and fragmentation are among the main drivers of terrestrial biodiversity decline worldwide. However, the effect of fragmentation per se at a given level of habitat amount remains debated, and experimental evidence is still scarce. To disentangle the effects of habitat amount and fragmentation, we conducted a landscape-scale experiment in which a wide gradient of habitat amount (nine levels, from 1% to 100%) was crossed with three levels of fragmentation, ranging from clumped to highly fragmented configurations. We investigated the responses of ground-dwelling arthropods over the first four years of the experiment. Total arthropod captures, as well as captures of several taxonomic groups including beetles, declined significantly with increasing habitat loss. Arthropod biomass also declined, reflecting both reduced capture rates and a filtering towards smaller-bodied species. In contrast, the effects of habitat fragmentation were mostly neutral, although significant effects were detected on the occurrence of some taxa. The results of this experiment will contribute to the ongoing debate on habitat loss versus fragmentation, providing essential knowledge for applied spatial conservation of insects.

Landscape composition outperforms configuration in predicting bee communities across different habitats in France

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Abstract

Understanding how landscape composition or configuration shapes bee communities is essential for designing landscape management that supports pollinator communities. In this study, we evaluated whether the local diversity of bee communities across different habitats is explained by landscape composition or configuration metrics. We also assessed the effect of landscape attributes and local environmental variables (temperature, wind, precipitation, and altitude) on bee composition dissimilarity (species turnover) along the coastal-to-inland gradient in southwestern France. Bees were sampled using bowl traps in five regional natural parks between spring and autumn 2022, covering eight habitat types: spruce plantations (n= 3), peatlands (n= 4), tall-herb meadows (n= 4), calcareous grasslands (n= 6), grey dunes (n= 8), dry heaths (n= 10), wet heaths (n= 13), and prairies (n= 27), totaling 75 sampling sites. Landscape variables included compositional (percentage of classes, compositional heterogeneity) and configurational (edge density, number of patches) metrics. We sampled 15,962 individuals from 258 species, with *Lasioglossum malachurum* (Kirby, 1802) being the most abundant species (N= 4,453; 27.9%). Bee communities were explained solely by landscape composition attributes. Increasing landscape heterogeneity positively affected bee abundance and diversity (H'), whereas a higher cover (%) of coniferous forest negatively affected species richness. The direction of the effect of landscape metrics on bee communities varied among habitat types. Moreover, higher cover (%) of coniferous forest, spatial distance, and altitude drove compositional changes in bee communities, increasing species turnover. Natural habitats in southwestern France were historically replaced by monoculture pine plantations for timber, resulting in landscape homogenization, reduced habitat heterogeneity, and limited floral and nesting resources. Our results highlight that promoting mosaics of natural and semi-natural habitats and enhancing compositional heterogeneity at the landscape scale are critical for sustaining bee communities.

Historical baselines reveal long-term trends in ground-beetle diversity in Dutch coastal dunes

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Abstract

Insect populations are changing worldwide, yet most datasets cover only the past few decades, leaving long-term trends poorly resolved. Historical baselines are essential to understand how communities respond to sustained environmental change. We analyse a unique long-term dataset of ground-beetle (Carabidae) communities from the Dutch coastal dunes, originally collected between 1953 and 1960 using pitfall traps and resurveyed in 2023–2025 at the same location. This provides a rare opportunity to quantify community change across more than seventy years in a relatively undisturbed dune ecosystem.

The forthcoming analyses address three core questions:

- How have species richness and diversity changed since the 1950s?
- Which functional and habitat-associated groups show the strongest long-term shifts across dune habitats?
- How has community structure changed, as inferred from Joint Species Distribution Models (JSDMs), including patterns of co-occurrence, shared environmental responses, and network-level reorganisation?

To answer these questions, we integrate diversity metrics, negative binomial GLMMs and hierarchical JSDMs to disentangle environmental, habitat and species - species components of community change. This modelling framework allows us to quantify not only which species have changed, but how the community as a whole has reconfigured over seven decades.

By integrating modern statistical approaches with mid-20th-century baselines, this study will provide one of the longest perspectives on insect biodiversity dynamics. The project demonstrates the scientific value of historical datasets and outlines a transparent framework for comparing ecological communities across widely separated sampling eras.

Habitat specific pollinator assemblages and interaction networks in a gypsum dominated landscape

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Abstract

Pollinators are nowadays widely known as key contributors for ecosystem services; however, they are increasingly threatened by effects of climate change and human activities. This study aims to characterize the pollinator community on the eastern side of a site characterized by the geological feature of the gypsum, the Vena del Gesso Romagnola Regional Park, by analyzing pollinators communities and plant–pollinator interactions. This place is UNESCO-recognized as world heritage site, as the extensive gypsum outcrops and formations shaped the landscape and its distinctive habitats. Sampling sites were selected at three representative gypsum outcrops. At each location, two standardized transects, one on the gypsum outcrop and one in the adjacent grassland, and two Malaise traps were set up, and collected specimens of wild bees (Apoidea), hoverflies (Syrphidae) and butterflies (Lepidoptera) were identified morphologically. Using data from this monitoring, interaction between pollinators and plants were analyzed through bipartite networks metrics. Results from transect surveys and preliminary Malaise trap identifications reveal contrasting responses of pollinator communities associated with gypsum outcrops and grasslands, along with a seasonal turnover in pollinator assemblages. Meteorological data were then integrated to further assess the influence of seasonality on communities sampled in grassland and gypsum environments.

How landscape structure shapes the spread of invasive insect pests

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Abstract

Invasive insect pests are a major component of global change, affecting the vitality and functioning of agricultural and forest ecosystems and, causing substantial ecological impacts and economic losses. Landscape structure strongly shapes the establishment and spread of these species through the influence of habitat composition, connectivity and human activities. Understanding how landscape configuration and land use mediate invasion processes is therefore essential for implementing effective prevention, surveillance and management strategies. Although simulation models, such as those based on reaction–diffusion equations, are widely used to study invasion dynamics, they seldom incorporate the structure and composition of the landscapes crossed by the invasive species and their spatial heterogeneity.

Using case studies, it is analysed how combining spatial analyses with ecological modelling across different modelling approaches can improve predictions of spread of invasive species. Particular attention is given to the role of urbanization and forest management, illustrated through two European invasive species: the pinewood nematode and its insect vector *Monochamus galloprovincialis*, and the African citrus psyllid *Trioza erytreae*. We also discuss how landscape-level insights can inform more effective surveillance design and adaptive management strategies, for example, reducing habitat connectivity.

Together, these perspectives stress the need to use a landscape-based approach for managing insect invasive pests.

The impact on a diverse beetle community from the dieback of a dominant canopy tree species (kauri, *Agathis australis*) in New Zealand.

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Henley BLACK, Samuel AGUILAR-ARGUELLO

Abstract

Kauri (*Agathis australis*) is a dominant emergent canopy tree species that is endemic to northern New Zealand. Kauri dieback disease, caused by the soil-borne oomycete pathogen *Phytophthora agathidicida*, has spread through much of New Zealand's kauri forest in the last 20 years, killing thousands of trees. However, whether kauri dieback affects the broader biological community in kauri forests is largely unknown. Here we test whether dieback of kauri trees affected ecologically important beetle communities by sampling beetles using flight-intercept and pitfall traps at three pairs of symptomatic (widespread dieback of kauri trees) and asymptomatic (little or no dieback) forest sites in Waitākere Ranges Regional Park, on the North Island of New Zealand. We collected 4366 individual beetles from 377 species and found that beetle abundance and species richness were significantly lower (34% lower abundance and 19% lower species richness) in symptomatic sites than in asymptomatic sites, whereas community composition showed no significant difference. The lower abundance and species richness observed in symptomatic sites were consistent across feeding guilds and not just those directly associated with living or dead kauri trees, suggesting that the changes in beetle abundance and richness may be related to environmental changes caused by the loss of dominant canopy trees rather than the loss of kauri trees specifically. Our results may be applicable to many forest systems where the loss of dominant tree species to pests, disease, or climate change, can lead to flow-on effects to the broader biological community. Our study presents evidence that plant diseases may have impacts that extend beyond species directly associated with that host plant.

Native, introduced and invasive ambrosia beetles in Hungary

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Abstract

Over the past few decades, damage caused by bark and ambrosia beetles (Curculionidae, Scolytinae) has increasingly impacted both European and Hungarian forests. This increase in damage is attributed to both altered climatic conditions and abiotic effects like the introduction of non-native, invasive bark and ambrosia beetles. While considerable information is available regarding bark beetles, the knowledge of ambrosia beetles is still limited, particularly for non-native species.

Ambrosia beetles have particular importance for forest management because of their ability to reduce timber quality, especially when infesting high value timber. According to their inbreeding biology a single fertilized female can easily establish a small invading population in a new environment, threatening biodiversity and complicating forest management strategies. Further, ambrosia beetles rely on their symbiotic fungi transported in their mycangia. Fungi associated with ambrosia beetles vary by species, but they are often highly pathogenic to the host tree, causing tree mortality even on large scale. Thus, understanding the biology, life cycle, and ecological role of these beetles is crucial for developing appropriate monitoring systems and management strategies. Current strategies include monitoring with traps (e.g., ethanol-baited traps), and some management guidelines, but more research is needed to better understand their dynamics and to improve long-term forest protection policies.

The presentation provides an overview of native and introduced ambrosia beetles in Hungary, including both the 11 native and the 4 introduced/invasive species. The study highlights species belonging to the genus *Xyleborus*, *Xyleborinus*, *Trypodendron* and *Platypus*, alongside introduced species of the genus *Anisandrus*, *Gnathothrichus* and *Xylosandrus*. Monitoring and control methods and forest management experiences will also be presented.

What lies behind a successful pest and vulnerable forest ecosystem? Effect of diversity, forest structure and prey defence strategy on predation risk

Magnus JONSSON (University of Helsinki, Magnus.jonsson@helsinki.fi)

Emy GUIBAULT, Venla KORHONEN, Katja KOSKENPATO, Carita LINDSTEDT

Abstract

Climate change and environmental homogenization are expected to facilitate the expansion of new potential pest insects as well as increase the vulnerability of forest ecosystems to outbreaks. However, at present, we lack empirical data on how the ecology of pest insects interacts with the local environmental conditions and shape outbreak risk. Here we study this from a predator-prey interaction perspective. We ask 1) how do anti-predator defences of pest insects affect their success in boreal forests, and 2) how is predation risk shaped by the diversity and structure of forests and predator communities? We tested these questions by conducting a field predation experiment where we manipulated the gregariousness, unpalatability and defensive colouration of dummy prey and tested their effects on predation risk. We also measured environmental variables along the prey transects to analyse how they shape overall predation risk across defence treatments. Our results show that the predation risk was always lowest for gregarious prey irrespective of other defence strategies. Furthermore, our results indicate that intensive forest management, homogeneous tree structure and a low dead wood continuum increase the susceptibility to pest insect invasions as the predation risk was lower in those locations in comparison to more natural state forests. Altogether, our results indicate that maintaining diversity in forests can make them more resistant to pest outbreaks. Furthermore, gregariousness can facilitate pest insects to form outbreaks by increasing their survival against generalist predators.

The role of broadleaved hedgerows in forest arthropod conservation in pine plantations

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Inge VAN HALDER, Hervé JACTEL

Abstract

Forests are key ecosystems for biodiversity conservation. Monospecific and intensively managed forests generally support lower biodiversity than mixed semi-natural forests. However, diversifying forest, at stand or landscape level, remains a logistical challenge for forest managers.

Building on the concept of bocage, an agricultural landscape characterized by a dense network of hedgerows, we hypothesized that broadleaved hedgerows embedded within monospecific conifer plantations could enhance forest arthropod biodiversity. We tested this hypothesis in the Landes de Gascogne Forest, the largest planted forest in Europe, predominantly composed of monospecific maritime pine (*Pinus pinaster*) stands.

We surveyed arthropod communities, focusing on butterflies, carabid beetles, and spiders, in broadleaved hedgerows and at pine stand edges. Using airborne LiDAR data, we also assessed how the vertical and horizontal structure of hedgerows influenced arthropod communities.

Our results showed that broadleaved hedgerows supported arthropod communities distinct from those found at pine stand edges. Species richness of forest specialist arthropods, as well as that of rare species, was significantly higher in hedgerows. Among the structural metrics measured, canopy density was a key factor explaining forest arthropod diversity. Moreover, hedgerows influenced ecological traits across arthropod groups.

Overall, our findings highlight the importance of broadleaved hedgerows within conifer plantation landscapes for forest arthropod conservation. Combined with previous evidence of their role in reducing insect pest infestations, broadleaved hedgerows emerge as a promising Nature-based Solution with direct applications for sustainable forest management.

Forest structure matters: responses of saproxylic beetles to management

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Giovanni TRENTANOVI, Silvia GISONDI, Francesco CHIANUCCI, Pio Federico ROVERSI, Alessandro CAMPANARO

Abstract

European forests host around 80% of terrestrial biodiversity, about one quarter of which is composed of saproxylic organisms—species that depend, for at least one stage of their life cycle, on dead or decaying wood or organisms linked to this resource. Among them, beetles represent the most species-rich group and play key ecological roles, serving as excellent indicators for assessing the effects of forest management on biodiversity and ecosystem functioning.

This contribution analysed how saproxylic beetle assemblages respond to different silvicultural regimes. The study was carried out in mountainous beech forests in Northern Apennines (Italy), consisting of transitional stands under conversion to high forests by different silvicultural regimes: (i) natural evolution (unthinned control), (ii) traditional conversion via periodic thinning (iii) anticipated seed-cutting. Monthly beetle data were collected through window traps from April 2023 to March 2024. Species data were integrated with tree inventory measurements related to forest stand and canopy structure.

More than 12,000 beetle individuals were collected, representing 145 species from 35 families. In general, individual abundances and species richness do not differ among stands, but considering biodiversity indexes, such as Shannon diversity and Evenness, the natural evolution stand hosts a more diverse and balanced community. Considering species composition, differences are reported for each management regime, highlighting how silviculture can act as a filter for a number of species. Finally, deadwood and canopy cover, as well as the number of standing dead trees, were positively associated with higher compositional diversity. These findings highlight the importance of maintaining and restoring structural complexity in managed forests to enhance biodiversity and support ecosystem processes.

Bark beetle diapause: Using eco-physiology and genomics to predict outbreaks

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Abstract

The spruce bark beetle *Ips typographus* is the most important forest insect in Europe. Its phenology and voltinism are strongly shaped by a specific developmental program, i.e. diapause. *Ips typographus* is characterized by a high plasticity of diapause responses, which affects its potential for eruptive population outbreaks. First, the diapause phenotype affects voltinism: facultative (regulated by environmental factors) and obligate (independent of environmental regulators) diapause expression results in multivoltine or univoltine life cycles, respectively. Using genomics and machine learning approaches we detected genetic loci that are associated with diapause phenotype, which can subsequently be used to predict diapause expression and thus voltinism under natural conditions. Second, facultative diapause is primarily under photoperiodic control and diapause is induced when daylength drops below specific thresholds. To respond to local habitat conditions, daylength values to induce diapause vary along latitude. Third, facultative diapause induction (primarily regulated by photoperiod) is also affected by temperature as warm conditions suspend photoperiodic cues and postpone the entry into diapause later in the season. Taken together, both internal and external regulators contribute to the complex diapause biology of *I. typographus*, which are additionally affected by a changing climate. This information can be implemented into practical tools to predict outbreaks for effective management measures.

Inter-continental introgression in the winter pine processionary moth species complex: phylogenetic and genomic perspectives

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Pierre NOUHAUD, Christian BURBAN, Raphaël LEBLOIS, Laure SAUNÉ, Eftichia DIMITRIOU, Dimitrios AVTZIS

Abstract

The pine processionary moth, *Thaumetopoea pityocampa* (Lepidoptera: Notodontidae) is a defoliator of forest trees and a threat to human and animal health due to its urticating larval setae. It belongs to a Mediterranean species complex comprising 2 (*T. pityocampa* and *T. wilkinsoni*) to 5 species (with the recently described *T. cretensis*, *T. hellenica* and *T. mediterranea*) depending on authors and studies. *T. hellenica* was described from Greece from mitochondrial data only, and found phylogenetically close to the *T. pityocampa* Eastern-North African mitochondrial clade present in Libya. A number of previous molecular studies based on mitochondrial information and a few nuclear sequences evidenced the occurrence of mito-nuclear discordance, which tends to blur the evolutionary scenario and question species delimitation in the complex.

Using mitochondrial and RAD-seq markers on a set of individuals sampled all over the Mediterranean range of the complex, we propose a robust phylogeny and decipher cases of mitochondrial introgressions and nuclear-mitochondrial discordance, which raises doubts about the validity of some recently described species. In particular, the occurrence of *T. hellenica* in Greece could correspond to a mitochondrial introgression. To explore this situation, we sampled pine processionary caterpillars all over Greece with a special focus in the Attica region where *T. hellenica* was previously detected. The sampling was completed with few individuals from Libya where *T. hellenica* is also supposed to occur. Whole-genome sequencing showed that individuals collected in the Attica region mostly have *hellenica*-like mitochondrial haplotypes, with a high haplotypic diversity. On the contrary, their nuclear genomes are mostly *pityocampa*-like, but still bear signs of past introgression from *T. hellenica*. Interestingly, the introgressed genomic regions were different between individuals, suggesting that the hybridization event was relatively ancient. New analyses will be necessary to estimate the age of the introgression and the evolutionary forces that shaped this intriguing pattern.

An emerging threat: The potential European spread of *Xylotrechus chinensis*

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Carole KERDELHUÉ, Alain ROQUES

Abstract

Xylotrechus chinensis (Chevrolat, 1852) (Coleoptera: Cerambycidae – tiger longhorn beetle) is an Asian wood-boring species recently detected in four European countries (France, Greece, Italy, and Spain), where it is causing significant mortality in *Morus* trees. We analyzed its ecological niche dynamics to compare the climatic niche in Asia with that in its European invaded range and to assess its potential distribution under the assumption of niche conservatism.

We found no evidence of a climatic niche shift, and the range of climatic conditions occupied by European populations falls within that observed in Asia, except for maximum summer temperatures, which are slightly higher in Europe. Ecological niche analyses allowed us to quantify five processes—abandonment, pioneering, unfilling, expansion, and stability—and to map their spatial patterns across Europe. Overall, 8.6% of the European land area corresponded to climatic conditions occupied both in Asia and Europe (“stability”). Another 41.1% corresponded to climates occupied in the native range but not yet colonized in Europe (“unfilling” and “abandonment”), likely due to limited dispersal capacity and the still recent establishment of the species in Europe. European populations also occurred in climatic conditions for which no observations exist in Asia (“expansion” + “pioneering”, 4%), corresponding to “temperate with dry and hot summer” climates in the Köppen–Geiger classification, occurring in mainland Greece and Crete. The remainder of the European land area was not climatically suitable for the species.

We conclude that (i) European populations of *X. chinensis* show no evidence of a climatic niche shift, (ii) suitable climates are widespread across the continent, (iii) *X. chinensis* current distribution remains limited by its recent introduction, and (iv) the species is likely to establish in many regions, provided suitable host trees are present.

Distribution of the genetic diversity of the Oak splendour beetle *Agrilus biguttatus* (Coleoptera: Buprestidae) across Europe

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Elodie LE SOUCHU, Emmanuelle MAGNOUX, Aurélien SALLÉ, Radek PLEWA, Marie-Anne AUGER-ROZENBERG

Abstract

Environmental and climatic changes shaped the distribution of temperate-adapted species. In Europe, it should be particularly significant for the thermophilous and heliophilous species *Agrilus biguttatus*, a xylophagous Coleopteran species aggravating oak forest decline, which expands its distribution area northward. The principal objective of this study was to investigate the phylogeography and genetic structure of several populations of *A. biguttatus* in order to improve our comprehension of its evolutionary history. We sequenced a mitochondrial COI fragment in 30 European populations and screened genetic variation in 199 individuals from 12 populations at 12 new microsatellite markers developed for the first time for this species. The dominance of a single COI haplotype among only 15 others coupled with a negative Tajima's D in the sampled area fit with a population expansion model. The microsatellite analyses indicated the existence of two well-defined clusters, one in the eastern part of Europe (Belarus and Poland) and another one in the western part (France, the Netherlands and Belgium). The western populations exhibited an apparent lack of genetic structuring, with some admixture between populations. Nevertheless, a trend towards genetic differentiation between distant populations was detected, suggesting gene flow and population expansion in Europe. We hypothesised that changes in climate and in the geographical distribution of oaks after post-glacial colonisation shaped the distribution of this temperate-adapted insect. However, the recent global changes and human-mediated transportation of infested logs may have accelerated its expansion.

Visual Ecology of Cerambycidae: Color Sensitivity and Trap Optimization for Improved Pest Detection

Laura Rita BESANA (University of Padua, Laurarita.besana@phd.unipd.it)

Domen LAZAR, Gregor BELUŠIČ, Giacomo SANTOIEEMMA, Giacomo CAVALETTO, Davide RASSATI

Abstract

Longhorn beetles (Coleoptera: Cerambycidae) constitute one of the world's most diverse beetle families, including numerous forest pests and several invasive species. Effective detection and monitoring of a newly emerged pest are crucial to maximize eradication success rates and minimize management costs. Recent studies have shown that visual cues, in addition to chemical volatiles, significantly enhance trap attractiveness. However, despite color sensitivity being fundamental to understanding the visual ecology of longhorn beetles, this aspect has remained unexplored. To address this gap, we conducted electrophysiological recordings on five longhorn beetle species across three subfamilies during 2024–2025. Preliminary findings reveal dichromatic vision in one prionine and two cerambycine species, while three lepturine species exhibit trichromatic vision. These results suggest that the expanded color sensitivity found in lepturines may have evolved more recently in conjunction with their primarily flower-visiting behavior. Additionally, we conducted a field trapping experiment in 2025 to assess longhorn beetle responses to various visual stimuli. Six traps in three colors (black, yellow, and fluorescent yellow) were deployed, both with and without UV LEDs. The experiment was replicated across ten blocks in the Euganean Hills region of Veneto, Italy. Preliminary data shows that flower-visiting longhorn beetles exhibit a strong preference for fluorescent yellow and yellow traps over black ones. UV LED illumination has a pronounced effect on crepuscular and nocturnal species, which demonstrated significantly higher attraction to illuminated traps. Together, these results advance our understanding of the physiological and behavioral foundations of color vision in longhorn beetles and reveal promising opportunities for optimizing monitoring protocols through the incorporation of visual cues.

In silico work as a first step towards valid molecular confirmation of alien *Cnestus* species

Elena L. T. BACHER (AGES, Elena.bacher@ages.at)

Chiara POHN, Richard A. GOTTSBERGER, Helga REISENZEIN

Abstract

In the face of climate change and globalization, invasive insect species have become a pervasive problem. Reliable molecular confirmation of morphologically identified alien species requires careful preparatory in silico work to ensure downstream results are valid. Because public sequence databases contain records of varying quality, a comprehensive inventory is essential to vet all available sequences attributed to the target species and its close relatives, along with understanding each database's content moderation and purpose. This includes assessing taxonomic correctness, metadata completeness, and phylogenetic coherence, allowing researchers to evaluate reference data reliability before and during species level identification.

Such quality control is especially critical for the subfamily Scolytinae, whose extreme inbreeding and high intraspecific variability further amplify the risk of incorrect identifications. The importance of this in silico approach is highlighted by the recent first detection of the invasive species *Cnestus mutilatus* (Blandford, 1894) in Austria. A multilocus strategy was employed to sequence the specimens in questions, furthermore, multiple barcoding primer sets were used to expose amplification bias and enhance genetic resolution. After performing in depth in silico work to assess the available sequences and their quality, as well as creating multiple alignments and performing tree-based ID, preliminary results indicate a close relationship to specimens previously recorded from Slovenia. This can suggest possible introduction routes or regional dispersal patterns.

Overall, this contribution underscores that rigorous in silico preparation—such as compiling a comprehensive database inventory and vetting sequences—is a crucial first step for the accurate molecular verification of morphologically identified *Cnestus* species. In a second step, it forms the basis for the development of a genus-specific real-time PCR assay for *Cnestus*. This foundation ensures reliable species level identification and tracing of invasion pathways, thereby improving surveillance and informing regulatory measures against alien Scolytinae.

Climate warming drives the range expansion of the pine processionary moth *Thaumetopoea pityocampa* (Lepidoptera, Notodontidae) in the European Alps

Sonja MADER (Department of Ecosystem Management, Climate and Biodiversity, Institute of Forest Entomology, Forest Pathology and Forest Protection, BOKU University, Vienna, Austria., Sonja.mader@students.boku.ac.at)

Lukas MICHOR, Andrea BATTISTI, Gernot HOCH, Axel SCHOPF, Kahraman IPEKTAL, Christian STAUFFER, Peter BAIER, Martin SCHEBECK

Abstract

The pine processionary moth (PPM) *Thaumetopoea pityocampa*, primarily native to the Mediterranean, is a model to study temperature-driven range shifts. The PPM is a challenging forest insect that defoliates pine trees and causes health problems due to the urticating setae of its larvae. An unprecedented outbreak in the Austrian Southern Alps since 2016/17 initiated the spread into novel regions of the PPM's alpine range. As major parts of the PPM life cycle are temperature-driven, we used historic climatic data to assess climate change effects on the recent range expansion in the Austrian Southern Alps. We applied a mechanistic model to reconstruct temperature conditions on a fine local scale and infer regions permissive for feeding and survival, and hence regions suitable for establishment and spread. Breakpoint analysis indicated a significant rise in PPM feeding activity in the Austrian Southern Alps since the 1980s, driven by global warming. Further, temperatures permissive for feeding were met at increasing frequencies from the year 2000 onwards. Additionally, we found that milder winter temperatures between 2011 and 2024 resulted in lower cold-related larval mortality.

Our findings demonstrate that climate-change driven temperature increases facilitated further PPM expansion towards higher latitudes/elevations in the Alps, particularly to regions near the recent outbreak. Our results can be implemented into surveillance programs to assess pine defoliation and hazards for human and animal health, along with further potential expansion of PPM in the Austrian Southern Alps.

Reimagining Human-Nature Relationships: Global Collaborations with People and Wasps

Seirian SUMNER (University College London, S.sumner@ucl.ac.uk)

Abstract

Human societies have never been more disconnected from nature. This separation has profound implications for our motivation and ability to address biodiversity loss and climate change. If we cannot notice, name, and understand the nature around us, we are unlikely to nurture it. We tend to value only the charismatic elements of nature that society has taught us to appreciate - such as bees as pollinators - while neglecting or even fearing those we do not understand. Wasps exemplify this bias: we fear their stings and rarely recognize their vital roles as pest controllers and pollinators.

However, this is largely a Global North perspective. By contrast, many communities in the Global South - particularly indigenous peoples - maintain close connections with nature. This stems partly from their reliance on the land for food, shelter, and medicine, and partly from cultural beliefs and traditions that foster respect for species often overlooked elsewhere. Collaborating with scientists and Indigenous communities in the Global South offers an opportunity to reset our relationship with nature.

In this talk, I will share personal experiences of how such collaborations have enriched my research, opened new avenues in wasp science, and demonstrated how we can begin to transform some of our most challenging relationships with the natural world.

Sustainable North–South Cooperation in Medical and Veterinary Entomology: The Model of Institut Pasteur du Cambodge

Sébastien BOYER (Medical and Veterinary Entomology Unit, Institut Pasteur du Cambodge, Sboyer@pasteur-kh.org)

Abstract

The Medical and Veterinary Entomology Unit at the Institut Pasteur du Cambodge (IPC) serves as a strategic regional platform in Southeast Asia, a tropical region characterized by insect diversity and public health challenges

Our unit's trajectory highlights how strong North–South cooperation is essential for responding to the alarming loss of biodiversity and the threat of emerging infectious diseases.

Modern cooperation extends beyond taxonomic inventories into high-level fundamental and applied research. We integrate emerging technologies to bridge infrastructure gaps, such as (i) Machine Learning & Big Data: Utilizing MALDI-TOF MS and AI for rapid mosquito and tick species identification, (ii) Medical Geography: Developing agent-based modeling and risk mapping to understand the impacts of climate change and rapid land-use modifications on vector distribution and pathogen emergence and (iii) Pathogen Discovery: Collaborating on NGS and multiplex chip technologies to identify viruses in various biological models, including sand flies and bat ectoparasites.

A core pillar of our sustainability model is the mentorship of the next generation of scientists, through joint programs with French universities. Since 2020, we have conducted 35 training sessions for national partners, including the Ministry of Health and local universities to decentralize expertise and build long-term research autonomy in Cambodia.

We also implement a One Health approach that links entomological research directly to public health responses. This includes supporting national authorities with expertise on emerging vectors and publishing national recommendations based on shared field data.

Our recent unit illustrates that sustainable cooperation is achieved through bilateral knowledge sharing and the integration of research with capacity building. By combining European infrastructure with deep local field expertise, we create a resilient framework for understanding and mitigating the threats posed by environmental change and vector-borne diseases in the tropics.

#12423

INSECTS & SOCIETY: Global Entomology: Strengthening N-S Cooperation

01/07/2026 at 11:30, Montlouis

Insects for Peace as a living laboratory for North–South cooperation in applied entomology

Karol BARRAGÁN-FONSECA (Universidad Nacional de Colombia, Kbbarraganf@unal.edu.co)

Natalia NARANJO-GUEVARA, María LLINÁS-SOTO, Duverney CHAVERRA-RODRIGUEZ, Marcel DICKE

Abstract

Insects for Peace is a Colombian applied entomology initiative focused on implementing insect-based circular production systems with rural communities, peace signatories and Indigenous groups to support food sovereignty, reduce reliance on external agricultural inputs and promote local bioeconomies. These activities are carried out through long-term North–South partnerships involving European universities, research centres and private-sector actors. Within this cooperation framework, Insects for Peace operates as a field-based research and training platform in which production systems are designed, tested and adapted through continuous interaction between communities, Colombian researchers and European partners. The initiative also serves as a case study for the International Office for Sustainability in Bogotá, where social, environmental and economic dimensions are analysed using shared evaluation approaches. Joint activities include workshops, protocol development, and monitoring visits. By linking tropical field sites with collaborative learning processes and sustained institutional engagement across regions, the initiative illustrates how cooperation between temperate and tropical countries can contribute to applied entomology, local innovation and long-term scientific partnerships. The presentation will discuss practical lessons related to governance arrangements, knowledge exchange and partnership development.

Local-international collaborations to discover Neotropical species interactions and hidden biodiversity declines.

Lee DYER (University of Nevada Reno, Ldyer@unr.edu)

Humberto GARCIA LOPEZ, Lora RICHARDS

Abstract

Undiscovered insect diversity is a classic feature of tropical forests, and even for described species, basic life history traits, such as trophic relationships, remain poorly documented for most insects. This problem is exacerbated by clear declines in caterpillar and tritrophic interaction diversity with negative consequences for ecosystem functioning, and specifics of these declines are difficult to estimate. Rather than relying on traditional approaches to close knowledge gaps, a more sustainable approach is to continue or initiate fully collaborative North–South partnerships that integrate local expertise and tradition with research and community engagement. Over the past three decades, we have worked towards developing sustainable collaborative research programs in the Neotropics between universities and local communities. These partnerships combine long-term standardized sampling of plants, caterpillars, and parasitoids with regional courses, museum development, and community-led outreach. In these projects, local participants are involved in all aspects of the research and have contributed to substantial species discovery and estimates of insect declines. This approach has generated unique long-term datasets on species interactions while strengthening local research infrastructure, encouraging multilingual and intercultural scientific communication, and supporting community autonomy in biodiversity discovery and protection.

Improving organic waste treatments through insect bioconversion: lessons from Indonesia

Pierre-Olivier MAQUART (Institut de Recherche pour le Développement - UMR 247, Pierre-olivier.maquart@ird.fr)

Intan PURBA, Chloé GENEVAY, Jonathan FILÉE, Agus D. PERMANA

Abstract

Organic waste management remains a major challenge in many countries of the Global South, where rapid urban growth often exceeds waste treatment infrastructure capacity. In Indonesia, organic waste constitutes a substantial share of municipal refuse, generating environmental pollution, public health concerns and significant greenhouse gas emissions.

The larvae of *Hermetia illucens*, the Black Soldier Fly, offer an innovative and low-cost solution by converting organic waste into valuable products: insect protein for animal feed and organic residues for soil amendment. Their deployment is increasingly considered a promising tool for circular economy development under tropical conditions.

This presentation draws on field observations conducted in Black Soldier Fly production units established across Java, representing a diversity of local organizational models involving municipalities, private actors and local communities. Beyond technical production, the originality of this emerging network lies in the fact that insect-based bioconversion is integrated into decentralized waste treatment pathways while remaining economically self-sustaining and generating significant local employment.

This raises important questions regarding scalability, local appropriation, governance and transferability to other tropical contexts. The Indonesian case also highlights the importance of international scientific cooperation in documenting, evaluating and strengthening such systems, while facilitating technology transfer to other countries. It provides an example of how North-South collaboration can contribute both to scientific knowledge production and to the identification of sustainable solutions adapted to local environmental challenges.

Taxonomy and Systematics. The lessons from the Global South.

Philippe LE GALL (UMR EGCE IRD CNRS Paris Saclay, Philippe.le-gall@ird.fr)

Germain MBOCK, LOUIS ROGER KAMGANG

Abstract

While tropical environments are the largest reservoir of biodiversity, they are also the least known in terms of description and functionality. Taxonomic expertise is essential to enable the monitoring of ecosystems and biodiversity, to support for governments in the management of the Nagoya Protocol and its corollaries and for the development of the use of biodiversity, like wood, edible insects and natural substances fields where there is a considerable need for traceability. We are facing a glaring lack of local expertise in relation to these issues plus the strong inequality in access to reference collections (with the exception of Botany). We are illustrating here some of the responses proposed on the African continent by our team at IRD. They are mainly based on the deployment of Field schools, developed yearly in Central Africa, Gabon and Cameroon, from 2011. This approach consists in training graduate, Master's and doctoral students in insect collection, taxonomy, ecological monitoring, and socio-cultural studies, including entomophagy. It open new perspectives for these students and new opportunities through the contact in the field with experimented searchers. The Ecotrop set-up has trained more than 300 students and has enabled some of them to produce a thesis and build a successful career.

Hidden diversity on urban carcasses - the role of microhabitats in insect succession

Danuta KADŁUB (University of the National Education Commission, Krakow, Kadlub.danuta@doktorant.uken.krakow.pl)

Andrzej GÓRZ

Abstract

Urban areas are increasingly recognised as important reservoirs of biodiversity, shaped by strong environmental gradients and fine-scale habitat heterogeneity. Within cities, differences in vegetation structure, exposure and substrate create a mosaic of microhabitats that can strongly influence ecological processes. One such process is the decomposition of animal remains, which provides a short-lived but resource-rich habitat colonised by diverse assemblages of necrophilous insects. Despite their ecological importance, the role of urban microhabitats in shaping necrophilous insect communities remains poorly understood.

In this study, we examine how microhabitat structure influences insect communities colonising animal remains in the city of Kraków, comparing sites located in the city centre and closer to its periphery. Three distinct urban microhabitats were studied: (1) an enclosed ruderal habitat; (2) a more wooded area with partial shading; and (3) an open grassland habitat.

In each microhabitat, carcasses of domestic pigs (*Sus scrofa domestica*) were placed during spring, summer and autumn, and insect communities were monitored through daily manual sampling and pitfall trapping. In total, more than 200 beetle species representing 26 families were identified. Seasonal variation played a significant role, with the highest diversity and evenness observed in summer, while autumn communities showed lower activity and were dominated by a few species. In spring, insect communities were markedly less diverse and showed little differentiation among microhabitats.

Our findings suggest that microhabitat structure, rather than the general site location (city centre versus urban periphery), has a strong influence on the composition and diversity of necrophilous insect communities. This highlights the importance of accounting for microhabitat-level variation when studying insect succession in urban environments. The results also underline how environmental conditions, such as temperature and moisture, shape the species that colonise animal remains at different times of the year.

The compound method for estimating post-mortem interval based on insect evidence

Szymon MATUSZEWSKI (Adam Mickiewicz University, Szymmat@amu.edu.pl)

Abstract

The most frequent use of insects in legal contexts is to estimate the post-mortem interval (PMI). Forensic entomologists usually base their estimates on the age of the oldest life stages of blow flies or other insect species that colonize cadavers shortly after death (i.e. early colonizers). This approach can yield an accurate approximation of PMI, especially when there was no delay in cadaver colonization. However, it omits the time preceding colonization of the cadaver (i.e. the pre-appearance interval, PAI), and therefore the estimated interval is usually reported in such cases as the minimum PMI. This bias is inherent in this approach. Unfortunately, it has serious implications for the applicability of the approach and the practical utility of the resulting conclusions.

First, the importance of PAI increases for middle colonizers and increases dramatically for late colonizers. Therefore, its omission renders the use of such insect evidence pointless, as the resulting error may simply be larger than the minimum PMI estimated from insect age. Second, PAI can be long even for early colonizers. Blow flies in Central Europe colonize cadavers in spring frequently with a delay of at least several days. Furthermore, there are barriers to colonization that cause significant delays in every season. Consequently, even for early colonizers PAI may be longer than the estimated age of insect evidence.

Accordingly, the systematic omission of PAI during entomological estimations of PMI significantly compromises the accuracy of resulting estimates. Therefore, a method was proposed that combines estimates of insect age with PAI (i.e. the compound method). In my talk, I will discuss the structure of the method and focus on PAI, detailing how it can be estimated in various scenarios. The talk will be illustrated with case reports, showing the benefits of the method and discussing the prospects for its more often use.

Beyond Murder: Why Every Entomological Case Matters

Lena LUTZ (Institute of Legal Medicine, University Hospital, Goethe-University Frankfurt am Main, Lutz@med.uni-frankfurt.de)

Jens AMENDT

Abstract

Forensic entomology is a subdiscipline of forensic science in which insect evidence is analyzed to support legal investigations. Traditionally, the age determination of necrophagous insects developing on a corpse combined with the analysis of species composition and succession dynamics is used to estimate the minimum post-mortem interval (PMI_{min}), defined as the time between first insect colonization and the discovery of the body. Beyond PMI_{min} estimation in homicide investigations, insect evidence can contribute to a wide range of forensic questions, including proof of body relocation, support in the investigation of sexual crimes, the recovery and genotyping of human DNA from insects, and the detection of neglect, such as insect infestation prior to death. While these applications are well established and highly relevant, the potential of forensic entomology extends far further. This presentation argues that forensic entomology can serve as a bridge between forensic science and adjacent fields such as sociology, ethics, and urban research. We highlight the value of routine case analysis, including forensically non-critical cases, that do not require a formal expert opinion. The structured processing and scientific evaluation of such cases can generate an important database to strengthen the professional interpretation and assessment of entomological evidence in medicolegal investigations. Furthermore, this approach opens new research avenues, including the study of e.g. biological and social indicators of unnoticed deaths in urban environments and legal aspects of criminal responsibility in cases of third-party neglect, while fostering interdisciplinary collaboration.

Can microclimate and insect thermal limit data improve species distribution models?

Candice OWEN (Chester Invertebrate Research Group, University of Chester, C.owen@chester.ac.uk)

Clarke VAN STEENDEREN, Guy SUTTON

Abstract

Species distribution models for invasive and other species typically utilise data obtained at a broad-scale, such as global climate variables from the WorldClim database. Only a few investigations have included finer-resolution data, such as that provided by microclimates across a landscape or the thermal limits of the species in question. This study used the invasive Argentine ant, *Linepithema humile* (Hymenoptera: Formicidae), to illustrate how microclimate data can be tailored to the focal taxon's recorded Critical Thermal Minima (CTmin) value, and incorporated as a predictor variable in MaxEnt modelling. We compared model performance and suitable area predictions in scenarios with and without microclimate data thresholded by thermal limits as a predictor variable. Models were then independently validated on the known invaded range of *L. humile*. The results suggested that although model performance was comparable across many of the different scenarios, estimates of suitable area in some invaded regions varied depending on the model design. These findings offer valuable insights into the possible over- and underestimation of climatically-suitable areas for invasive or other species using finer-scale data in MaxEnt models, which has consequences for model use to inform conservation and invasive species monitoring programmes.

Occurrence and forensic relevance of *Chrysomya albiceps* (Insecta: Diptera: Calliphoridae) in Poland and Germany

Patrycja ZBIERALSKA (Department of Biology, Evolution and Insect Conservation, Centre for Forensic Biology and Entomology, University of Wrocław, ul. Przybyszewskiego 65, PL-51-148 Wrocław, Poland, Patrycja.zbieralska@uwr.edu.pl)

Lena LUTZ, Katarzyna PALACZ-ZIÓŁEK, Agata THANNHÄUSER, Łukasz SZLESZKOWSKI, Jens AMENDT, Marcin KADEJ

Abstract

Chrysomya albiceps (Wiedemann, 1819), a blowfly species of forensic significance, has expanded its geographic range throughout Central Europe in recent decades. In Poland, the species was first recorded in 2008, marking the northernmost occurrence of this taxon in Europe at the time. Subsequent observations across the country, including mass occurrences of adults and larvae in Łódź during the summers of 2013 and 2014, confirmed the establishment of the species. In a forensic context, the species was confirmed in 2014 in an apartment, based on larvae collected from the body of a man in an advanced stage of putrefactive decomposition. In Germany, *C. albiceps* has been repeatedly reported since the 1990s, particularly in the southern regions, aligning with a broader pattern of expansion observed in Austria, the Czech Republic, and Slovakia. In addition to distributional records from field observations, *C. albiceps* has been increasingly detected in forensic autopsies, demonstrating its relevance in real-case investigations. The forensic importance of *C. albiceps* arises from its synanthropic behavior and unique larval ecology. This behavior can significantly alter the composition and abundance of necrophagous insect communities – for example, reducing densities of *Lucilia sericata* larvae by up to 99% – which may bias post-mortem interval (PMI) estimates. This presentation synthesizes current knowledge on the distribution, ecology, and forensic significance of *C. albiceps* and presents data based on entomological samples collected during autopsies in Poland and Germany. The findings highlight the necessity for continuous monitoring and incorporation of species-specific biological traits into forensic casework to improve the accuracy of PMI estimation under changing entomofaunal conditions. This also encourages conducting local developmental studies on this species for Central Europe.

From parasitism to keratin resource - hexapod succession on hair

Katarzyna PALACZ-ZIÓŁEK (Department of Biology, Evolution and Insect Conservation, Centre for Forensic Biology and Entomology, University of Wrocław, ul. Przybyszewskiego 65, PL-51-148 Wrocław, Poland , Katarzyna.palacz-ziolek@uwr.edu.pl)

Monika KRZYŻANOWSKA, Marcin KADEJ

Abstract

Human hair and animal fur create a unique microhabitat for insects, evolving from a living substrate to the final stages of keratin decomposition. This presentation analyzes the succession of insects: from hematophagous ectoparasites living on the hair of living humans or animals, through the colonization of keratinophagous beetles (Dermestidae) on corpses, to storage or museum pests. It compares hair degradation methods of specific organisms and points out potential gaps and opportunities for exploiting existing links between hair substrate and hexapods.

In living humans or animals, hair provides protection and a place for lice (*Pediculus humanus capitis*, *Pthirus pubis*) and fleas (*Ctenocephalides* spp.) to lay their eggs. These insects feed on blood and skin, not keratin. After the death of the host, the body becomes a niche for fly larvae, which feed on the soft tissues around the hair. Finally, the keratin substrate is preferentially colonized by Tineidae and Dermestidae larvae. However, the methods of fiber degradation vary between species.

In Tineola moths, keratin degradation is suggested to involve cysteine-metabolizing enzymes that break disulfide bonds in keratin, together with the activity of serine proteases and the intestinal microbiome. In Dermestidae it is assumed that symbiotic microorganisms in the digestive tract play a key role in keratin degradation. In lice, the ability to break down keratin is limited and probably depends on symbiotic relationships with bacteria or fungi.

The review highlights forensic and medical implications: from diagnosing neglect to estimating PMI and exposure conditions. It identifies gaps in knowledge, including insect-fungus interactions and the impact of environmental variables on keratinophagy. The results suggest the need for standards for hair sampling in entomological analyses, but also highlight the broader importance of protecting museum artifacts and storage facilities.

Assessment of the effect of height on the distribution of Diptera of forensic interest in an urban context

Asia Beatrice LANCELLOTTI (University of Genoa, Lancellottiasiabeatrice@gmail.com)

Sofia ROTTA, Giuseppina CARTA, Stefano VANIN

Abstract

Forensic entomology studies insects and other arthropods involved in decomposition, primarily to estimate the minimum post-mortem interval (minPMI) and eventual transfer of the cadaver. Although this discipline is widely accepted in forensic investigations, there are still numerous under-researched factors that can influence insect colonization and the accuracy of estimates. One such factor is the height at which a body is located relative to the ground level, despite some observations from legal cases suggesting that it may affect the composition and arrival of necrophagous entomofauna.

This study evaluates the effect of height on colonization by analyzing the composition of entomological communities at different heights along a building in an urban environment. Conducted in Genoa since March 2024, the investigation includes bi-weekly sampling sessions using baited traps placed at three levels of the same building. Environmental temperature was also recorded to evaluate its potential influence.

Between March 2024 and November 2025, 16,986 adult specimens were collected, the majority being dipterans (16,260), followed by hymenopterans (595), mites (101), beetles (23), and spiders (7). Statistical analysis revealed a significant decrease of insects as height increased. The temperatures recorded at the collection sites, on the other hand, did not show significant differences, excluding a direct influence on the variation in colonization.

The analysis of dipterans revealed a strong predominance at ground level, but with a differential distribution of families at higher levels. For example, Sarcophagidae showed a greater capacity for colonization at higher floors.

Furthermore, two alien species - *Synthesiomyia nudiseta* Van der Wulp, 1883 and *Chrysomya megacephala* (Fabricius, 1794) - were detected during the study.

These results suggest that cadavers found at higher floors undergo slower and reduced colonization, thus affecting decomposition and entomological succession. The forensic implications of this research are significant, as reduced entomological activity may alter the estimation of minPMI.

#10824

PHYSIOLOGY & BIOCHEMISTRY: Endocrinology and hormonal regulation in insects

01/07/2026 at 14:00, Villandry

Insect insulins: similar, yet different

Jose L. MAESTRO (Institute of Evolutionary Biology (CSIC-UPF), Joseluis.maestro@ibe.upf-csic.es)

Abstract

The insulin/insulin-like growth factor signalling (IIS) pathway, present in all metazoans and remarkably conserved throughout evolution, regulates key biological processes such as cell growth and proliferation, circulating sugar levels, longevity, stress resistance, or, for example, insect caste determination. The pathway is activated when its ligands, mainly called insulin-like peptides (ILP) in insects, bind to the insulin receptor (InR), a tyrosine kinase membrane receptor.

Whereas in vertebrates, particularly in mammals, insulin and insulin-like growth factors (IGFs) each bind to their own receptors, although some cross-reactivity can occur, insects typically possess one or a few receptors but exhibit a great diversity in the number of ligands, with some species having more than 30 genes coding for ILPs. So, how is the activity of such a crucial pathway regulated? The answer most likely lies less in differences in receptor-binding affinity and more in the spatial and temporal pattern of ligand expression, and in their distinct modes of action: endocrine or paracrine.

In this talk we will review the roles of the IIS pathway in insects, with particular emphasis on its involvement in the regulation of growth, molting, reproduction or the regulation of other hormones, paying special attention to the results obtained in the cockroach *Blattella germanica*.

Microscopical Characterization of the Corpus Allatum in Mosquitoes: Insights into Juvenile Hormone Feedback and Gland Complex Organization

Fernando Gabriel NORIEGA (University of South Bohemia, Czech Republic, Noriegaf@fiu.edu)

Abstract

In the larvae of the mosquito *Aedes aegypti*, the three most important endocrine glands, the corpora allata (CA), the corpora cardiaca (CC), and the prothoracic gland (PG), together form the glandular complexes (GC). Using confocal laser scanning microscopy in combination with immunohistochemistry, in situ hybridization, ultrastructural expansion microscopy, and apoptosis studies, we were able to identify the different cell types of the GC and follow their fate during metamorphosis.

The regulation of CA activity is very complex, as the CA integrates multiple stimulatory and inhibitory signals to determine the final juvenile hormone (JH) synthesis rate. Using a CRISPR/Cas9 approach, we generated mosquitoes with weak JH signaling that triggered CA hypertrophy and hyperplasia phenotypes. Our hypothesis is that a compensatory feedback loop maintains JH homeostasis, and therefore reduced JH signaling results in CA hypertrophy and hyperplasia in mosquitoes.

These studies provide the foundation for a more detailed understanding of the structure and changes in a major endocrine organ of mosquitoes, which are vectors of several important infectious diseases.

The clock-related neuropeptide Pigment Dispersing Factor is essential for the photoperiodic reproductive switch of the pea aphid

Francesca Sara COLIZZI (IGEPP - INRAE (Le Rheu), Francesca-sara.colizzi@inrae.fr)

Gaël LE TRIONNAIRE, Romuald CLOTEAU, Nathalie PRUNIER-LETERME, Sylvie HUDARVEDIAN

Abstract

The pea aphid, *Acyrtosiphon pisum*, is a paradigmatic photoperiodic species with a life cycle closely linked to seasonal changes in day length. The neuropeptide pigment-dispersing factor (PDF) is known to regulate circadian and seasonal responses in other insect species, but its presence in *A. pisum* had not been confirmed until our recent study. Indeed, we identified a PDF-coding gene and developed a specific antibody that stained four neurons in each brain hemisphere, co-expressing the circadian core-clock protein Period. These neurons exhibit daily and seasonal plasticity, similar to that observed in *Drosophila* PDF neurons, and their terminals overlap with insulin-like peptide (ILP)-positive neurosecretory cells and Cryptochrome (CRY)-positive clock neurons. Given ILP's suggested role in seasonal adaptations and CRY's potential function as a circadian photoreceptor for day-length measurement, our findings suggest PDF plays a key role in regulating aphid seasonal timing.

To test this hypothesis, we generated pdf knockout mutants via the CRISPR/Cas9 system and found that, while these mutants were viable and showed no defects under long-day conditions, they completely lost the ability to produce sexual females under short-day photoperiods. This demonstrates that PDF is essential for the short-day-induced production of sexual females. In contrast, male production was unaffected, indicating that male and female sexual morph production relies on distinct photoperiodic pathways, with PDF being specifically required for female sexual differentiation.

This study is crucial for two reasons. First, it provides the first evidence that PDF is a core component of the aphid photoperiodic system and a critical regulator of seasonal female sexual differentiation. Second, it establishes a CRISPR/Cas9-based functional genetics approach in *A. pisum*, paving the way for mutants in insulin-like peptides and other candidate genes to further elucidate the photoperiodic pathway.

Revisiting the dogma about the anti-metamorphic role of juvenile hormone

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Abstract

Sir Vincent B. Wigglesworth described juvenile hormone (JH) as an "inhibitory hormone" that prevents insect metamorphosis. Using CRISPR-Cas9, we generated *Aedes aegypti* mutants that lack the key enzyme for JH biosynthesis, juvenile hormone acid methyl transferase (*jhamt*). These mutants are deficient in JH signalling. Homozygous *jhamt*^{-/-} mosquito larvae hatched normally, but were smaller than WT larvae and developed slightly slower. After reaching the L4 stage, all homozygous *jhamt*^{-/-} larvae died 6-7 hours before pupation, suggesting that JH is essential for the transition from larva to pupa but dispensable for earlier larval stages. To test this crucial role of JH, we applied the JH mimic methoprene at different times and concentrations during larval development. Concentrations of 0.01 to 1 ppb applied at certain larval stages were sufficient to allow normal pupation and emergence of the adults. In addition, we observed that the titers of ecdysteroids in the last larval stage (L4) were significantly lower in *jhamt*^{-/-} mutants. Our results suggest that the transition to pupa in mosquitoes is controlled by a delicate relationship between JH and ecdysteroids signalling, with JH being absolutely necessary for normal metamorphosis.

The role of juvenile hormone in innate immunity

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Abstract

Drosophila melanogaster is an establish model for studying of innate immunity and its relationships to development and physiology. However, the mechanism responsible for energy allocation between these processes is not fully understood. Our data point to involvement of juvenile hormone (JH). JH is considered to be pro-development in a growing larva, ensuring the animal reaches body mass sufficient for metamorphosis. In adult females, JH is known to be pro-reproductive and immunosuppressive. Adversely, immunity requires a lot of energy, competing for resources with development. This prompted us to anticipate a detrimental effect on immune competence if JH signaling were to be heightened in immune cells. Contrary to our expectations overexpression of JH receptor in immune cells led to their excessive proliferation and differentiation into lamellocytes, activated immune cells typically observed only in larvae infected by a parasitoid wasps or other pathogens. As a result, the larvae were pre-conditioned for the wasp infection and became super resistant to it. However, JH signaling does not simply promote immunity. RNAi of JH receptor also induced increased resistance to wasp infection although not cell differentiation. Additionally, activation of sessile immune cells that is normally mediated by Ecdysone during pre-pupal stage was impaired by the receptor overexpression. We propose that JH is a program setting signal that instructs the immune cells on how to act and what stage of life they are in. For proper function an optimal level of JH is necessary.

Dissecting global neuropeptide precursor processing phenotypes in *Tribolium castaneum* using CRISPR-imaging lines and neuron-specific gene knockout

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Vera TERBLANCHE

Abstract

Neuropeptides are small proteinaceous molecules that play important roles in various physiological processes and daily behaviours in multicellular organisms. The maturation of most insect neuropeptide precursors requires precise cleavage mediated by two conserved prohormone convertases (PCs). Recent work in *Tribolium castaneum* showed that *PC1/3* (absent in dipteran genomes) and *PC2* (*Drosophila*: *amontillado*) play non-redundant roles in larval growth and survival. Further elucidating the role of PCs, we found that only *PC1/3* knockdown led to an abnormal shift from lipid storage to an increase in circulating sugars and glycogen reserve. To analyse through which cells and organs both proteases exert their functions, we used CRISPR-Cas9-mediated homology-directed repair (HDR) to establish imaging lines for both proteases. Based on these reporter lines and staining with PC2 antibody, PC1/3 and PC2 were confirmed to be co-expressed in pairs of neurons in the tritocerebrum and most intestinal endocrine cells. PC1/3 was specifically expressed in clusters of secretory neurons in suboesophageal ganglion (SOG). We screened for neuropeptides that produce a similar phenotype as PC1/3 and may be processed by this enzyme. Then, we found that *Allatostatin-B* (*Mip*), *periviscerokinin* (*PVK*), and *Allatostatin-C* (*AstC*) were also involved in regulating larval growth and feeding. However, only *capa-PVK* knockout showed similar effects on metabolite levels as *PC1/3*-deficient larvae. To solve the puzzle of cell-specific function and neuropeptide targets of PC1/3, we worked towards establishing a binary CRISPR-based neuron-specific knockout system, which has not previously established outside dipterans. We have already been successful in expressing transgenic Cas9 in SOG and the lines will be ready for phenotypic analysis soon. These findings will advance the understanding of cell-specific functions of this prohormone convertase and on possible differences in neuropeptide processing between beetles and dipterans.

Octopaminergic and Tyraminergetic Control of *Ixodes ricinus* Salivary Glands

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Abstract

Octopamine, the invertebrate functional analog of vertebrate adrenaline, and its biosynthetic precursor tyramine are key regulators of physiological processes in arthropods. In ticks, catecholaminergic and cholinergic agonists are commonly used to induce salivation; however, the contribution of octopaminergic and tyraminergetic signaling remains poorly defined. We investigated the effects of octopamine and tyramine on salivary secretion in partially fed female *Ixodes ricinus*. In vivo injection of both amines induced salivation, but with significantly lower secretion rates and volumes compared to classical catecholaminergic and cholinergic stimulants. Genome mining of *Ixodes ricinus* identified two adrenergic-like octopamine receptors (Oct α 2R, Oct β R) and two tyramine receptors (TyrR1, TyrR2). All four receptors were chemically synthesized, heterologously expressed, and pharmacologically characterized, revealing distinct ligand sensitivities and signaling properties. To determine their anatomical distribution, we generated specific antibodies and examined all these receptor localizations in the synganglion and salivary glands. Immunohistochemical analyses revealed Oct β R-positive axonal projections in type II and III acini terminating on the single octopamine-positive myoepithelial cell of each acinus. In contrast, Oct α 2R and TyrR1 appeared non-axonal and were directly expressed by salivary gland epithelial cells. Together, these results provide new insights into octopaminergic and tyraminergetic control of tick salivary gland function and contribute to a mechanistic framework for neurotransmitter-mediated regulation of complex salivary secretion.

Outsmarting wireworms: combining semiochemicals and entomopathogens for sustainable pest management

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Fanny RUHLAND

Abstract

Wireworms (Coleoptera: Elateridae) are polyphagous soil-dwelling pests causing significant crop losses worldwide. The recent ban on neonicotinoids in Europe has created an urgent need for sustainable control alternatives. Here, we present an integrated research program addressing wireworm management through chemical ecology and biological control.

Our investigations into wireworm host-finding behaviour revealed that larvae use root-emitted volatile organic compounds (VOCs) to locate host plants. In barley, we identified a blend of aldehydes that attracts *Agriotes sordidus*. Similarly, maize varieties with contrasted field susceptibility showed differential VOC profiles, with less susceptible varieties releasing more diverse blends. In potato, laboratory bioassays confirmed that wireworm feeding activity correlates with variety susceptibility, affecting both larval development and weight gain.

Building on these findings, we developed an attract-and-kill strategy combining plant semiochemicals with entomopathogenic fungi.

We screened 11 entomopathogenic fungal (EPF) strains and identified two highly virulent candidates that significantly reduced larval survival in contact-based assays.

A biodegradable formulation combining wireworms' attractants with EPF successfully attracted wireworms and achieved up to 74% mortality under laboratory conditions. Applied in sugar beet fields, the formulation led to increased leaf dry mass.

We also evaluated the efficacy of entomopathogenic nematodes (EPN) to control wireworms, with the aim to include them in the attract-and-kill formulation. A comparative study of 16 EPN populations revealed that nematode morphometry, particularly leaner infective juveniles, influences virulence against wireworms. We also characterized the volatile signatures of EPN-infected insect cadavers, identifying specific VOCs that attracted *Agriotes* larvae, opening new perspectives for biological control applications.

While individually insufficient, these methods appear complementary and compatible, emphasizing the need for integrated pest management strategies combining multiple approaches to maintain crop yields while preserving biodiversity.

Drift Exposure in Flower Strips: Functional Responses of Arthropods and Implications for Ecosystem Services

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Abstract

Drift deposition of plant protection products from treated crops can temporarily suppress beneficial arthropods and the services they provide. Flower strips are widely implemented to enhance biological control, pollination, and soil-related functions, yet their position along field edges exposes arthropods to spray drift. How drift affects functional groups, and whether flower strip design mitigates these impacts, remains insufficiently quantified under realistic conditions.

We combined measured drift deposition with controlled exposure experiments to assess how realistic drift levels of the broad-spectrum insecticide acetamiprid affect arthropod functional groups in 6-m-wide flower strips. Drift deposition was first quantified using tracer applications, showing up to 28% of the field rate in the first metre and a rapid decline thereafter (2022). These values were used to simulate high (28%), medium (1.2%), and low (0.4%) drift-rate exposures in a two-year field experiment, together with positive (full-rate) and negative (water) controls. Parasitoids, predators, pollinators, detritivores, and herbivores were monitored using pan and sticky traps installed during acetamiprid application, as well as suction sampling and pitfall traps throughout the season from June to August (2023-2024).

Short-term knockdown effects were concentrated in the first metre and were evident in parasitoids, detritivores and herbivores, while predators and pollinators appeared to be unaffected. Across the 6-m strips, no functional group exhibited persistent seasonal reductions at drift-rate exposure, in contrast to full-rate applications, which caused strong and lasting declines in multiple beneficial guilds.

These results demonstrate that realistic drift exposure can temporarily reduce activity of beneficial taxa near the crop edge but does not compromise the seasonal integrity of functional groups across wider flower strips. By linking drift deposition, functional responses, and habitat design, this work provides empirical support for using flower strips to sustain ecosystem services in agricultural landscapes and identifies the first metre as a priority zone for drift-reduction measures.

Enhancing semi-natural grassland quality promotes invertebrate community diversity and composition

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Abstract

European semi-natural grasslands are under increasing pressure from agricultural intensification, creating a need for conservation strategies that enhance habitat quality and support invertebrate communities which underpin key ecological functions. In Ireland, management interventions such as delayed mowing and the establishment of early and late cover (ELC) have been implemented through an agri-environmental scheme (AES) to conserve Corncrake on semi-natural grasslands. We aimed to test the ecological contribution of enhancing semi-natural grassland quality through this AES on invertebrate community diversity and composition.

We adopted a field based, multi-scale approach to investigate how local habitat management and grassland quality shape the abundance, diversity, and composition of invertebrate communities, with a particular emphasis on carabid assemblages. First, we compared early and late cover (tall patches of vegetation that provide Corncrake with cover when grazed or cut vegetation in grasslands is too short) with adjacent grasslands to investigate the contributions of this cover to invertebrate abundance and diversity. Second, we sampled invertebrate orders and carabid species across semi-natural grasslands spanning a gradient of habitat quality assessed using a results-based scorecard, and related community responses to sward and soil characteristics.

ELC habitats supported significantly higher abundance of ground-dwelling invertebrates, particularly during the early and later stages of the sampling season when surrounding grassland vegetation was short. At the grassland-quality scale, invertebrate orders primarily responded to sward structure and soil moisture, whereas carabid abundance, richness, and community composition increased with higher grassland quality characterised by structurally open and heterogeneous swards. Carabid assemblages showed moderate concordance with broader invertebrate communities and provided distinct indicator species for high-quality grasslands, highlighting their potential as complementary indicator species alongside plant-based metrics.

Our findings demonstrate that results-based management and targeted habitat creation can promote structural conditions that enhance invertebrate communities and support functionally important carabid assemblages on semi-natural grasslands.

Disrupting insect pests through crop diversification: An oilseed rape -faba beans case study

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Abstract

Crop diversification at the plot level, through intercropping or companion planting, involves growing two or more plant species in proximity and is increasingly adopted as a sustainable agronomic practice. Beyond optimizing land use and soil fertility, it can reduce insect pest impact. Such protection may arise directly, via visual, physical, or chemical disruption, or indirectly, through host plant modifications induced by the companion plant. Oilseed rape (OSR, *Brassica napus*), a major crop in Europe, is highly susceptible to a complex of insect pests. Studying the OSR–faba bean (FB, *Vicia faba*) companion planting system offers insights into how crop diversification reduces pest pressure and the ecological mechanisms involved.

Two complementary field trials were conducted under open-field conditions with natural insect immigration. The first trial, carried out over two consecutive years, aimed to evaluate the direct effects of FB companion plants on the incidence of the complex of OSR insect pests. The second trial focused on indirect effects by assessing how companion planting influences the morphology and metabolism of OSR plants, and how these changes may affect pest–host interactions with *Psylliodes chrysocephala*.

FB companion plants provided physical and/or visual disruption, leading to a reduction in pest incidence across the OSR pest complex. However, this effect did not fully account for the overall decrease in pest pressure observed. Companion planting also induced significant morphological and metabolic modifications in OSR, altering ecophysiological traits such as morphological structure and metabolite profiles (glucosinolates). These changes likely influenced insect host selection, contributing further to pest suppression.

The OSR–FB companion planting system reduces pest pressure through combined direct and indirect mechanisms, with physical and visual disruption playing a central role. These findings deepen understanding of how crop diversification disrupts insect pests and provide a framework to evaluate the mechanisms underlying pest regulation in diversified cropping systems.

First surveys on some natural antagonists of the invasive alien species *Zelus renardii* (Hemiptera: Reduviidae)

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Abstract

Zelus renardii (Hemiptera: Reduviidae) is native to America and is rapidly spreading worldwide, especially in the Mediterranean area. As a generalist predator, it feeds on phytophagous insects, but also on other predators. In fact, the literature reports that in its native area *Z. renardii* preys on *Chrysoperla* spp., a group of natural predators used in biocontrol, leading to the release of aphid populations from regulation. Considering the potential impact of *Z. renardii* on ecosystem services, it is essential to investigate the interaction with some of its natural antagonists, such as egg parasitoids and entomopathogenic fungi.

A three-year survey (2023–2025) on egg parasitoids (Hymenoptera) was carried out in Sardinia (Italy) where *Z. renardii* was first recorded in 2020. Field egg masses of *Z. renardii* and native *Rhynochoris* spp. (Hemiptera: Reduviidae) were collected, and viable sentinel egg masses were exposed at several sites.

Zelus renardii underwent negligible parasitism, exclusively by *Anastatus bifasciatus*: only 1/38 field-collected and 3/284 sentinel egg masses were parasitized. In contrast, egg masses of native reduviids showed high susceptibility to different parasitoid species, particularly *Hadronotus leptocorisae*. To verify field results, no-choice tests were conducted under laboratory conditions by offering *Z. renardii* and *Rhynochoris* spp. egg masses to *H. leptocorisae* and *A. bifasciatus* females. Results indicated that parasitoids largely rejected *Z. renardii* egg masses. Moreover, to assess the potential of the entomopathogenic fungus *Bauveria bassiana* as a biocontrol agent, egg masses and two nymphal stages of *Z. renardii* were exposed to different concentrations of fungal conidia. Tests showed a concentration-dependent decrease in the vitality of the assayed nymphal instars, newly emerged nymphs, and the number of hatched eggs. Our study provides a baseline on the effectiveness of some natural antagonists of *Z. renardii*, useful in case further studies will confirm its impact in newly invaded areas.

Multi-scale drivers of arthropod predator distribution and diversity for predictive biocontrol in Mediterranean citrus landscapes.

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Abstract

Arthropod predators play a central role in regulating pest populations in agricultural landscapes, yet the local and landscape-level factors influencing their effectiveness remain poorly understood. Promoting predator presence, diversity, and activity while limiting crop damage is crucial for sustainable food production. We established a landscape monitoring network across Corsican citrus orchards, spanning a wide gradient of semi-natural habitats and agricultural practices. From 2021 to 2022 and over three seasons, we recorded predator abundance at the tree scale ($n = 1000$) for four species important for current and future biological pest control: the green lacewing (*Chrysoperla carnea* spp.), the pine ladybird (*Exochomus quadripustulatus*), the mealybug destroyer (*Cryptolaemus montrouzieri*), and the harlequin ladybird (*Harmonia axyridis*). Thanks to the large size and spatial extent of the sample for this type of study, we were able to implement a multi-step statistical framework designed to examine the main ecological drivers of predator distribution across multiple spatial and temporal scales, and the interacting effects of farming and landscape on predator diversity and pest infestation severity. Overall, predator abundance was about twice as high in organic orchards (mean $\pm$ SE: 19 ± 3) compared to conventional orchards (10 ± 2). Clear species-specific temporal and farming type trends were also observed. At the field scale, predator diversity was influenced by interactions between farming type and landscape context, with conventional orchards embedded in landscapes of low semi-natural habitat continuity exhibiting lower diversity values. This research enhances our understanding of predator ecology and contribute to a broader surveillance program characterizing arthropod communities and trophic interactions for predictive biocontrol in the Corsican agricultural landscape.

Entomopathogenic Nematodes: An effective treatment for sustainable whitefly control in mulberry (*Morus alba* L.) cultivation.

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Abstract

Whiteflies are economically important pests that infest a wide range of plants, with mulberry (*Morus alba* L.) being among their preferred hosts. However, when mulberry leaves are infested by whiteflies, they become unsuitable for both silkworm (*Bombyx mori* L., Lepidoptera: Bombycidae) rearing and ornamental use. In the present study, we evaluated the efficacy of two entomopathogenic nematodes (EPNs), *Steinernema carpocapsae* (Weiser, 1955) (Rhabditida: Steinernematidae) and *Steinernema feltiae* (Rhabditida: Steinernematidae), as potential biological control agents against mulberry whiteflies.

Laboratory bioassays were conducted using *S. carpocapsae* and *S. feltiae* applied at three concentration rates each using a handheld sprayer on infested mulberry leaves. A biological insecticide containing spinosad served as a positive control, while water-sprayed leaves served as the untreated control.

Post-treatment, dead nymphs were counted daily for 5 days, and total mortality was calculated. Both EPNs and spinosad significantly increased whitefly mortality within 24 hours of application. Over the 5-day trial, higher EPN concentrations achieved more than 60% nymphal mortality compared with the untreated control.

These findings provide the first known evidence of the potential of *S. carpocapsae* and *S. feltiae* as effective biological control agents against mulberry whiteflies, highlighting their role in promoting sustainable pest management alternatives to conventional pesticides that may harm non-target organisms.

Evidence based plant protection: prospects of the future farm advisory

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Abstract

Modern agricultural practices strongly demand a shift toward precision agriculture; however, the working frame is constantly altered due to the changing environmental conditions, the rise or invasion of novel pests, and the ban of a wide range of chemical insecticides. The rational use of pest control means based on scientific evidence utilizing to both product efficacy levels and pest pressure estimations has proven the past years that a) it is feasible and b) it has a positive impact with regard to estimated damage levels and reliance to chemical insecticides. The particular approach has been implemented in two major cropping systems: for the control of olive fruit fly *Bactrocera oleae* in the Region of Crete and the control of tomato borer *Phthorimaea absoluta* in greenhouse tomato. Two distinct cropping systems with different issues in implementation of the 'Evidence based Plant Protection' scheme. In this presentation, the progress achieved and the problems resolved over the past 5 years will be presented, in addition with an insight of the potential positive impact on crop production and sustainability if an area wide adoption of the proposed approach is achieved. Evidence based Plant Protection schemes applied on olive crops were supported by the Region of Crete and the Ministry of Agriculture while schemes applied on greenhouse tomato were supported by research projects 'ZeroTuta' (M16ΣΥΝ2-00271, M16) και 'Innovative Plant Protection and Environment' (TAEDER-053567).

RNA interference as a new tool for Integrated Pest Management: developing protocols for the evaluation of non-target effects on beneficial species

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Abstract

RNA interference (RNAi)-based biocontrol products represent promising, selective alternatives to conventional pesticides. However, their classification as Plant Protection Products (PPPs) in the EU subjects them to risk assessment frameworks that do not fully account for their unique mode of action as well as for their biological and environmental properties. Given EFSA's favourable view on the potential of these technologies for sustainable pest management, there is a clear need for dedicated workflows and protocols to evaluate possible off-target effects on beneficial arthropods inhabiting the same ecological compartments.

In this study, we developed protocols for testing double-stranded RNAs (dsRNAs) with insecticidal activity against the target pests *Popillia japonica* (Japanese beetle), *Halyomorpha halys* (brown marmorated stink bug), and *Scaphoideus titanus* (leafhopper vector of *flavescence dorée* phytoplasmas) and on a set of non-target organisms relevant for existing IPM programs against these pests. Our aim was to assess the compatibility of the use of RNAi-based products with current biocontrol strategies and to evaluate their potential for synergistic integration. Moreover, to preserve key ecosystem service providers, all dsRNA products were also tested on *Apis mellifera* as a representative pollinator species and emblematic off-target organism in PPP application scenarios.

Each beneficial species was exposed both to the pest-specific dsRNA targeting the gene sequence of the co-occurring pest, and to a dsRNA designed on its own homologous gene. Species-specific exposure protocols were developed and optimised according to each organism's ecological characteristics, while ensuring feasibility under laboratory conditions. We assessed survival rates and analysed gene-expression patterns across treatments to evaluate how each dsRNA affected the tested beneficial species.

These results deliver unprecedented evidence on RNAi responsiveness in different biocontrol agents and offer critical data for refining off-target risk assessment procedures. By generating specific, ecologically relevant insights, this study contributes to the development of regulatory workflows tailored to dsRNA-based technologies.

AgriPV Systems as Drivers of Insect-Mediated Ecosystem Services in European Agriculture

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Abstract

Agricultural intensification has simplified landscapes and reduced habitat heterogeneity, negatively affecting beneficial insects that provide key ecosystem services such as pollination and pest suppression. Agricultural Photovoltaics (AgriPV), integrating solar energy production with crop cultivation, was investigated as a novel approach to restore biodiversity within intensively managed systems. This study assessed how AgriPV infrastructure combined with perennial flower strips influenced insect communities and their associated ecosystem services.

The research was carried out at Aarhus University's AgriPV test facility in Denmark, comprising a 1 MW installation over 2 ha with north-south oriented, single-axis tracking panels. Beneath the panels, 1 m-wide biodiversity strips were established using locally sourced wildflower seed mixes adapted to shade gradients. Ten crop species were cultivated between panel rows, with seven selected for insect monitoring (bread wheat, malting barley, winter oilseed rape, faba bean, potato, barley/pea mix, and buckwheat).

Flower-visiting insects (bees, hoverflies, butterflies) were surveyed through timed transect walks, complemented by pitfall trapping of ground-dwelling arthropods across three habitat types: (1) flower strips under panels, (2) adjacent crop rows, and (3) reference fields without panels or strips. Sampling was conducted monthly from April to August 2025. Collected specimens were preserved for taxonomic identification, and data analysis is currently underway to evaluate insect abundance, diversity, and functional roles in relation to habitat configuration and crop phenology.

Preliminary observations suggest that AgriPV systems created microhabitats and resource continuity, potentially enhancing beneficial insect activity and supporting pollination and natural pest control. The study aims to identify plant species most effective for supporting pollinators and predators under partial shade and assess overwintering potential within biodiversity strips. These findings will inform the design of multifunctional agricultural landscapes that optimize renewable energy production and biodiversity-based ecosystem services, contributing to EU sustainability goals.

Little known pest, *Euproctis lunata* (Erebidae: Lepidoptera) of castor plants: Insights into its biology and entomopathogenic fungi based sustainable management

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Abstract

Castor hairy caterpillar, *Euproctis lunata* Walker (Erebidae: Lepidoptera), a least-known defoliating pest of castor plants (*Ricinus communis*), has recently gained attention due to considerable losses of castor plants. No comprehensive study is available on this pest in Pakistan, leaving a critical gap in understanding its biology and impact on castor crops and how to manage this pest in a sustainable way. We determined the developmental biology of *E. lunata* on castor plant and studied the management of larvae using two entomopathogenic fungi, *Metarhizium anisopliae* and *Beauveria bassiana* as potential biocontrol agents. Larvae grew through six instars, with a 21.4-day duration. The pupal stage completed in 12.4 days, and adult moths lived for 5.10 days. Pathogenicity trials showed higher virulence of *B. bassiana* against *E. lunata* larvae compared to *M. anisopliae*. At 10^9 conidia/mL concentration, *B. bassiana* caused 62.5-87.5% larval mortality up to 15 days, while *M. anisopliae* induced 47.5-80.0% mortality. Further, probit analysis confirmed *B. bassiana* as the more potent pathogenic fungi, with a lower LC_{50} value of 1.4×10^5 conidia/mL and LC_{90} of 6.1×10^9 conidia/mL. The findings provide useful information on *E. lunata* biology and demonstrate the potential of *B. bassiana* fungus for eco-friendly and sustainable management of this pest. Future studies should include extensive field surveys to map the distribution and infestation levels of this pest on castor plants and nearby cropping systems across diverse agro-ecological zones of Pakistan.

Beneficial Entomofauna in {*Opuntia ficus indica*} Cultivation

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Abstract

The use of functional biodiversity is essential for strengthening the ecological stability of agroecosystems. Beneficial entomofauna, composed of organisms that contribute to biological control, pollination, and the regulation of ecosystem processes, is a key component in traditional crops such as the prickly pear cactus (*Opuntia ficus indica*), widely cultivated in Mexico for its nutritional, cultural, and economic value. The active presence of this entomofauna reduces dependence on external inputs, improves the health of the agroecosystem, and increases its capacity to respond to disturbances. With the aim of identifying the beneficial entomofauna associated with prickly pear cultivation, the study was carried out on a prickly pear plot located in the municipality of Tlalnepantla, Morelos (latitude: 19°03'29.3" N, longitude: 98°55'32.8" W, altitude: 2070 m above sea level), during the period February-April 2025. Direct and indirect sampling was carried out to collect the entomofauna present, which was separated, identified, and preserved in the entomology laboratory of the Center for the development of biotic products. A total of 10,000 specimens were obtained, distributed across four main orders: Diptera, Coleoptera, Lepidoptera, and Neuroptera, several of which are reported as natural enemies of important pests for *Opuntia* spp. The dominance of diptera and coleoptera suggests high functional activity in terms of biological control. These results highlight the potential of beneficial entomofauna as a structural pillar of agroecological resilience in prickly pear systems, especially in areas adjacent to biological conservation zones, where ecological connectivity can enhance ecosystem services.

Different insecticide exposure routes influence toxicity and behavioural responses in *Bombus terrestris*.

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Abstract

The global decline of pollinators has emerged as a major scientific concern, with the widespread use of certain insecticides identified as a key driver of this trend. Consequently, proper regulation and evaluation of insecticide impacts on pollinators are crucial. Current risk assessments focus mainly on lethal dose estimates using *Apis mellifera* as a surrogate species, often neglecting wild pollinators and sublethal effects that may compromise essential functions such as pollination. This study investigates, under laboratory conditions, the effects of sublethal exposure to two insecticides with distinct modes of action —thiacloprid (neonicotinoid) and deltamethrin (pyrethroid)— on worker bumblebees (*Bombus terrestris* (Linnaeus, 1758)) derived from wild-caught queens.

Individuals were subjected to toxicity assays via three exposure pathways: oral ingestion, topical thoracic application, and contact with an insecticide-treated surface. Deltamethrin exposure resulted in mortality rates ranging from 10% to 40%. All exposure routes notably reduced nectar intake, with thoracic topical application producing the most pronounced decrease. Thiacloprid caused lower mortality (0–20%); however, marked differences in nectar consumption were observed among exposure pathways, with oral ingestion exerting the strongest effect. Regarding non-lethal outcomes, clear sublethal effects were detected across the different exposure routes. For deltamethrin, 75–90% of treated workers displayed behavioural impairments, mainly affecting movement and defensive responses, with thoracic application being the most detrimental route. In workers exposed to thiacloprid, 80–95% exhibited disruptions in mobility, coordination and defensive behaviour, particularly following oral exposure. Our results demonstrate that exposure pathway is a key determinant of insecticide effects. Overall, these findings emphasize the need to include wild pollinators beyond *Apis* species and to incorporate sublethal effects in insecticide risk assessments in order to better understand the true impact of insecticide use.

More than biodiversity loss: rainforest conversion to monoculture plantations selects for land-use specific functional braconid wasp communities

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Abstract

The conversion of rainforests into rubber and oil palm plantations drives biodiversity loss in Southeast Asia. Parasitoid wasps are highly diverse and play an essential role in ecosystems by regulating herbivore populations. Declines in density and diversity of braconids (Hymenoptera: Braconidae), a major group of parasitoid wasps, after land-use change is well-documented, but potential functional losses remain elusive. We studied taxonomic and functional dimensions of braconid wasps, sampled by canopy fogging from 32 research plots in Jambi Province, Sumatra, Indonesia. Four land-use systems were compared: (1) lowland rainforest, (2) jungle rubber (low impact rubber agroforestry), and smallholder monocultures of (3) rubber and (4) oil palm. The abundance, biomass, richness, and rarity of braconids was about 50% lower in rubber and oil palm than in rainforest. In jungle rubber, braconid wasps were generally as abundant and diverse as in rainforest. Taxonomic community composition differed substantially between rainforest and jungle rubber on the one hand, and monocultures on the other, mediated by aboveground temperature, vegetation cover, tree biomass, stand structural complexity and herbivore host abundance. Functional community composition was similar in rainforest and jungle rubber, but differed from and between monocultures, mediated by aboveground temperature, vegetation cover, tree height, and the density of trees and understory plants. Functional trait analysis suggests that rubber plantations, like rainforest and jungle rubber, are dominated by large idiobiont braconids targeting concealed beetle larvae hidden in wood, whereas oil palm plantations are dominated by small koinobiont braconids attacking caterpillars and eggs on the foliage. The findings demonstrate that functional decline parallels species decline in braconid communities after rainforest transformation to cash crop monocultures, and imply that plantation types select for braconid communities that differ in life strategies and host taxa. Overall, the results point to land-use specific taxonomic and functional parasitoid wasp communities in tropical landscapes.

The fly's defensive repertoire: genes, cells and behaviour

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Abstract

To better understand the evolution of complex traits, we study the defensive responses of *Drosophila* against two major challenges in their ecology: parasitoids and noxious fungi. Complex traits are manifestations of intricate gene interaction networks, and evolution of complex traits revolves around the genetic variation in such networks. We characterized the natural variation in immunity against parasitoids, within and among *Drosophila* species, and used experimental evolution to assess how rapid evolution impacts the genetic variation in gene networks. By mapping how the genome changed during the evolution of immunity in *Drosophila*, we uncover the gene network changes associated with the gain, loss and increase of parasitoid resistance. The acquisition of parasitoid resistance in the melanogaster species group is associated with an evolutionary innovation, i.e. a novel type of differentiated hemocyte (i.e. insect blood cell). The molecular mechanism for this evolutionary innovation combines co-option of existing gene interaction networks, recent gene duplications and rapid divergence of a relatively small set of genes. In comparison, the fly's defensive responses against noxious fungi, which compete with *Drosophila* larvae for food, utilize different gene networks. Moreover, this defense relies partly on social behaviour, in particular, aggregations of larvae that jointly combat the noxious fungi. Experimental evolution and transcriptome analyses reveal that the fly's defenses against the chemical warfare of the noxious fungi involves large, diversified gene families. Combined, this emphasizes how two ecological challenges may result in the evolution of complex traits with very different genetic architectures.

Accidental introductions of parasitoids and predators in Germany - an underestimated chance for better biological control of invasive pest insects?

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Abstract

The unintentional introduction of non-native and potentially invasive organisms into Europe and—due to its central location—more or less inevitably also into Germany is of great significance for biodiversity and many human activities, including agriculture and forestry. Plant pests are subject to a precautionary legal framework at the international, EU, and national levels. Their potential introduction through global transport or other routes is strictly monitored on the basis of comprehensive lists of (un)regulated quarantine pests and comprehensive plant health measures. Despite these measures, invasive pests still enter and cause major problems in agriculture. Classical biological control, i.e., the planned importation and release of well-adapted, highly specialized natural enemies, can be an option for improving sustainable pest management. However, there is currently no practical framework in Germany for the regulation and registration of non-native biological control agents. Nevertheless, monitoring in Germany has shown that several non-native parasitoids (e.g., *Leptopilina japonica*, *Eriborus* sp.) of some serious invasive pests are already present in this region, some in adventive populations, others successfully established for several years and even spread to other regions and countries. We provide an overview of the species that occur and have been recently discovered, and also report on prospects for the use of these natural enemies against serious invasive pests, e.g., the Spotted Wing *Drosophila* or the box tree pyralid moth.

Classical biological control of the diamondback moth in the USA: potential of *Diadegma semiclausum* as a candidate agent

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Abstract

The diamondback moth (*Plutella xylostella*) is a major pest of cruciferous crops and is known for developing high levels of insecticide resistance. Classical biological control using the specialist larval parasitoid *Diadegma semiclausum* may provide a sustainable management option in the USA. We compared life-history traits of three *D. semiclausum* populations from France, Greece, and the Netherlands on their local *P. xylostella* populations and two USA populations (one insecticide-resistant, one susceptible). Semi-field trials assessed performance on four commercial crucifer varieties, and a competition experiment was conducted with *Diadegma insulare*, the primary native parasitoid of diamondback moth in North America.

All *D. semiclausum* populations successfully developed on USA hosts, though parasitism success was lower on insecticide-resistant hosts. Parasitism rates were higher on the original host populations than on the USA populations. In semi-field cages, parasitism rates were similar across crop varieties and positively correlated with ambient temperature. *D. semiclausum* parasitism rate was 6.7 times higher than that of *D. insulare*, and the two species showed additive parasitism when combined.

These findings provide baseline data to support the selection of *D. semiclausum* populations most likely to succeed if introduced in the USA. They also suggest that *D. semiclausum* could enhance diamondback moth control alongside *D. insulare*, offering a promising avenue for integrated biological control programs.

Inundative release of *Muscidifurax raptor* Girault and Sanders, and *Pachycrepoideus vindemiae* Rondani (Hymenoptera: Pteromalidae) to control of *Piophilidae* *casei* Linnaeus (Diptera: Piophilidae) in ham pro

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Abstract

The use of biological control within an IPM approach in stored food production is expected to increase, due to both the limitations of chemical methods and the rising focus on environmental sustainability. However, comprehensive biological control strategies for animal-derived products like meats, fish, and cheeses are still lacking. Dry-cured ham is an example of a preserved animal product that can be infested by various arthropods, such as *Piophilidae casei* Linnaeus (Diptera: Piophilidae), when stored. This study aimed to assess the effectiveness of releasing the pupal parasitoids *Pachycrepoideus vindemiae* Rondani and *Muscidifurax raptor* Girault and Sanders (Hymenoptera: Pteromalidae) in controlling this dangerous fly in customized cages in a ham production facility in Northern Italy. Data on total parasitism (TP), emergence rates (ER), sex ratio (SR), and longevity (LO) were collected for *M. raptor* and *P. vindemiae* during the biological control experiments. It was found that both parasitoids could successfully parasitize pupae of *P. casei* in ham production, avoiding ham contamination. While the LO and SR data did not show a significant difference between the two parasitoids, *P. vindemiae* demonstrated a significantly higher TP and ER, resulting in the best candidate for biological control of *P. casei*. An assessment of the potential use of these parasitoids in ham facility is discussed.

Woolly Apple Aphid and Natural Enemy Activity in Net-Covered Organic Orchards in Emilia-Romagna

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Abstract

The woolly apple aphid (WAA), *Eriosoma lanigerum*, is re-emerging as a key pest in European apple orchards. Important aspects of its ecology remain unclear, as does the effectiveness of natural predators in current orchard conditions. To investigate the population dynamics of the WAA in protected orchards, a two-year field study was launched in 2024 across four organic apple orchards in Emilia-Romagna. All the apple orchards are covered with single-row nets, widely adopted to limit pest invasion and extreme-weather damage.

The focus of monitoring in 2024 was on the WAA and its primary parasitoid, *Aphelinus mali*. Aphid colonies in the canopy were assessed and classified, and parasitisation levels were evaluated using a stereomicroscope on selected colony samples. Yellow sticky traps provided information on the flight activity of *A. mali*, while double-sided sticky bands around the bases of the trunks enabled detection of WAA movement between the canopy and roots. Data loggers were used to monitor temperature and humidity under the nets.

Monitoring continued in 2025 and a complementary biological control strategy involving the release of the predatory hoverfly *Sphaerophoria rueppellii* was implemented to evaluate its performance under the nets and its compatibility with the WAA–*A. mali* system.

Preliminary results suggest that WAA infestations peak in late May/early June. Initially, colonies develop at the rootstock and on older woody tissues before spreading to new shoots. Field parasitisation by *A. mali* was high, often exceeding 50%. Early indications suggest that releases of *S. rueppellii* may also contribute to WAA suppression. Further analyses will clarify the seasonal movement patterns of the WAA and the activity of *A. mali* under the nets, as well as the contribution of *S. rueppellii* to reducing the pest population. This information will inform the development of more effective and sustainable management strategies for protected organic orchards.

Assessing Biological Control Agent Releases for Aphid Management under Exclusion Nets in Apple Orchards

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Abstract

In orchards, native natural enemies (NE) tend to establish too late in the season to provide effective aphid control. Augmentative biological control represents a promising strategy to enhance early-season aphid regulation. However, it remains difficult to implement in open-field due to released NE dispersal, intraguild interactions, weather dependency. In apple production, the rosy apple aphid *Dysaphis plantaginea* is one of the most problematic pests. Its early-season occurrence, high reproductive capacity, and severe damage potential even at low densities make it a major threat. The increasing use of anti-hail and codling moth exclusion nets during the growing season may offer new opportunities to improve the efficacy of augmentative biocontrol against aphids. In this study, we aimed to evaluate the potential synergistic effects of netting and augmentative biocontrol against *D. plantaginea*. Three netting configurations were evaluated : single-row, full block, and anti-hail nets (Control). Five NE were tested separately : two generalist predators (green lacewings and earwigs), two specialist predators (hoverflies and lady beetles), and a parasitoid. We assessed whether net presence and type modulated effectiveness of augmentative biological control through (i) increases in released NE abundance and detection probability and (ii) resulting impacts on aphid populations monitored on marked shoots. Preliminary analyses show that releases positively affected the timing of first detection and total abundance of lady beetles and green lacewings in marked shoots, although green lacewings detection remained very low. Releases also increased the detection probability of detecting earwigs in tree-beating samples. In contrast, no release effect was observed for hoverflies or parasitoids. Netting systems influenced parasitoid abundance, which was higher under full-block nets. Aphid infestation levels were consistently lower under anti-hail nets. Further analyses will clarify the effects of NE releases on aphids regulation. This combination of management levers may provide an innovative pathway toward improved biological control strategies.

Cryptic but functionally divergent: *Chrysoperla lucasina* outperforms *Chrysoperla carnea* in predation of early developmental stages of *Nezara viridula*

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Abstract

Invasive pests increasingly threaten the stability of integrated pest management programs in greenhouse cropping systems, where biological control strategies are typically tailored to established pest complexes. However, cryptic diversity within commercially used natural enemies may conceal important differences in their functional traits and pest suppression potential. *Nezara viridula* (Hemiptera: Pentatomidae) has emerged as a major pest in European greenhouses, where current biocontrol programs are poorly equipped to suppress it. Eight commercially available generalist arthropod predators commonly used in greenhouse solanaceous crops in Europe were assessed for their ability to suppress *N. viridula*. Their impact on its eggs and early nymphal instars was assessed through standardized laboratory assays, as well as greenhouse cage trials using fruit-bearing sweet pepper plants. Predation was mainly exhibited by larvae of *Chrysoperla* species (Neuroptera: Chrysopidae), revealing clear functional divergence between the cryptic species *C. carnea* and *C. lucasina*. Notably, *C. lucasina* was the only predator to attack *N. viridula* eggs, albeit at low levels. Against nymphal instars, third-instar *C. lucasina* larvae exhibited the highest predation, while second-instar *C. lucasina* often outperformed second-instar *C. carnea* and sometimes even matched the efficacy of third-instar *C. carnea*. All other predators showed little or no predation. In greenhouse cage trials, third-instar *C. lucasina* significantly reduced the survival of both first- and second-instar *N. viridula* nymphs under the structurally complex on-plant conditions. Across all assays, first-instar *N. viridula* nymphs were generally more vulnerable to predation than second-instar nymphs. These results identify *C. lucasina* as a promising candidate for augmentative biological control of *N. viridula*, warranting further evaluation under longer exposure periods, mixed-prey environments, and in combination with other biocontrol agents, such as egg parasitoids. Importantly, this study highlights how cryptic species within commercially used predators can differ markedly in efficacy, an underrecognized aspect of functional diversity in biological control.

Interaction of *Leptopilina japonica* Novkovi? & Kimura, 2011 with native European *Drosophila* and parasitoids

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Abstract

The larval-pupal parasitoid *Leptopilina japonica* Novković & Kimura, 2011 (Hymenoptera: Figitidae) is a natural enemy of the invasive *Drosophila suzukii* (Matsumura, 1931) (Diptera: Drosophilidae). Both species originate from East Asia, and while the fly has been an invasive pest for almost 20 years, the parasitoid has started to follow its host only in recent years. To date, *L. japonica* has been reported from six European countries. We investigated three types of interactions of *L. japonica* with native fauna:

First, we tested, how pupal parasitoids against *D. suzukii* were affected by puparia which contained *L. japonica* pupae. While *Pachycrepoideus vindemniae* (Rondani, 1875) successfully hyperparasitised *L. japonica*, *Trichopria drosophilae* (Perkins, 1910) avoided parasitised puparia altogether.

Second, we conducted hybridization experiments of *L. japonica* with native *Leptopilina*. Behavioural analysis was combined with different experimental settings to cover the chances of interspecific mating on a spectrum from more to less artificial circumstances.

Third, we conducted a field monitoring with different substrates in multiple locations in Germany throughout one year (June to October) and observed natural infestation with flies and parasitoids. Substrates and habitats were chosen to attract the highest possible diversity of Drosophilids and puparia were individually incubated.

By testing multiple aspects of interaction with native parasitoids and possible non-target host species, our results help to determine, whether *L. japonica* is a suitable biocontrol agent against *D. suzukii*, and if the species should be promoted or possibly used for augmentative releases.

Revealing parasitoid–pest interactions: quantifying parasitism in cabbage stem flea beetle using molecular approaches

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Abstract

Revealing parasitoid–pest interactions: quantifying parasitism in cabbage stem flea beetle using molecular approaches

The cabbage stem flea beetle (CSFB, *Psylliodes chrysocephala* L.) is the most damaging autumn pest of winter oilseed rape (*Brassica napus*) in Europe, with both life stages affecting plant survival and yield. Limited effectiveness of chemical control has led to a significant decline in sown area across the EU and UK.

Biological control by parasitoids is a key ecosystem service that helps reduce crop yield losses. Yet knowledge of CSFB–parasitoid interactions remains limited. Information on parasitoids biology, diversity, and the effects of management practices on their populations is scarce, limiting the development of strategies to enhance natural enemy populations and their use in integrated pest management strategies. Traditional methods to assess parasitoid–host relationships, such as rearing or dissection, can be effective but are technically demanding, time-consuming, and prone to error. Molecular tools now offer powerful alternatives. DNA-based techniques, including metabarcoding, enable rapid and reliable identification of parasitoids and their host associations.

Here, we used these molecular approaches to reveal parasitoid–pest interactions and quantify parasitism rates. By scaling up sample processing, these techniques enable us to reveal how agricultural practices and environmental conditions shape parasitoid diversity, phenology, and ecological function—essential knowledge for developing integrated pest management strategies in oilseed rape production.

Exploring the bacterial microbiota of parasitoid species used for biological control

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Abstract

Insect biology largely depends on the diversity of the microorganisms with which insects interact closely, forming their microbiota. The bacterial dimension of the insect microbiota has received increasing attention in recent years, as it has been shown to play a central role in the evolutionary ecology of insects, influencing their phenotype in many ways. Surprisingly, despite the significant attention paid to the virobiota of parasitoid wasps (Hymenoptera), their bacterial microbiota remains poorly studied, even though it may strongly affect fitness and reproductive behavior, key aspects in the context of mass production for biological control. For instance, some parasitoids can be associated with heritable symbionts that act as reproductive manipulators (e.g., *Wolbachia* and *Cardinium*). These symbionts tend to manipulate their hosts by skewing the sex ratio towards females. To address this knowledge gap, we analysed the functional bacterial diversity of six industrially produced aphid parasitoid species: *Aphidius ervi*, *Aphidius colemani*, *Aphelinus abdominalis*, *Aphidius matricariae*, *Ephedrus cerasicola* and *Praon volucre*. Commercial samples were obtained from the major insect-producing companies, along with wild strains selected by Viridaxis S.A. We hypothesized that aphid parasitoid microbiota is more diverse than is commonly reported, and that the closer the species are from a phylogenetic point of view, the more bacteria they will share. We also tested for the presence of heritable bacteria with a potential role in inducing parthenogenesis in Hymenoptera, which could influence mass production efficiency. After DNA extraction, bacterial diversity was assessed using a metabarcoding approach based on Oxford Nanopore sequencing. The first results show, for some species, a tendency to produce more males than females at emergence. Preliminary results are presented for the parasitoid species, including bacterial prevalence levels. This study represents a first step towards understanding the relationship between parasitoids and their bacterial symbionts, and towards optimizing the biological control of aphids.

Combating a plant pathogen with ladybird beetles

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Abstract

Powdery mildew (PM), caused by *Podosphaera aphanis*, is one of the most destructive diseases in greenhouse strawberry production worldwide. The pathogen infects young leaves, flowers, and fruits, leading to malformations and yield losses of up to 30%. Current management relies on sulfur, fungicides, UVC light, climatic regulation, and resistant cultivars, yet these measures face limitations such as reduced efficacy, negative side effects on natural enemies and workers, labour-intensive application, and high technological costs. Biological control options for PM remain limited, and existing agents such as fungivorous mites show primarily preventative effects and have not been evaluated on strawberry. Mycophagous ladybird beetles represent a largely unexplored group of macro-biocontrol agents for PM. *Psyllobora vigintiduopunctata* (P22), an obligate consumer of powdery mildew, is native to Europe and capable of removing large quantities of spores and mycelium as both larvae and adults. In this study, we evaluated the control efficacy of P22 against strawberry PM under both curative and preventative settings in cages. We also examined how supplementary food and release density influence P22 population dynamics and disease suppression, and tested compatibility with a commonly used “green” spraying program. A single release of P22 adults effectively controlled PM within four weeks in the curative trial and prevented disease establishment in the preventative trial. PM suppression in both trials was significantly better than in the control and comparable to the spray scheme. Spraying was not compatible with either adults or larvae. P22 population dynamics depended on PM availability, while supplementary food increased survival and abundance of newly emerged adults when PM was scarce. No significant difference in disease suppression was observed between one- and two-couple releases. These findings demonstrate the potential of ladybird beetles for biological control of PM, and further assessment at commercial scales is warranted.

Potential of Bumblebee-Mediated Vectoring of the entomopathogenic fungus *Beauveria bassiana* for Thrips Management in Strawberries

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Abstract

Thrips are increasingly problematic in early-season tunnel strawberry production, with few effective control options. The entomopathogenic fungus *Beauveria bassiana* is a promising biocontrol agent, but direct targeting of thrips remains difficult. Api-vectoring of microbial control agents is used against grey mold in strawberry production using the 'Flying Doctors' hive design (BioBest, Belgium), while few attempts for insect pest control with this method have been made. This study assessed the potential of bumblebees (*Bombus terrestris*) to vector *B. bassiana* (BotaniGard WP) to strawberry flowers to control Western flower thrips (*Frankliniella occidentalis*), and evaluated *B. bassiana* effects on bumblebees (survival individually vs. in groups) and hives (activity and contamination). Laboratory and greenhouse experiments examined thrips and bumblebee survival under different *B. bassiana* concentrations, vectoring capacity, thrips control efficacy, bumblebee activity, and fungal spread in hives. Thrips were highly susceptible, with ~50% mortality at low conidia concentrations. Bumblebee workers exposed to BotaniGard WP died completely when exposed individually, while groups of six workers had ~33% mortality. In greenhouse trials, bumblebees deposited ~10⁵ colony forming units (CFU) per flower, but also carried the fungus into hives, where 10²–10³ CFU were detected in hive areas and up to 10⁵ CFU in cells. Despite hive contamination, bumblebee survival was unaffected at the hive level, and foraging activity remained stable. However, api-vectoring did not significantly reduce thrips populations, likely due to climatic conditions affecting thrips abundance. These findings highlight both the potential and limitations of api-vectoring for insect pest control. While bumblebees can efficiently distribute *B. bassiana* without major survival impacts, efficacy against thrips under greenhouse conditions was low. This work supports further research to optimize protocols, assess risks, and expand the multifunctionality of commercial bumblebee hives for targeted biopesticide delivery beyond plant pathogen control.

Signals in the dark: enhancing *Cydia pomonella* monitoring with kairomones and UV light traps

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Abstract

Climate change, through rising temperatures and increasingly irregular precipitation patterns, is altering the phenology of *Cydia pomonella*. Higher temperatures can lead to additional generations per season, while prolonged rainfall may delay mating events, complicating population dynamics. These shifts, combined with the reduced reliability of *C. pomonella* adult monitoring in orchards under mating disruption, have renewed interest in monitoring strategies capable of attracting both sexes and providing insights into the reproductive status of this pest population. In this study, we evaluated and compared kairomone-based lures, PHEROCON Megalure CM Dual 4K and PHEROCON CM DA Combo + AA, which attract both *C. pomonella* males and females in orchards treated with mating disruption. These were tested alongside a custom-designed UV light trap, developed to offer a better attractivity to the kairomone traps. Field trials were conducted in Switzerland and Italy to assess the performance of these trap-lure combinations. Results from the first year of field trials (2024) show that all trap-attractant combinations consistently captured both *C. pomonella* males and females across a range of mating statuses throughout the season. Notably, UV light traps yielded a 5-fold increase in total captures. Further results and detailed analyses will be presented during the conference. This dual-approach framework addresses critical gaps in *C. pomonella* monitoring by generating reliable capture data under mating disruption, including information on female mating status. By establishing a robust, multimodal monitoring system, our work lays the groundwork for future integration with climatological data, with the ultimate goal of improving population forecasting models and enhancing orchard resilience under shifting agroecological and environmental conditions.

First European record of the Nearctic hyperparasitoid *Cheiloneurus swezeyi* and impacts on *Neodryinus typhlocybae* populations

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Abstract

The introduction of the Nearctic parasitoid *Neodryinus typhlocybae* (Hymenoptera: Dryinidae) in Europe has been considered a successful example of biological control against the invasive pest *Metcalfa pruinosa* (Hemiptera: Flatidae). Recent reports of increasing *M. pruinosa* populations prompted research to assess biotic factors that may interfere with the activity of the introduced parasitoid. Among these, hyperparasitoids represent a critical yet unexplored component of this system.

In a three-year study, 5,993 cocoons of *N. typhlocybae* were sampled from 28 semi-natural sites in northeastern Italy. Cocoon fate, hyperparasitoid assemblage, emergence patterns, and the influence of vegetation structure on hyperparasitism were examined. Hyperparasitoids were characterized by an integrative approach combining morphological characters and mitochondrial cytochrome c oxidase subunit I (COI) sequencing.

Results showed that adult *N. typhlocybae* emerged from only about 15% of the cocoons, while 31% yielded hyperparasitoids. The Nearctic hyperparasitoid *Cheiloneurus swezeyi* (Hymenoptera: Encyrtidae) was detected for the first time in Europe. This species is known as the primary antagonist of *N. typhlocybae* in its native range. *C. swezeyi* and the native *Pachyneuron muscarum* (Hymenoptera: Pteromalidae) represented the two hyperparasitoids with the greatest impact on the emergence of the primary parasitoid. Multiple individuals of *C. swezeyi* frequently emerged from single cocoons, with an average exceeding five individuals per host. Hyperparasitism by *C. swezeyi* was high in the lower vegetation layer (<0.5 m above ground), a pattern consistent with the high proportion of wingless females and their limited dispersal ability. Molecular analyses revealed six different COI haplotypes of *C. swezeyi*.

These findings indicate that *C. swezeyi* represents an emerging component of the *M. pruinosa*–*N. typhlocybae* system, potentially reducing the efficacy of the biological control program. Continued monitoring of hyperparasitoids is therefore essential to define the distribution of *C. swezeyi* across Europe and to assess the long-term success of biological control programs.

From Factory to Field: Sex Pheromone of *Plutella xylostella* produced in yeast cell-factories validated in laboratory and field trials

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Abstract

The use of insect sex pheromones in Mating Disruption (MD) represents a sustainable alternative to conventional insecticides for agricultural pest control. Notably, this method remains effective against insecticide-resistant pest populations. Furthermore, the novel production of pheromones in engineered yeast cell factories—a cost-effective and innovative platform—is a ground-breaking technology poised to transform modern plant protection strategies. *Plutella xylostella* (DBM) (L.) (Lepidoptera: Plutellidae) is a cosmopolitan pest of brassicas. To validate and compare the performance of yeast-derived sex pheromone components with those chemically synthesized, we studied the behavioral and electrophysiological response (EAG) of male DBM adults. In addition, by coupling gas chromatography with electroantennographic detection (GC-EAD), we examined whether any residual impurities present in yeast-derived pheromone components can be perceived by the insects' antennae and thus interfere with their normal behavior. Furthermore, we assessed the performance of the yeast-derived pheromones under field conditions through monitoring and MD trials in cabbage fields in Greece. We demonstrated that the pheromone blend —comprising (Z)-11-hexadecenal and (Z)-11-hexadecenyl acetate derived from (Z)-11-hexadecen-1-ol produced by yeast cell-factories— was as efficient and specific for monitoring and MD in cabbage fields as the conventional ternary synthetic blend [(Z)-11-hexadecenal and (Z)-11-hexadecenyl acetate and (Z)-11-hexadecen-1-ol]. Notably, the yeast-derived mixture contained small amounts of unoxidized (Z)-11-hexadecen-1-ol due to incomplete oxidation. For MD trials a hydro-degradable pheromone dispenser—designed to gradually dissolve and continuously release pheromone throughout the growing season—has been successfully tested in frequently irrigated fields, thereby eliminating the need for manual removal. These precise, time-efficient, and economically viable technologies are in line with European Commission initiatives like the Green Deal's Farm to Fork Strategy and the Biodiversity Strategy, promoting food sustainability while preserving biodiversity.

Exploring *Anagyrus* species as biological control agents against invasive mealybugs in Mediterranean agroecosystems

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Abstract

Invasive mealybugs (Hemiptera: Pseudococcidae) pose an important threat to Mediterranean agriculture, causing significant economic losses and increasing pesticide reliance. Biological control using encyrtid parasitoids is a sustainable alternative. This work integrates two studies that evaluate the efficacy and specificity of parasitoids within the genus *Anagyrus* against mealybug species recently introduced in Spain and Italy. The first study investigated the host selection behavior and specificity of *Anagyrus fusciventris* targeting *Pseudococcus longispinus*, a key pest in Spanish persimmon orchards. To assess the environmental safety of potential inoculative releases, no-choice tests were conducted involving three non-target species (*Planococcus citri*, *Delottococcus aberiae*, and *Paracoccus burnerae*). While *A. fusciventris* attempted to parasitize non-target hosts, the three mealybugs encapsulated the parasitoid eggs. These results suggest that *A. fusciventris* is a highly specialized and safe candidate for managing *P. longispinus* with low impact on non-target mealybug populations. The second study explored the potential of *Anagyrus matritensis* to control *Phenacoccus solenopsis* in Italy. Since its detection in Sicily, this highly polyphagous pest has threatened horticultural crops such as tomato (*Solanum lycopersicum*). Field surveys identified *A. matritensis* and other parasitoids in the island. Laboratory choice and no-choice assays were performed to determine the host stage preference and biological parameters of this parasitoid. Our results highlight the suitability of *A. matritensis* for conservative biological control programs. Similarly, the high density of the specific encyrtid endoparasitoid *Aenasius arizonensis* in the field suggest it can be another potential biological control agent against *P. solenopsis* in Italy. Further research is investigating the role of food supplements to optimize the rearing of these parasitoid species. Our results demonstrated that providing alternative food supplies increase parasitoid fitness, but these effects were species dependent. Overall, these studies will contribute to design the protocols to implement biological control programs against invasive mealybugs in Mediterranean agroecosystems.

Evaluation of sustainable strategies for the management of *Lygus* spp. in berry and vegetable crops

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Abstract

Lygus spp. (Hemiptera: Miridae) are highly polyphagous insects causing substantial damage in berry and vegetable crops. Their feeding on stems and fruits induces tissue deformation, shoot wilting, and lateral bud proliferation, resulting in economic losses due to downgraded produce and reduced yields. Management of these pests is particularly challenging due to their high mobility, broad host range, and the presence of multiple morphologically similar species.

Despite their economic importance, the biology and ecology of many *Lygus* species remain poorly understood. Key aspects such as host plant selection, chemical ecology, and behavioral responses to plant odors are largely unknown, limiting the development of targeted and effective integrated pest management (IPM) strategies. A better understanding of these fundamental traits is essential to design sustainable interventions and to improve the predictability and efficiency of control measures.

At the same time, restrictions on certain synthetic insecticides and the increasing demand to reduce pesticide use in high-value specialty crops create a pressing need for practical, sustainable solutions. Current approaches, including biological control agents, physical barriers, mechanical removal, trap crops, and push-pull systems, show variable efficacy depending on environmental conditions, crop type, and pest behavior, and there is urgent need for an integrated strategy to reliably control *Lygus* populations.

Ongoing research at Agroscope combines fundamental and applied approaches. Efforts aim both to improve knowledge of *Lygus* biology, behavior, and chemical ecology, and to evaluate integrated strategies that combine biological, physical, and cultural measures. This dual approach seeks to generate sustainable, evidence-based management solutions while increasing our understanding of these poorly known pests. The insights gained are expected to support more resilient and environmentally responsible crop production across Europe.

Use of egg parasitoids to control pests in soybean

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Abstract

Augmentative Biological Control (ABC) is one of the essential strategies for more sustainable agriculture, especially in commodity crops as soybean, where the overdependency on chemical insecticides for high yields has been a major concern. Due to their high parasitism potential, the egg parasitoids *Telenomus podisi* and *Trichogramma pretiosum* have been considered among the most promising biocontrol agents for stink bugs and lepidopterans, respectively. Field releases of those parasitoids in soybean fields have reached up to 90% parasitism, efficiently reducing the use of chemicals. Despite the promising results, field efficacy is depended on a well-established releasing recommendation. Insecticide applications should be avoided in the field for approximately 10 days before releasing the parasitoids. Neither can chemicals be used 5 and 14 days after releasing *Tr. pretiosum* and *Te. podisi*, respectively. In addition, pest monitoring must be carefully performed in order to release fed-parasitoid adults at early pest infestation. Releasing must be performed respecting parasitoid dispersion capacity which is 8 meters for *Tr. pretiosum* and 25-30 meters for *Te. podisi*. Adoption of IPM, including the use of selective insecticides only when Economic Thresholds are reached or surpassed, will promote a more sustainable management and a more favorable agroecosystem for the ABC to succeed. Both parasitoid species are officially registered for pest control in agriculture and commercially available in Brazil, released in approximately 350,000 hectares in the country last crop season. Recent low carbon soybean certification can be a new incentive for increasing IPM and ABC adoption in the pursuit of a more sustainable and resilient agriculture.

Prospecting soil-dwelling predatory mites as biocontrol agents against insect pests in Mediterranean vineyards

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Abstract

Soil-dwelling predatory mites of the Laelapidae family (Mesostigmata) are promising biocontrol agents, feeding on various soil microinvertebrates, including crop pests. We assessed the potential of two laelapid species, *Gaeolaelaps aculeifer* and *Cosmolaelaps* sp. 1 (under description), collected from French Mediterranean vineyard soils, to feed on four prey types: (i) a factitious astigmatid mite used for mass rearing, (ii) free-living nematodes, and two soil-associated crop pests: (iii) *Drosophila suzukii* larvae and (iv) grape phylloxera (*Daktulosphaira vitifoliae*). A no-prey control was also included.

Bioassays were performed under controlled conditions. Each Petri dish contained one or five predator females and one prey species. Predation and egg production were recorded every 24h over four days. Ten replicates per prey-predator combination were tested, with the experiment repeated across three weeks (n=30 per treatment). Egg counts were analyzed using GLMs with a log link and predator number as offset; means were compared via Tukey's method (emmeans).

Gaeolaelaps aculeifer showed high reproductive output on astigmatid mites (5.48 ± 0.26) and nematodes (5.22 ± 0.25), moderate on *D. suzukii* (2.15 ± 0.08), and very low on phylloxera (0.30 ± 0.05), similar to starvation. *Cosmolaelaps* sp. 1 reproduced best on nematodes (0.51 ± 0.07), moderately on astigmatid mites (0.32 ± 0.05), and poorly on both pests, indicating they are unsuitable prey.

Our findings indicate that *G. aculeifer* is a promising biological control agent for targeting the soil stages of *D. suzukii*, while *Cosmolaelaps* sp. 1 may be better suited for environments rich in nematodes. Both species can be reared on factitious prey, facilitating mass production. This bioassays is the first step in a series of prospective studies, aimed at developing the operational use of these mites in integrated pest management programs.

Synergistic effects of astigmatid mite mixtures on the performance of selected *Orius laevigatus* (Fieber) (Hemiptera: Anthocoridae) strains

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Abstract

The successful establishment of predatory insects in crops is a critical factor for effective biological control, often depending on the availability and quality of food sources during the initial release phases. This study evaluated the population dynamics and field establishment of two strains of *Orius laevigatus*, a commercially available population (Agrobío) and a strain selected for feeding on astigmatid mites (MITE2), under different supplemental feeding regimes in cage trials. The treatments included single-prey diets, a complex mixture of three astigmatid mite species (*Acarus siro* (Linnaeus), *Tyrophagus entomophagus* (Laboulbène) (Acari: Acaridae), and *Carpoglyphus lactis* (Linnaeus) (Acari: Carpoglyphidae)), and a traditional *Ephestia kuehniella* eggs as control. Our results showed that the specific treatment provided had an impact on the total predator population throughout the study. Our findings demonstrate that providing a diverse mixture of mite species significantly enhances the establishment and growth of *O. laevigatus* populations in the field compared to single-species supplementation. Notably, the selected strain MITE2 showed a superior response to these mixtures, achieving population levels that significantly exceeded those of the commercial strain and even surpassed the densities observed with the optimal traditional diet of *E. kuehniella*. This evidence suggests that the combination of the MITE2 line and the field release of multi-species mite mixtures provides a major strategic advantage: it allows the predator to remain and establish in the crop without the need of expensive supplementary diets or the presence of the target pest. This ensures that the natural enemy is already present and at high densities when the pest eventually appears, representing a significant advancement in preventive and sustainable pest management.

Assessing the potential role of the native parasitoid *Exorista larvarum* (L.) as a biocontrol agent against *Cydalima perspectalis* (Walker): a laboratory evaluation

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Abstract

The Box Tree Moth (BTM), *Cydalima perspectalis* (Walker) (Lepidoptera: Crambidae), is an insect pest native to East Asia that has quickly spread across the Holarctic region through the trade of infested ornamental plants. Since its first record in Europe in 2006, it has posed a serious threat to *Buxus* species in both urban and natural environments. While several natural enemies control BTM populations in its native range, only a few native species have been recorded in field conditions in Europe, exhibiting low parasitism rates. Recently, the tachinid fly *Exorista larvarum* (L.) (Diptera: Tachinidae), a native larval endoparasitoid, has been observed parasitising BTM in field conditions in Europe. In this study, the potential of *E. larvarum* as a biocontrol agent against BTM was evaluated in laboratory conditions. A colony of *E. larvarum*, maintained on the greater wax moth *Galleria mellonella* (L.) (Lepidoptera: Pyralidae), was used to assess host acceptance and suitability through no-choice and choice tests. Acceptance rates were high for both hosts (no-choice: 97% for BTM, 88% for *G. mellonella*; choice: 60% for BTM, 100% for *G. mellonella*). Larval mortality was also high (no-choice: 71% for BTM, 89% for *G. mellonella*; choice: 71% for BTM, 97% for *G. mellonella*). Conversely, host suitability varied significantly between the exotic and factitious hosts: puparia formation and adult emergence were higher in *G. mellonella*, unlike BTM (no-choice: 83% vs. 3%; choice: 87% vs. 11%). Although *E. larvarum* showed a preference for *G. mellonella*, our findings suggest that this parasitoid species can complete its life cycle on BTM, albeit at very low rates, contrary to previous studies. These results may suggest emerging changes in the behavioural dynamics of this host–parasitoid relationship, highlighting the need for further research to clarify the potential role of *E. larvarum* as a BTM biocontrol agent.

Interactions between *Liriomyza huidobrensis* and *Neochrysocharis formosa* under varying biotic and abiotic factors

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Abstract

Recently established in Australia following an invasion in 2020, the Serpentine leafminer (SLM) *Liriomyza huidobrensis* is a high risk pest of significant economic importance. SLM poses a serious threat to the horticulture sector, particularly the protected cropping systems, prompting the need for the development of sustainable management tools. *Neochrysocharis formosa* is one of the most common larval endoparasitoids of late second- to early third-instar SLM larvae and is considered a promising biocontrol agent. In this study, interaction between SLM and *N. formosa* was assessed under different temperatures (17, 25, and 30°C) and insect host densities (low, medium, and high). The development of both the host and parasitoid was also assessed under varying constant temperature conditions. Temperature had strong effect on the developmental period of SLM, which was the longest (39.1 ± 0.5 days) at 17 °C. At 30°C, SLM larvae could develop up to the pupal stage, but no adults emerged. The developmental time of *N. formosa* decreased significantly with increasing temperature from approximately 23.4 ± 0.9 days at 17 °C to approximately seven days at 30 °C. The mean number of *L. huidobrensis* larvae killed by the parasitoids increased with temperature up to 30 °C. At all tested temperatures, larval mortality through larval-feeding and stinging was higher than that caused by parasitism. The mortality caused by feeding and stinging became prominent as the insect host-density increased. The results demonstrate the influence of temperature and host-density on the interaction between SLM and *N. formosa*. The findings highlight the importance of non-reproductive host-killing behaviours in determining biocontrol effectiveness and provide valuable insights for optimising the use of *N. formosa* in integrated management programs targeting *L. huidobrensis* under varying environmental conditions..

Do endosymbionts affect sexual ornament expression?

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Abstract

Endosymbionts are prevalent in insects and almost exclusively transmitted in the cytoplasm of eggs from mother to offspring. Because their transmission depends on females, many endosymbionts enhance female fitness or manipulate host reproduction. For example, some endosymbionts bias the sex-ratio by male-killing or feminising genetic males to increase their transmission success. The possibility that endosymbionts with sex-specific effects have an impact on sexual selection has been recognised. However, the potential that sex-ratio biasing endosymbiont affect the expression of sexually selected male traits is largely overlooked. Here, I will discuss how endosymbiont-driven sex-specific selection shape sexually selected traits. I will also explore whether the presence of a naturally occurring maternally inherited bacteria that cause female-biased sex ratio, is associated with reduced trait value of a sexually selected signal, focusing on the pierid butterfly *Eurema hecabe*. Males of *E. hecabe* express a visual sexually dimorphic signal - a bright, exaggerated ultraviolet (UV) iridescence across most of their dorsal wing surface. This signal is sexually selected, with females preferring males with bright UV reflectance in the lab and in the field. We quantified whether a naturally occurring sex-ratio distorter contribute to generating variation in UV trait expression. Long-term field data of naturally occurring variation in trait expression was combined with experimental manipulations through exposing male genotypes to both short-term and long-term feminising selection and the resulting changes in UV reflectance quantified. Our results indicate that sex-ratio-biasing endosymbionts substantially erodes UV trait value. These findings suggest that reproductive manipulators can influence the evolution of sexually selected traits and may contribute to maintaining variation in male ornamentation within natural populations.

Interpreting pre-copulatory processes via post-copulatory sexual selection in the black soldier fly (*Hermetia illucens*)

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Abstract

Sexual selection – male–male competition and female choice – occurs both before and after copulation. These two timeframes are not independent; information from one can help elucidate processes occurring in the other. In the black soldier fly *Hermetia illucens* (BSF), the determinants of pre-copulatory sexual selection are still largely unknown. A notable feature of this species is that it is mass-reared and has been studied almost exclusively under laboratory conditions. Our research showed that sexual selection in BSF can occur in several ways after mating. In the context of male competition, males transfer seminal fluid that reduces female sexual receptivity, and a sperm plug that blocks rival sperm from reaching the female's sperm storage organs. We also found that males invest more in sperm production in the context of intrasexual competition. Regarding female choice, we showed that females can partially degrade male ejaculate, which may allow them to select which spermatozoa to store. We discuss how these observations provide valuable insights into pre-copulatory sexual selection in BSF. Altogether, these findings offer a framework for interpreting rare observations of reproductive behaviours in this insect, including same-sex interactions often interpreted as male–male aggression and putative leks, thereby providing further insights into its mating system.

Precise, individualized foraging flights in honey bees revealed by multicopter drone-based tracking

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Abstract

Honey bees perform repeated long-distance commutes between the nest and food sources, yet tracking these flights in natural environments remains a significant challenge. This technical challenge has limited our understanding of “real world” navigational strategies. To address this, we utilized a novel drone-based tracking system to record high-resolution flight paths of individual honey bees travelling between the hive and a feeder 122m away within an agricultural landscape. This approach allowed for the precise assessment of inter- and intra- individual variation during a consistent foraging task.

We found that bees developed idiosyncratic routes, employing distinct solutions to travel around a conspicuous tree blocking the direct flight path. Repeated flights over the same route made by the same individual showed remarkable navigational precision and differed less than flights of different bees over the same route. Bees exhibited precision in navigation that exceeds that reported in the waggle dance, implying that variability in the waggle dance does not reflect a limit in the bee’s navigational capacity and underlying spatial representation.

Variability in flight paths over the same route, although low overall, was not uniform. Bee flight variability was lower near a prominent proximal landmark (the aforementioned tree) and higher above a visually repetitive corn field. Furthermore, changes in flight precision and travel alignment suggest that bees make use of different navigational strategies on different parts of their journey and that individual bees can differ in the strategies they employ. These findings indicate the importance of landscape structure, particularly proximal landmarks, in honey bee flight precision and the navigation strategies honey bees employ.

Individual-based model for investigating symbiont acquisition pattern of *Riptortus pedestris* (Hemiptera: Alydidae) shaped by environmental factors

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Joo-Young KIM, Doo-Hyung LEE

Abstract

Riptortus pedestris (Hemiptera: Alydidae) acquires its symbiont from the soil environment at each generation, acquiring symbiotic benefits including increased development during nymphal stage and enhanced dispersal capacity during adult stage. However, symbiont acquisition of the nymph depends on random encounter with symbiont-harboring soil, making it unreliable. In addition, environmental factors including predator pressure or food abundance can affect symbiont acquisition process of the nymph by altering behavior of the nymphs. In our study, we aimed to investigate how symbiont acquisition is shaped by insect's physiology and behavior in response to environmental factors including predation pressure and food abundance. For this, we developed an individual-based model simulating symbiont acquisition process of *R. pedestris* nymphs based on empirical data acquired from laboratory experiments. Then, we evaluated symbiont acquisition rate of the insect under various environmental scenarios, varying with predation pressure, food availability of host plant, and density of vegetation. Furthermore, these scenarios were simulated in two vegetative environments, soybean field, a homogeneous habitat with suitable host plants, and forest, a heterogeneous habitat with non-host and host plants. Our simulation results showed that predation pressure decreased symbiont acquisition rate of the insect largely, while its effect was mitigated at high vegetation density. Food availability of host plants had different effects in the two vegetative environments. In soybean field, high food availability of host plants prevented the insects to descend to the soil from the plants, resulting in low soil contact and subsequently low symbiont acquisition rate. On the other hand, in forest, where host plants were scarce compared to the soybean field, high food availability increased survival of the insect, resulting in high symbiont acquisition rate. Our results show how environmental factors affect symbiont acquisition process of the insect, helping us understand symbiont acquisition of the insect in the field.

Prey Preference and Body Size as drivers of Intraguild Predation in a Psyllophagous Ladybird Community: Anticipating the Impact of Introducing *Harmonia conformis* for Biological Control

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Abstract

Despite its potential to undermine biological control programs, the role of Intraguild Predation (IGP) within psyllophagous ladybird communities remains poorly documented. We investigated IGP interactions among four ladybird species associated with psyllids, including three species established on La Réunion (*Olla V-nigrum*, *Exochomus laeviusculus* and *Coccinella septempunctata*) and one not present yet, *Harmonia conformis*, a candidate biological control agent against the invasive psyllid *Acizzia uncatoides*. This study is motivated by the need to predict potential non-target effects associated with such an introduction.

Using quarantine laboratory facilities, we combined Y-tube olfactometer assays without alternative prey and choice tests offering both heterospecific eggs and psyllid larvae. This approach allowed us to assess intraguild egg detection, feeding preferences and the intensity of intraguild predation among the psyllophagous ladybird community.

Our results show no olfactory discrimination among heterospecific eggs, suggesting limited long range detection of intraguild prey. When both prey types were available, *H. conformis* exhibited the highest predation rates and significantly preferred psyllid larvae in two out of three interspecific contexts. Equal consumption of eggs and larvae was only observed with *E. laeviusculus* eggs, likely due to egg size and accessibility, as more eggs are required for satiation and experimental conditions nullified egg-hiding defenses typical of Chilocorinae. Conversely, none of the resident species preferred *H. conformis* eggs, except *C. septempunctata*, whose aphidophagous and generalist diet explains its non-selective consumption of substitute prey.

Overall, IGP intensity in this system appears weak and mainly driven by predator body size, trophic specialization and prey accessibility. Given the strong imbalance in egg-to-psyllid ratios during natural psyllid outbreaks, IGP in this system seems to be marginal. By providing evidence that IGP remains marginal compared to target predation, these results provide foundation for the final regulatory decision, ensuring that biological control efforts do not compromise local biodiversity.

Honeybees have consequences for foraging bumblebees in a mass flowering heathland

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Abstract

Heather is an essential food source for wild bumblebees, as well as for managed honeybees that are moved to heathlands in late summer for honey production. When honeybee activity increases, however, competition for floral resources between honeybees and bumblebees may arise.

We investigated how varying numbers of honeybee hives in upland heathlands affected honeybee abundance, nectar availability, and several aspects of bumblebee foraging - including bumblebee abundance, body size, species composition, flower handling time, and pollen collection—at two distances from the hives. As expected, more hives led to higher honeybee numbers, but they did not alter bumblebee abundance or the relative proportions of bumblebee species. However, additional hives were associated with shorter flower handling times and a higher percentage of pollen-collecting bumblebees, likely reflecting behavioural adjustments to reduced resource availability. Bumblebee worker size also decreased as hive numbers increased, suggesting either that larger workers were displaced to avoid competition, that colonies recruited smaller foragers in response to diminished rewards, or both.

Our findings demonstrate that honeybees can influence bumblebee foraging behaviour, even in habitats that are relatively rich in resources. This underscores the importance of evaluating long-term population consequences and accounting for interactions between wild and managed bees in management and conservation planning, to safeguard wild bumblebee populations while supporting productive honey harvesting.

Long-term memory in the anucleate nervous system of tiny parasitoid wasp *Megaphragma viggianii* (Hymenoptera: Trichogrammatidae)

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Abstract

Microinsects have become important model organisms in neurobiology because they retain complex behavioral repertoires while possessing tens to hundreds of times fewer neurons than larger insects and mammals. The parasitoid wasp *Megaphragma viggianii* Fusu, Polaszek & Polilov, 2022 (Hymenoptera: Trichogrammatidae) is a unique example: by the time it emerges from the pupa, it loses about 97% of the nuclei in its central nervous system. This poses a fundamental question about the ability of such insects to form long-term memory, which is generally assumed to depend on protein synthesis requiring nuclear DNA.

We examined the capacity of *M. viggianii* for associative learning and the formation of memory traces. We used a thermal maze, designed for miniature insects, to elicit and assess associative responses. At any given time, the maze contained a single thermally favorable zone. In the experimental group, this zone was consistently paired with a visual cue, whereas no such contingency was provided to the control group. Elevated temperatures in the rest of the arena motivated individuals to actively search for the favorable zone. Across repeated trials, wasps in the test group learned to use the visual cue to locate the comfortable area, resulting in a reduction in search time.

In our study, we demonstrate the ability of *M. viggianii* to retain memory traces for up to 24 hours after training and propose that the observed retention represents true long-term memory, drawing on evidence that this type of memory is blocked by protein-synthesis inhibitors in the closely related parasitoid wasp *Trichogramma telengai* (Hymenoptera: Trichogrammatidae).

These results indicate the possible existence of previously undescribed molecular mechanisms enabling long-term memory formation in the absence of neuronal nuclei and highlight the evolutionary plasticity of memory systems.

This work was supported by the Russian Science Foundation (project no. 22-74-10008-P, <https://rscf.ru/en/project/22-74-10008-P>).

To sting or not to sting: differential responsiveness to the alarm pheromone in honeybees

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Abstract

Honeybees defend their nest against large predators thanks to a collective effort to harass and sting the intruder. Typically the threat is detected by a few bees, which then need to quickly mobilize their nestmates into a defensive response. At the core of this recruitment is the sting alarm pheromone (SAP), a complex odour blend released when the bees' stinger is exposed. The SAP attracts and primes nearby workers for attack, thus providing a seemingly simple communication channel during defensive events. However, when taking a closer look at this system we found that the decision to sting of bees receiving this signal was dependent on both their age and their task: young (<10 days) and old (>30 days) bees had an increased likelihood to sting in the presence of SAP, irrespective of their task. Middle-aged (11-29 days) bees, however, only responded by stinging if they were foragers. Middle-aged nurses did not sting in response to SAP exposure. To unravel the molecular mechanisms underlying this differential responsiveness to the alarm pheromone, we quantified the levels of a large panel of neuromodulators. We also used calcium-imaging to study the neuronal activity evoked by the alarm pheromone in the primary olfactory area, the antennal lobes. Overall, our results shed light on the mechanisms by which a single signal can trigger different responses, ultimately resulting in division of labour during an episodic task.

Service from beyond – fluorescent evidence for cannibalistic necrophagy in ants

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Abstract

Nitrogen availability strongly constrains growth and reproduction across animal taxa, yet organisms vary widely in how they obtain this limiting resource. In ants, protein requirements are typically met by preying on other arthropods. Such resources, however, can fluctuate markedly in abundance, particularly in temperate and boreal environments where seasonal scarcity is common. An alternative and potentially reliable nitrogen source within colonies is the consumption of dead nestmates, a behavior known as cannibalistic necrophagy. Although this behavior is well documented in some social insects (such as termites), direct evidence for its occurrence in ants remains scarce.

Here, we experimentally tested whether ant workers can exploit conspecific corpses as a nutritional resource. To do this, we used colony fragments of a red wood ant species (*Formica polyctena*). Workers were first fed liquid food containing fine fluorescent dye. Following this, they were freeze-killed and their corpses were presented to starved nestmates. The digestive tracts of the food-deprived ants were subsequently dissected and examined using fluorescence microscopy. The corpses of the ants feeding on fluorescently marked food were also screened for any signs of damage.

Three days after being presented to starved nestmates, the corpses of workers that had fed on fluorescently marked food were either dismantled completely, or small holes were gnawed on the ventral surface of their gaster. We detected a strong fluorescent signal in the crop and midgut of the living recipient workers, demonstrating that nutrients originating from nestmate corpses had indeed been ingested.

Our results provide direct experimental evidence that ant colonies can recycle nutrients from deceased nestmates through necrophagy. By allowing nitrogen recycling, necrophagy may enhance colony resilience during periods of food shortage. This mechanism could be particularly important in large colonies, where internal nutrient recycling may contribute substantially to ecological persistence and evolutionary success.

Does short-term thermal history alter contest behavior and outcome in two competing parasitoids?

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Mathieu BUSSY, Solène LIÉGEOIS, Sylvain PINCEBOURDE

Abstract

Dyadic contests for indivisible resources are widespread throughout the animal kingdom. According to the Contest Theory, contest resolution depends on the asymmetry between competitors in terms of their ability to gain access and keep the resource (Resource Holding Potential, or RHP), as well as the value they place on the contested resource (Resource Value, or RV). As temperature can influence contestants' physiological and behavioral performances as well as how much they value the resource, their thermal history could modulate contest dynamics. Here, we investigated how short-term thermal exposure of competitors affects the behaviour and outcome of contests between two parasitoid wasps, *Dinarmus basalis* and *Eupelmus vuilleti*, when competing for the same host, *Callosobruchus maculatus*. Focal females were exposed for 24 hours to either their optimal temperature (34 °C) or a suboptimal temperature (25 °C or 40 °C) before competing for a host that was maintained at 34°C. Contests were set up against an intraspecific or an interspecific opponent female, maintained at the optimal temperature (34°C). Contrary to our expectations, the short-term thermal history of females did not significantly affect their aggressiveness, latency to exploit host, or victory in either species. Only differences in egg load between opponents consistently explained contest resolution, with females with more mature eggs being more likely to win. These results are consistent with previous studies: females with more ready-to-lay eggs are more motivated to oviposit and therefore place a higher value on the host. Although females exposed to 40 °C were less likely to exploit the host, no consistent temperature-driven asymmetry in RHP or RV emerged. These results indicate that recent thermal experience does not modulate competitive performance in these parasitoid species. We suggest that intrinsic host quality, rather than environmental factors, primarily drives contest resolution in this system.

Integrating sociality into the pace-of-life syndrome: insights from ontogenic and interspecific levels.

Tristan ROBINEAU (Museum and Institute of Zoology, PAS, Tristan.robineau2@gmail.com)

Benedetta BARONI, João VASCONCELLOS-NETO, Hania BABIK, Giuseppe MANNINO, Francesca BARBERO, Magdalena WITEK, Violette CHIARA

Abstract

The emergence of sociality has been a major turnover, and social organizations can be found in many taxa. Yet, the proximal mechanisms supporting the emergence of sociality remain poorly understood. The pace-of-life (POL) syndrome hypothesis states that behavior,

physiology, and life-history traits are intercorrelated and can be distributed along a slow/fast continuum. Species with higher levels of sociality generally exhibit slow life-history traits such as a long life-span or fewer offspring. This intercorrelation of traits has often been interpreted as a consequence of social life, with the idea that social life is the main evolutionary advantage, around which the other traits are organized.

We propose a refreshing perspective on the origin of social life: sociality can be considered a POL trait, and a shift toward a slower POL may underlie its emergence.

The novelty of our approach is to consider the POL syndrome as the regent of the sociality level.

First, we proposed a comparative approach and studied four *Anelosimus* species, ranging from social to nearly solitary spiders. We measured their exploration, activity, boldness, and metabolic rate. Our results confirmed a switch toward slower POL characteristics as sociality increased.

We also studied the POL-sociality relationship from an intra-individual perspective. We used *Agelena labyrinthica* solitary spiders. Like all the solitary species of spiders, the juveniles of *A. labyrinthica* have a gregarious phase that ends with dispersal, leading to solitary life. We measured POL traits of the juveniles during this transitional phase. Our results showed a shift toward faster POL characteristics with the start of solitary life.

These studies shed light on the relationship between POL and sociality, both at the interspecies and intraindividual levels, improving our understanding of the mechanisms driving the emergence of social behavior.

Quantifying the fitness costs and benefits of female aggression

Andrew SPIRES (University of Oxford, Andrew.spires@biology.ox.ac.uk)

Eleanor BATH, Ashleigh GRIFFIN, Beth MORTIMER, Irem SEPIL

Abstract

Intrasexual competition is a widespread and pervasive evolutionary selection pressure as individuals compete with conspecifics for limited resources to maximise their survival and reproductive success. Although winning contests often yields clear benefits, such as access to mates or nesting sites, aggressive actions also impose costs, many of which are harder to quantify, including non-lethal injuries and energetic expenditure. Disentangling the fitness consequences of aggression therefore remains challenging, and most studies rely on linking correlations between aggression and fitness outcomes. In particular, the fitness effects of aggression in females are poorly understood. Female competition has historically been overlooked, in part because females typically compete over reproductive or ecological resources and display less intense aggression.

To directly test the effects of aggression on female fitness, we experimentally manipulated female aggression in *Drosophila melanogaster*. We blocked synaptic transmission of neurons involved in regulating female aggression, thereby reducing female aggression. Using mated females, we quantified their reproductive success under differing levels of competition relative to genetic controls. Similarly, we assayed lifespan under starvation conditions in both manipulated and control unmated females to capture the metabolic costs of aggression.

Our results detect a fitness cost of aggression: females with increased aggression show reduced stress resistance under high competition conditions. However, we found no evidence that more aggressive females benefit through increased reproductive success. The absence of a detectable fitness benefit suggests that female aggression in *Drosophila melanogaster* may be shaped by intralocus sexual conflict, or alternatively, that the potential advantages may only emerge when measuring female lifetime reproductive success or grand-offspring production.

Evaluating attraction properties of two mealybugs to *Anagyrus pseudococchi* and *Nephus includens* using four arm olfactometer and wind-tunnel

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Çağlar KALKAN, Gül SATAR, Miraç YAYLA, Asio MAHAD OSMAN

Abstract

Planococcus citri is a major pest of citrus and numerous ornamental and cultivated plants. Although this species has many natural enemies, chemical control remains the dominant management strategy worldwide because, under field conditions, natural enemy responses are often delayed, and economic damage may occur before effective suppression is achieved. Nevertheless, biological control is a cornerstone of sustainable agriculture, and its success relies heavily on the conservation and enhancement of natural enemies within agroecosystems. In the biological control of *P. citri*, *Anagyrus pseudococchi* and *Nephus includens* are among the most important natural enemies. Supporting these beneficial organisms through alternative prey resources within orchards may help maintain pest populations below the economic injury threshold. However, for such strategies to be effective, it is essential to understand how natural enemies respond to odors emitted by both the target pest and alternative prey. Therefore, this study evaluated the behavioral responses of *A. pseudococchi* and *N. includens* to odors from the *P. citri* and the alternative prey *Planococcus vovae* using a four-arm olfactometer and a wind tunnel.

In four-arm olfactometer assays, *N. includens* showed a stronger orientation toward arms containing only mealybugs than toward arms containing mealybug+host plant or clean host plant, regardless of prey species. In contrast, *A. pseudococchi* exhibited similarly high orientation toward arms containing mealybugs alone and mealybug+host plant, with significantly lower responses to the remaining treatments.

In wind tunnel experiments conducted separately with pest alone, pest + host plant, and host plant alone, *N. includens* exhibited the strongest orientation toward odor sources consisting of mealybugs together with their host plants. Similar patterns were observed for *A. pseudococchi*, although females responded more strongly than males.

Overall, these results indicate that trophic interactions among Citrus+*P. citri*–*N. includens*/*A. pseudococchi*–Cypress+*P. vovae* are promising for the development of a banker plant system aimed at enhancing biological control.

Sugar-driven behavioral plasticity disrupts ant–mealybug mutualism and alters interactions with predators

Marie BOUREL (CIRAD, Mariebourel37@gmail.com)

Bernard Raymond ABUFERA, Willy SUZANNE, Philippe TIXIER, Dominique CARVAL

Abstract

Ant–hemipteran associations rely on the exchange of carbohydrate-rich honeydew for ant protection and care, but the outcomes of these interactions are highly context-dependent. Variation in carbohydrate availability, in particular, may induce a transition from cooperation to exploitation. Here, we investigated how sugar provisioning and host plant availability influence interactions between the African big-headed ant *Pheidole megacephala*, the pineapple mealybug *Dysmicoccus brevipes* and the ladybeetle *Exochomus laeviusculus*.

Under controlled conditions, we manipulated the presence of an alternative sugar source as well as the availability and distance of the host plant *Ananas comosus*. Sugar provisioning strongly favored antagonistic behaviors: ants ceased tending mealybugs and predated them, leading to complete mealybug disappearance within 25 days. Under sugar deprivation, ants maintained a minimal number of mealybugs, likely to secure honeydew as a long-term carbohydrate supply. When multiple mealybug-free pineapple plants were available, ants actively dispersed mealybugs across plants. In this situation, mealybugs persisted despite increased ant aggressiveness, suggesting that dispersal across multiple plants can buffer mutualism disruption by diluting predation pressure and ensuring continued resource access.

To evaluate cascading effects on biological control, we incorporated *E. laeviusculus* into a tri-trophic system. Sugar-fed ants were more aggressive toward both mealybugs and ladybeetles, yet predator efficiency remained unchanged. Ant presence, rather than diet-induced aggressiveness, was the main driver of interference, as both sugar-fed and deprived ants similarly reduced predation attempts. Thus, while sugar supplementation disrupts the ant–mealybug mutualism by promoting ant predation, it does not intensify interference with natural enemies.

Overall, our findings reveal that carbohydrate availability is a powerful driver of mutualism breakdown, although its disruptive effect can be counteracted when ants have access to multiple host plants. Sugar supplementation weakens ant protection of mealybugs without intensifying interference with natural enemies, highlighting carbohydrate manipulation as a promising strategy for integrated pest management.

Context-dependence of developmental plasticity in insects

Patricia BELDADE (Lisbon University, Pbeldade@fc.ul.pt)

Abstract

Environmental conditions shape phenotypic variation through effects at different levels and time-scales; changes in phenotype frequencies due to natural selection and changes in phenotype expression due to phenotypic plasticity. In particular, the temperature experienced during development can lead to the production of distinct adult phenotypes from the same genotype; a phenomenon called thermal developmental plasticity. This plasticity can match phenotype to ecological conditions and help organisms to cope with environmental heterogeneity, including differences between alternating seasons. I will use two insect models of seasonal plasticity to illustrate the importance of thermal plasticity in studies of variation in organismal phenotypes, and of the impact of climate change in natural populations. Temperature (T) during development affects a series of adult traits, some of which are invariable during adult life (e.g., body size and pigmentation) while others respond to adult environmental conditions (e.g., behaviour and immunity). I will present data documenting these effects and how thermal plasticity depends on genetic and environmental context. These types of interactions can impact how thermally plastic populations might cope and adapt to temperature perturbation.

#10589

EVOLUTIONARY GENETICS: Unraveling phenotypic plasticity

02/07/2026 at 11:00, Descartes

Plasticity of fatty acid synthesis and fat accumulation in a parasitoid insect

Bertanne VISSER (University of Liège , Bertanne.visser@uliege.be)

Maude QUICRAY, Mathilde SCHEIFLER

Abstract

Most insects can synthesize fatty acids and accumulate bulk fat reserves to fuel key functions for life. Fat metabolism is a dynamic and plastic process, also in the parasitic amber wasp *Leptopilina heterotoma*. The amber wasp is unique, however, because fat synthesis and accumulation can be switched on or completely off depending on the developmental environment (a lean or a fat host insect). Over the years, my team of researchers have investigated diverse aspects of plastic fat metabolism in the amber wasp, including the effects of fluctuating temperatures, age, and habitat type. During this presentation I will highlight our latest key findings, as well as a new direction of research on amber wasp fat metabolism.

Evolutionary trajectories of plasticity when encountering novel thermal conditions during southward range expansion of a damselfly

Swaegers JANNE (KULeuven, Janne.Swaegers@kuleuven.be)

Abstract

Although theory indicates the importance of plasticity for the speed of adaptation to novel environments, empirical data on the evolutionary trajectory of plasticity in new selective regimes remain scarce in natural populations. We harnessed range expansions of a damselfly from France into warmer regions in Spain as a natural experiment to test how transcriptional thermal plasticity evolves, and compared the outcomes with a native, locally thermally adapted sister species. A common-garden experiment of 11 populations revealed that plasticity evolution depended on the magnitude and duration of the warming treatment, with stressful high temperatures causing maintenance of ancestral plasticity. The frequency of plastic genes that became assimilated was higher with increasing duration of historical exposure to the thermal regime and when the warming treatment was more often encountered in the field. Specifically for chronic warming, transcriptomic plasticity first increased and subsequently decreased during range expansion, indicating evolved plastic responses precede constitutive evolutionary adaptations when coping with chronic warming. This mirrors the previously found patterns in phenotypic plasticity in the pace-of-life but interestingly our results now suggest that initial selection for 'chronic warming'-plasticity in the new edge populations mostly acts on other pathways than those that are involved in adaption in later stages. These findings are crucial to predict the role of plasticity in driving evolution in a warming world.

Molecular mechanisms involved in the control of reproductive mode plasticity in the pea aphid

Gael LE TRIONNAIRE (INRAE, Gael.le-trionnaire@inrae.fr)

Eglantine SOUCAT, Nathalie PRUNIER, Sylvie HUDAVERDIAN, Romuald CLOTEAU, Fabrice LEGEAI, Stéphanie ROBIN, Stéphanie LE BRAS, Jean-Christophe SIMON, Julie JAQUIÉRY

Abstract

Aphids are major crop pests worldwide. Such a success is largely explained by their unusual reproduction. They indeed reproduce by parthenogenesis during spring and summer - causing most of the economic losses on crops – and switch to sexual reproduction at autumn arrival by perceiving photoperiod shortening ending up with the production of overwintering eggs. In nature, lineages that are able to display this reproductive mode plasticity (also called polyphenism) are termed as Cyclical Parthenogenetic (CP) and coexist with lineages called OP (Obligate Parthenogenetic) that lost this ability. Using population genomics approaches, we identified a single genomic region that genetically discriminates natural CP and OP populations. This region contains 32 genes, mutations in one (or more) of these being responsible for the OP phenotype (Rimbault et al., 2023). Transcriptomic analyses of CP and OP lineages (Huguet et al., 2024) also revealed that parthenogenetic to sexual embryogenesis transition relies on the co-activation of hundreds of genes co-localized in a specific region of the X chromosome also surprisingly enriched in transposable elements. Such an unusual pattern suggests some important epigenetic and post-transcriptional regulations to promote the activation of a sexual embryogenesis genetic program. In order to understand the molecular mechanisms underlying reproductive mode plasticity, we first used CRISPR-Cas9 targeted mutagenesis to test the role of candidate genes located within the genomic region discriminating CP and OP populations. Second, we performed ATAC-seq to investigate chromatin accessibility changes during embryogenesis switch in order to identify the gene networks (including putative Transcription Factors) shaping reproductive mode plasticity. These two complementary approaches should thus help us shedding light on the specific genes as well as the genome-wide mechanisms involved in the control of this phenomenon of ecological importance.

When parental conditions shape offspring tolerance to stress: Transgenerational plasticity in response to sublethal exposure to an insecticide in *Drosophila melanogaster*

Romain GAYET (Université Lyon 1; CNRS, Laboratoire de Biométrie et Biologie Evolutive (LBBE), Villeurbanne, France, Romain.gayet@etu.univ-lyon1.fr)

Géraldine MANSUY, Elorri SEGURA, Annaïs NGAKU, Christophe PLANTAMP, Emmanuel DESOUHANT, Patricia GIBERT

Abstract

Transgenerational plasticity (TGP) represents a form of non-genetic inheritance through which offspring express phenotypic responses to environmental conditions experienced by their parents. Such plastic responses might be particularly relevant in the context of human-induced environmental changes, which impose novel selection pressures and increase environmental variability. Among these, pesticides use creates highly stressful conditions for insect populations, and can promote rapid adaptive responses. Yet, whether TGP contributes adaptively to coping with such anthropogenic stressors remains unclear. Here, we investigated the occurrence of TGP in *Drosophila melanogaster*, in response to sublethal exposure to an anthranilic diamide insecticide (cyantraniliprole). We used the LD20 (environmental dose inducing 20% of mortality in the population) to inflict sublethal chemical stress to developing flies across two successive generations with a crossed-environment design: parents (P) were exposed to two conditions, Control (C) and Treated to cyantraniliprole (T). Offspring (F1) of each parental lot were also exposed to the same conditions, resulting in four modalities: (i) Control-Control (CC); (ii) Control-Treated (CT); (iii) Treated-Control (TC); (iv) Treated-Treated (TT). We then measured a range of phenotypic traits in F1 individuals to assess the phenotypic responses due to TGP. We demonstrated that TGP is expressed in insects in response to a chemical stress. Male offspring showed higher survival to the insecticide when their parents had been treated, indicating transgenerationally induced resistance. Insecticide exposure reduced wing size in F1 females, but this reduction was attenuated when parents had been exposed, suggesting a transgenerational mitigating effect. We also showed that consecutive exposure across two generations significantly increased the number of mature eggs in females, reflecting higher energetic investments in fecundity under stressful conditions. These results demonstrate the importance of considering phenotypic plasticity as a dynamic process, as TGP can alter reaction norms in offspring and shape new adaptive strategies in changing environments.

Identification of gene regulatory networks driving wing polyphenism in the pea aphid (*Acyrtosiphon pisum*)

Scott Zhe Yang YIM (University of Oxford , Scott.yimzheyang@biology.ox.ac.uk)

Abstract

Phenotypic plasticity is the ability of an organism to change its phenotype within the same genotypic background, in response to environmental perturbation. Polyphenism is an extreme case of phenotypic plasticity whereby a single genotype gives rise to multiple discrete phenotypes, which allows organisms to temporarily adapt to changes in environmental conditions. Discovering the regulatory mechanisms underlying polyphenism is critical to understanding how organisms can react and adapt to ongoing environmental challenges. Here, we used the model organism, pea aphid (*Acyrtosiphon pisum*), to study the regulatory mechanisms that drive polyphenism. In this species, under optimal conditions, the mother reproduces asexually, and all offspring are genetically identical. Upon exposure to environmental stimuli (crowding/starvation), the mother will produce winged offspring in the next generation. Since all offspring are genetically identical, the production of offspring with wings must have an epigenetic basis. Integrating ATAC-seq and RNA-seq, we have produced the first gene regulatory landscape of aphid wing formation. We leveraged winged and wingless third instar aphids which cover the critical period of wing formation. Through ATAC-seq footprinting analysis, we determine the genomic occupancy of specific transcription factors driving wing phenotype-specific gene regulatory networks. In addition, we also applied CUT&RUN provide insight into specific chromatin profiling in pea aphid. To the best of our knowledge, this study provides the first insight into the gene regulatory network driving wing polyphenism in pea aphids.

Molecular Bases of Genital Developmental Plasticity in Males

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Tatiana TEIXEIRA TORRES, Bruno GENEVCIOUS

Abstract

Competition for sexual partners is a determining factor for the reproductive success of males in polygamous species. Prolonged copulation is a common strategy in this context and it may prevent females from copulating with other males and exercising post-copulatory choice of partners. The mechanisms by which males manage to prolong copulation are still poorly understood for most animal groups. Even less is known about which types of phenotypes can be plastically affected by competition for partners. We tested the hypothesis that higher densities of competing males during development affect the formation of reproductive structures, copulation duration, and the expression of genes associated with genital development. To achieve this, Pentatomidae bugs (*Euschistus heros*) were reared to adulthood in groups of two or three individuals, resulting in seven scenarios with varying male-female ratios. Scenarios that included only females were excluded, resulting in five experimental conditions for which we obtained 40 biological replicates each. To evaluate the effects of competition on morphology, we removed the genitalia of all males and measured one clasper—structures males use to hold onto females during mating. Clasper length was consistently greater in males reared in the presence of competitors. These males also engaged in longer copulations, suggesting a link between developmental environment, genital morphology, and mating behaviour. We performed RNA-seq on dissected genitalia from immature individuals reared in the most contrasting scenarios (high vs. no male-male competition). Transcriptome analyses identified 168 differentially expressed genes (DEGs), with 116 upregulated in the no-competition group and 52 in the high-competition group. Using a functional genomics approach, candidate DEGs are now being silenced through RNA interference (RNAi) to assess their role in genital development. This knowledge not only advances our understanding of developmental plasticity but also contributes to broader insights into the evolutionary forces governing reproductive traits in polygamous species.

The smell of death: characterization and applications

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Abstract

After death, a body undergoes a complex decomposition process during which hundreds of volatile organic compounds (VOCs) are released into the surrounding environment. By exposing pig carcasses to decomposition in forests, meadows, and indoor settings, we revealed the strong influence of the environment on the cadaveric odor profile. We also demonstrated that the colonization of corpses by necrophagous insects not only accelerates decomposition but significantly alters the VOC composition. These insects possess specialized olfactory sensilla that enable them to perceive decomposition-derived chemicals and use them as cues to locate and colonize fresh cadavers. Remarkably, the parasitoids of these scavenging species exploit the same chemical signals. We further characterized the VOCs emitted by submerged and buried remains, as well as those present in soil layers located above and below buried rat carcasses. Since studies examining the odor of human corpses remain scarce and constrained by small sample sizes, we undertook a comprehensive characterization of the human cadaveric volatilome through periodic visits to a morgue. Using dynamic headspace collection, we collected the VOCs released by 20 human corpses at the fresh stage, and we assessed the influence of skin temperature, sex, age, body size and postmortem interval on the volatilome.

These findings have led to a collaboration with Belgian federal police officers specializing in the search for human remains. Through a series of behavioral assays, we demonstrated that human remains detection dogs responded positively to a simplified synthetic blend composed of the principal cadaveric molecules. Notably, we showed that these dogs do not target specific cadaveric compounds but rather respond to broader chemical families and are capable of detecting cadaveric cues at concentrations as low as 100 nanograms. This simplified blend is now used by dog handlers for the routine training of their animals.

Impact of heat stress on the production and perception of cuticular hydrocarbons in the buff-tailed bumblebee

Luce GAY (Laboratory of Zoology, Research Institute for Biosciences, Université de Mons, Luce.GAY@umons.ac.be)

Abstract

As an integral component of global change, the intensification and increased frequency of extreme climatic events such as heat waves are having major consequences for pollinating insects. Among these insects, bumblebees genus *Bombus* are among the species most affected by elevated temperatures. One of the most important aspects of *Bombus* physiology, yet one that has never been examined in the context of heat waves, is the composition of cuticular hydrocarbons. This mixture of alkanes and alkenes on the cuticle plays a key role in chemical communication and in limiting water loss.

To address this gap in the literature, the objective of this project is to evaluate the impact of heat waves on the production of cuticular hydrocarbons, on their perception and on the potential consequences for social interactions within the colony. Commercial bumblebee colonies will be exposed to simulated heat waves of varying intensities under ecologically relevant conditions. Hydrocarbon profiles will then be analysed both qualitatively and quantitatively. The perception of these molecules will be examined using neurobiological and behavioural approaches in order to assess how individuals subjected to heat stress recognise the colony's hydrocarbon profile.

The first experiments will be conducted shortly and will compare the cuticular hydrocarbon profiles of individuals exposed to heat waves lasting five to ten days at temperatures ranging from 28 °C standard conditions to 35 °C. These results will provide an initial understanding of the effects of heat waves before extending the investigation to behavioural aspects.

Taken together, the findings will offer a comprehensive assessment of the impact of heat waves on the social cohesion of vulnerable social pollinators.

Chemical sexual communication in coccinellids: mechanisms, cue specificity, and evolutionary patterns

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François VERHEGGEN

Abstract

The first sex pheromone ever identified in a lady beetle was recently discovered in the Asian lady beetle *Harmonia axyridis* (Coleoptera: Coccinellidae). Females display a stereotyped calling behavior that results in the release of a volatile blend -mainly composed of five terpenoid compounds- which attracts males and triggers copulation, but only in the presence of aphid prey. Although similar behaviors have been observed in other coccinellid species, pheromonal communication in closely related taxa remains poorly studied. Moreover, the precise olfactory cues triggering pheromone production in *H. axyridis*, as well as the potential influence of larval diet quantity and quality, remain unknown.

This study, which is an integral part of Anaïs Sion's PhD thesis, aims to (1) identify the olfactory cues that trigger sex pheromone production; (2) evaluate the impact of larval diet on adult pheromone output; (3) explore the conservation of sex pheromones across phylogenetically related species.

Using dynamic sampling of volatile organic compounds (VOCs) further analyzed by gas chromatography (TD-GC-MS-FID), we first demonstrate that exposure to aphid-emitted VOCs alone is sufficient to trigger sex pheromone production in *H. axyridis*. To identify specific cues that trigger pheromone emission, we exposed ladybeetles to aphid alarm pheromone or aphid honeydew, the experiment is underway. Additionally, larval diet quality and quantity had no significant effect on adult pheromone production, highlighting the pivotal role of some aphid-derived cues during adulthood.

In *H. quadripunctata*, we identified three female-specific compounds— β -caryophyllene, β -elemene, and α -humulene—also present in *H. axyridis*, suggesting a conserved communication mechanism. Further behavioral assays and analyses are needed to confirm their functional role.

This study contributes to our understanding of sexual communication in coccinellids, specifically in *H. axyridis* and may inform future phylogenetic analyses within this family.

Cracking the chemical code of ant-aphid mutualism

Christophe LUCAS (Institut de Recherche sur la Biologie de l'Insecte (UMR7261), CNRS, University of Tours, Tours, France, Christophe.lucas@univ-tours.fr)

Jesus FORONDA, Laurence BERVILLE, Estefania RODRIGUEZ, Aranzazu PEÑA, Elfie PERDEREAU, Mar MONTORO, Francisca RUANO

Abstract

The mutualistic relationship between ants and aphids is a complex phenomenon that relies on a combination of tactile and chemical cues. Recent research has shown that ants can modify the chemical profiles of aphids, but the specific mechanisms and compounds involved in this process are not well understood. This presentation will delve into the chemical mechanisms that govern the mutualistic relationship between *Tapinoma ibericum* ants and *Aphis gossypii* aphids, identifying key compounds involved in communication between these two species.

Using gas chromatography-mass spectrometry, we analyzed the chemical profiles of 14 colonies of aphids and ants, over 3 days of interactions. Results show that contacts with *T. ibericum* lead to a swift alteration of the aphids' cuticular chemical profiles, highlighting the dynamic nature of this mutualistic relationship. Moreover, a key finding is the identification of a specific compound (3,15-di-MeC27) which is highly abundant in attended aphids and is a major component of the ant's cuticle. This compound may serve as a recognition marker, facilitating communication between ants and aphids, but other identified compounds may also play a crucial role in this mutualistic interaction.

These discoveries have important implications for the development of novel pest control strategies. By manipulating specific chemical cues, it may be possible to disrupt the mutualistic relationship between ants and aphids, ultimately reducing aphid populations and mitigating their impact on crops. Further research is needed to fully explore the potential of this approach, but the findings of this study provide a promising starting point.

Decoding alarm signalling in *Dysaphis plantaginea*, the rosy apple aphid: from chemical identity to behavioural response

Eleonora FABRIS (Faculty of Agricultural, Environmental and Food Sciences, Free University of Bolzano-Bozen; Plant Protection Department, Institute for Plant Health, Laimburg Research Centre, Auer-Ora, Italy, Efabris@unibz.it)

Silvia SCHMIDT, John PICKETT, Sergio ANGELI

Abstract

Dysaphis plantaginea (Hemiptera: Aphidinae) (Passerini, 1860), the rosy apple aphid, is a major pest in European apple orchards, where it negatively affects tree health and fruit quality. As the use of broad-spectrum insecticides is increasingly restricted, alternative pest management strategies based on chemical ecology should be investigated. Alarm pheromones, composed of volatile compounds such as terpenes, play a central role in aphid defence by triggering escape responses in conspecifics while simultaneously attracting natural enemies. This dual ecological function makes them promising candidates for sustainable pest control. This study provides a comprehensive qualitative and quantitative chemical characterisation of the alarm pheromone of *D. plantaginea* across different instars. GC–MS analyses of epicuticular extracts and cornicle secretions were combined with behavioural assays to assess repellent activity. The results contribute to a deeper understanding of aphid chemical communication and support the development of environmentally friendly pest management strategies for apple orchards.

Olfactory cues in the reproduction of *Hermetia illucens* (BSF)

Silvana PIERSANTI (Dipartimento di Chimica, Biologia e Biotecnologie, University of Perugia, Via Elce di Sotto 8, 06123 Perugia, Italy, Silvana.piersanti@unipg.it)

Manuela REBORA, Giulia PETRONI, Giorgia CARBONI MARRI, Gianandrea SALERNO

Abstract

Every year, more than 200 billion black soldier flies are reared on an industrial scale to convert a wide range of organic by-products into high-value materials for agricultural and industrial applications. This bioconversion process supports the 2030 Sustainable Development Goals by reducing carbon dioxide emissions and promoting the sustainable management of organic waste, animal manure, and plant residues. Despite its industrial importance and an expanding body of research, critical gaps remain in our understanding of adult BSF chemical ecology—particularly the cues governing mate communication and sexual selection. Addressing these gaps is essential for optimising mass production.

In this context, the present study describes the fine structure of antennal sensilla in male and female BSF using scanning and transmission electron microscopy (SEM, TEM). Electrophysiological single-cell recordings (SCR) were performed to assess the ability of male and female antennae to perceive volatile organic compounds (VOCs) emitted by potential mates and by substrates suitable for mating and oviposition. Behavioural experiments were also conducted to investigate the attractiveness of these VOCs to both sexes.

Our results reveal three types of olfactory sensilla on the antennae, some of which responded to the tested VOCs. Y-tube olfactometer bioassays strongly support the role of conspecific VOCs in mate recognition and sexual selection. Additionally, the present data allow comparisons with previously obtained EAG responses to standard odorants, as well as behavioural insights into habitat selection across different oviposition substrates. These findings advance our understanding of BSF chemical ecology, which is crucial for optimising reproduction and improving global breeding systems.

Investigating the chemical profiles of mechanically injured brood in African honey bees (*Apis mellifera scutellata*) and comparison with the European honey bees (*Apis mellifera mellifera*)

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Keletso MALEBYE, Christian PIRK, Fanny MONDET

Abstract

In honey bees (*Apis mellifera*), hygienic behaviour (HB) is a social immunity trait which can improve disease and parasite resistance in the colony. This behaviour has been bred for economic purposes for decades with conventional selection methods such as the pin-killed brood assay (PKB). While European honey bee subspecies are known to release specific compounds upon injury, the chemical signals driving the hygienic efficiency of the resistant African honey bees remain undefined. To investigate if mechanical injury triggers a distinct chemical response in these two subspecies, we analysed pink-eyed pupae from colonies located in South Africa and colonies located in France. Volatile organic compounds (VOCs) and cuticular hydrocarbons (CHCs) from injured (pin-killed) and non-injured brood were collected via headspace solid-phase microextraction (HS-SPME) and solvent extraction, respectively. We found significant differences in VOC profiles between the two subspecies. However, contrary to findings in European honey bees, the mechanical injury in *A. m. scutellata* did not trigger specific chemical signature changes under the tested conditions. These results suggest a lack of a strong, immediate, injury-induced volatile or cuticular signature, contrasting with findings in some European honey bee subspecies where specific brood volatiles, such as β -ocimene and esters, are often implicated in signalling parasite presence or brood distress. This divergence in signalling suggests that African honey bees may utilize a different suite of defensive adaptations compared to European honey bees, which could explain the resilience of this subspecies against parasites in South Africa.

A biosynthetic survey and a heterologous production platform for molecules from biocontrol fungi

Pablo CRUZ-MORALES (Technical University of Denmark, Peruzm@dtu.dk)

Abstract

Pests are responsible for the loss of up to 40% of global crops. Widespread resistance to pesticides has emerged due to the overuse of a limited set of compounds and targets. Many fungal species form symbiotic relationships with plants while antagonizing insects, nematodes, and bacteria, making them valuable sources of sustainable biocontrol agents and biopesticides. However, despite their potential, only a few species are currently used in biocontrol, and their biosynthetic capabilities remain poorly understood.

Here, we used metabologenomic approaches to catalog the biosynthetic repertoire of 82 plant- and insect-associated species within the Hypocreales order. We annotated over 5,000 biosynthetic gene clusters (BGCs), assigned putative products to more than 1,000 of them, and experimentally linked over 100 BGCs to molecules. In parallel, we established black yeasts as novel heterologous hosts for fungal natural products. These hosts combine the genetic tractability of conventional yeasts with the metabolic robustness of filamentous fungi. We developed genetic engineering tools and automation protocols enabling cheap, efficient, and precise gene integration and genome editing, allowing us to heterologously produce several natural products from biocontrol species.

Our work highlights the vast and underexplored chemical repertoire of biocontrol fungi and demonstrates the potential of black yeasts for systematic discovery, characterization, and production of natural products with pest-controlling activities. We believe this provides a strong foundation for developing sustainable pest control strategies in agriculture.

Effects of ozone pollution on plant-pollinator chemical communication under climate change: the case of the Mediterranean fig tree and its specialized pollinator

Magali PROFFIT (Centre d'Ecologie Fonctionnelle et Evolutive (CEFE) UMR 5175, CNRS, Magali.proffit@cefe.cnrs.fr)

Alice KLOOP, Emilie BALTHAZAR, Solène LIEGEOIS, Emmanuel GRITTI, Joana SAUZE, Clément PIEL, Sébastien DEVIDAL, Benoit LAPEYRE, Finn KJELLBERG, Bruno BUATOIS, Florence NICOLÉ

Abstract

Anthropogenic environmental changes constitute a real threat to pollination and associated ecosystem services. Among these changes, it has been shown that increased levels of atmospheric pollutants such as ozone (O₃) can affect floral odors, a complex mixture of volatile organic compounds (VOCs) emitted by plants once they are present in the atmosphere, and consequently their recognition by pollinators. However, due to its high oxidizing potential, O₃ can also affect the physiology of organisms and thus the emission of floral odors by plants and their perception by pollinators. This threat could be further exacerbated by the increase in temperatures predicted in the coming years. In this study, we examined the impact of O₃ pollution, in the context of climate change, on all stages of chemical communication between plants and pollinators, using the highly specialized interaction between the Mediterranean fig tree and its pollinator. Insect and plant exposures were carried out separately in mesocosms at the European Ecotron in Montpellier, where we simulated realistic peaks of ozone pollution (120 ppb) and temperature increases (+3°C), separately and in combination. We showed that short exposure (3 hours) to each stress factor separately, but also in combination, affects the antennae detection sensitivity to floral VOCs, mobility and survival of pollinators. We also demonstrated that medium exposure (3 days) affects VOC emission by fig tree inflorescences immediately after exposure, but also 24 hours later. Experiments are currently in progress to try to understand, at the molecular level, the mechanisms of action of these two stress factors on VOC biosynthesis, as well as on the chemosensory genes of pollinators.

Climate change alters phloem feeder honeydew composition, reducing parasitoid fitness

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Pablo URBANEJA-BERNAT, Maria SCHULZE-SYLVESTER, Angeliki SYROPOULOU, Caroline MÜLLER, Rabea SCHWEIGER

Abstract

Honeydew excreted by phloem-feeding insects is a key carbohydrate resource for parasitoids and other beneficial insects, yet how climate change alters its nutritional quality and cascades through multitrophic interactions remains unknown. We hypothesized that elevated CO₂ (eCO₂) and water limitation modify honeydew chemistry in ways that impair the fitness of natural enemies relying on this resource. Using a tri-trophic system consisting of grapevine (*Vitis vinifera*), the vine mealybug *Planococcus ficus*, and its parasitoid *Anagyrus vladimiri*, we grew plants under ambient or elevated CO₂ and under well-watered or drought conditions in a full-factorial design. We quantified honeydew production, profiled primary metabolites via GC–MS, and measured parasitoid longevity and egg load when fed honeydew from each treatment. Honeydew quantity was unaffected by treatments, but its chemical composition shifted markedly. Elevated CO₂ reduced key sugars such as sucrose and erlose, whereas drought increased compounds including raffinose and myo-inositol. Parasitoids feeding on honeydew produced under eCO₂ showed reduced longevity and egg load, particularly when honeydew originated from well-watered plants. Our findings reveal that climate-driven changes in plant physiology can degrade honeydew nutritional quality, creating a climate-sensitive nutritional bottleneck at the third trophic level. These results highlight a previously underappreciated mechanism by which global change can impair natural enemy performance and underscore the importance of considering plant-derived food quality when designing resilient biological control strategies in vineyard systems.

Differences in the pheromone composition of two closely related lepidoptera species and the effects of climate change and pollution on insect sexual communication.

Marvin MINIO (University of Eastern Finland, Marvin.minio@uef.fi)

Delia PINTO ZEVALLOS

Abstract

Recognition of intra- and interspecific pheromonal compounds by sympatric species is important for strengthening behavioural and reproductive isolation. It has been suggested that both climate change-related elevated temperatures and air pollution will affect pheromone communication. We have conducted preliminary analyses for the identification of the pheromone of a least studied species within the genus *Plutella*, *P. porrectella*. In Europe, *P. porrectella* co-occurs with *P. xylostella*, a microlepidoptera model species that is a common pest of Brassicaceae species worldwide. In the context of predicted environmental conditions, the differences in the pheromone composition and calling behaviour of these closely related moths have been determined. Preliminary data will be presented and discussed in the context of climate change.

Beet Smells: The Role of Leaf and Root Volatiles in Host Plant Selection by *Pentastiridius leporinus*

Bruna CZARNOBAI DE JORGE (Julius Kühn-Institut (JKI) , Bruna.Czarnobai@julius-kuehn.de)

Jürgen GROSS

Abstract

Sugar beet production in Europe is increasingly constrained by Syndrome Basses Richesses (SBR), a severe bacterial disease of sugar beet and other crops, transmitted by the reed glass-winged planthopper *Pentastiridius leporinus*. SBR is a fast-spreading disease in Central Europe that causes significant yield losses and reduces the absolute sugar content of affected sugar beets. The disease is caused by two specific prokaryotic, phloem-limited pathogens: *Candidatus Arsenophonus phytopathogenicus* and *Candidatus Phytoplasma solani*.

The main challenge in pest management of *P. leporinus* is the absence of effective control options, creating an urgent need to better understand its biology and interactions with host plants.

The primary objective of this study is to identify differences in volatile organic compound (VOC) profiles among sugar beet varieties and to determine whether these differences are linked to attractant or repellent effects on *P. leporinus*. Leaf volatiles were collected from various sugar beet varieties using dynamic headspace sampling and analyzed by GC-MS. Electrophysiological recordings (EAG) were used to identify compounds detected by the antennae of adult planthoppers. Behavioral assays were then conducted to assess the attractiveness or deterrence of selected compounds and variety-specific volatile blends.

In addition to the aboveground cues, we also examined volatile emissions from the rhizosphere to identify which root-derived chemical signals might be detected by nymphal stages living in the soil. Rhizosphere volatiles were collected and compared across sugar beet varieties to find potential underground attractants important for nymphal host location.

By combining chemical analysis, electrophysiology, and behavioral experiments, we aim to identify key semiochemicals involved in host selection both above- and belowground. These results will establish a mechanistic foundation for developing new strategies to support the sustainable management of SBR in sugar beet cropping systems.

Chemical and biological analysis of insect holobionts as a model for interaction and biosynthesis of specialized metabolites

Véronique EPARVIER (CNRS-ICSN, Veronique.eparvier@cirs.fr)

Jérôme MURIENNE, Robin WISSON, David TOUBOUL, Rania HAMIDI

Abstract

The intricate symbiotic relationships between insects and microorganisms play a fundamental role in ecological stability and host fitness. Among social insects, termites exhibit a remarkable association with a diverse microbiome that supports key biological functions, including digestion, immunity, and pathogen defense.

This study investigates the symbiotic interaction between termites and occurring fungal strains of the genus *Scedosporium*, focusing on their potential role in nest protection. Our results demonstrate that *Scedosporium boydii* produces antimicrobial compounds, in particular tyroscherin and its derivatives, which effectively inhibit the entomopathogenic fungus *Beauveria bassiana*. Metabolomic analyses by LC-MS/MS and MS-imaging revealed complex chemical interactions within the termite ecosystem (metaholobionte), with tyroscherin (and its analogues) being widely distributed in the colony and produced only during biotic interactions.

We were able to demonstrate by genomics and metabolomics that *S. boydii* can be detected at different levels of the metaholobiont reinforcing its strong ecological association with these insects. These results underline the importance of microbial symbioses in termite ecology, and highlight the protective role of mutualistic fungi in mitigating biotic threats to termite colonies. These findings underscore the significance of microbial symbioses in termite ecology and highlight the protective role of mutualistic fungi in mitigating biotic threats to termite colonies.

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Beyond the antennae: tarsal chemodetection modulates oviposition in the moth *Spodoptera littoralis*

Sai ZHANG (INRAE, Versailles, France, Saizhang2016@163.com)

Arthur COMTE, Nicolas MONTAGNÉ, Guirong WANG, Emmanuelle JACQUIN-JOLY

Abstract

Insect odorant receptors (ORs) are key elements in mediating the detection of environmental volatiles. While insect ORs are primarily expressed in antennae, some ORs have also been identified in non-antennal tissues, like the ovipositor and tarsi, whose function in chemodetection remains unclear. In this study, transcriptomic analyses across different tissues of the noctuid moth *Spodoptera littoralis* revealed four ORs expressed in the ovipositor, with one additionally expressed in the tarsi. Using the *Drosophila* empty neuron system, we identified ligands for three of the four ORs. Oviposition and four-arm olfactometer behavioral assays demonstrated that most ligands elicited deterrent effects on oviposition and orientation behavior in female moths. To further determine which organ contributes to these behavioral responses, antennal and tarsal ablations were performed prior to the behavioral assays. The results suggest that one of the OR ligands, indole, is detected by the tarsus, while the remaining behaviorally active ligands are sensed via the antennae. Collectively, our findings reveal that olfactory detection in insects could rely on multi-organ integration with distinct, organ-specific functional specializations.

#10683

ECOLOGY & BEHAVIOR: Multitrophic interactions 3

02/07/2026 at 16:30, Ronsard

Effect of nectar-inhabiting microbes on the foraging behavior and performance of insect parasitoids

Antonino CUSUMANO (University of Palermo, Antonino.cusumano@unipa.it)

Abstract

[Keynote talk]

Floral nectar is ubiquitously colonized by microbes among which bacteria and yeasts are the most abundant. These microbes have the ability to alter nectar traits which can, in turn, affect the whole community of flower-visiting insects. There is increasing evidence that nectar-inhabiting microbes affect not only insect pollinators but also insect parasitoids, as microbe-mediated changes in nectar traits can alter their foraging behavior and life-history traits. For example, the production of microbial Volatile Organic Compounds (mVOCs) can affect the attraction of parasitoids to nectar. Furthermore, changes in sugar and amino acid composition due to microbial fermentation can impact parasitoid longevity. In this talk I will highlight the importance of considering the role of nectar-inhabiting microbes in shaping the interactions between parasitoids and their food resources.

Do plant volatiles shape species interactions in agroecological fields?

FOTEINI PASCHALIDOU (INRAE, Foteini.paschalidou@inrae.fr)

Abstract

Plant volatile organic compounds (VOCs) convey chemical information that mediates ecological interactions in plant-insect and plant-plant communication. Plant VOCs are important for biological pest control, as such chemical compounds have an ecological role in regulating pests either by deterring herbivores from feeding or oviposition, or indirectly by attracting natural enemies of herbivores. Plants that receive VOCs from herbivore-infested neighbours may also enter into an “alarmed” state in which they are primed and prepared to respond more strongly to future herbivore attacks. We have studied how VOCs shape plant-insect interactions in different scales from the lab to the field.

We studied whether Oviposition Induced Plant Volatile (OIPVs) emissions from *Brassica napus* enhance defences in non-damaged neighbouring *B. napus* when subsequently infested with *Pieris brassicae* larvae. We show that oviposition triggers the release of specific volatiles, i.e. α -pinene, dimethyl-trisulfide, and limonene, potentially serving as herbivore early warning cues for neighbouring non-damaged plants and we further tested the synthetic mixtures of these three compounds under field conditions to measure their effects on the insect communities.

From pathogenicity to trophic interactions: fungal volatile cues mediate wireworms belowground behavior

Fanny RUHLAND (Chemical and Behavioral Ecology, Gembloux-Agro-Bio-Tech, TERRA, University of Liège, Liège, Belgium, Fanny.ruhland@uliege.be)

Ismahen LALAYMIA, Nolan RÉGNIER, Elise DELAHAUT, Antoine BOULLIS, Stéphane DECLERCK, François J. VERHEGGEN

Abstract

The ban on several soil-active pesticides has encouraged interest in biological control strategies against wireworms. Entomopathogenic fungi (EPF) are promising alternatives, yet the mechanisms shaping their interactions with subterranean pests remain poorly understood. We screened 11 EPF strains for pathogenicity against wireworms during a five-hour direct exposure and monitored mortality for 12 weeks, identifying two potential virulent strains (MANEW: 35% mortality; and OARV: 57% mortality). These strains, together with the non-entomopathogenic fungus *Trichoderma harzianum* (TH), were then encapsulated in biodegradable beads to develop an “Attract-and-Kill” formulation.

We assessed the persistence of pathogenicity after encapsulation and quantified wireworms’ behavioral responses to fungal olfactory cues. Encapsulation preserved the pathogenicity of OARV (55% mortality) and enhanced that of MANEW (64% mortality). Whereas many insects are known to detect and avoid entomopathogenic fungi, we unexpectedly found that beads containing MANEW or TH attracted wireworms.

To decipher the chemical basis of this attraction, we focused on two types of fungal cues known to guide wireworms belowground: CO₂ emissions and volatile organic compounds (VOCs). CO₂ levels did not differ among treatments, but TD-GC/MS analyses revealed a complex blend of 80 compounds (terpenes, aldehydes, alkanes, ketones, alcohols) emitted by the fungi. Multivariate analyses showed distinct odor signatures for each fungus, with several characteristic compounds in MANEW and TH profiles previously described as toxins, bioregulators, or insect attractants.

Finally, we assess the consequences of these fungus–pest interactions for plant protection, in a microcosm experiment. Overall, our findings highlight a previously overlooked mechanism in EPF–host interactions: fungal VOCs can mediate wireworm orientation and may be exploited to enhance the efficacy as soil-based “Attract-and-Kill” strategies.

Parasitoids and their injection components indirectly alter plant responses via their caterpillar host, affecting later-arriving parasitoids

Sarah KALISVAART (Wageningen University, Sarah.kalisvaart@wur.nl)

Erik POELMAN, Maximilien ADAM, Alexander HAVERKAMP

Abstract

Herbivorous insects often change their host plant's phenotype when feeding, which may influence how other organisms interact with this plant. Upon parasitism, many parasitoids inject a combination of polydnavirus and venom into their host. In doing so, the behaviour and physiology of the host are modified. Since plants perceive herbivory through damage patterns and salivary components, parasitised herbivores may elicit different responses compared to their unparasitised counterparts. This plant-mediated effect of parasitism and its injection components can affect other insects that interact with the induced plant. However, most evidence for such plant-mediated effects comes from greenhouse or laboratory studies. Few studies have investigated the effect on the third trophic level.

In our study, we investigated the plant-mediated response of parasitism and its associated injection components, and how these responses affect subsequently arriving parasitoids. In greenhouse and open field experiments, we exposed wild *Brassica oleracea* plants to herbivory by unparasitised *Pieris brassicae* caterpillars, caterpillars parasitised by *Cotesia glomerata*, and caterpillars injected with polydnavirus and/or venom, and we used uninduced plants as control. 7 days after induction, *P. brassicae* were removed and plants were subsequently induced by *Plutella xylostella*, *Mamestra brassicae* or young *P. brassicae* caterpillars. We then observed the behaviour of their corresponding parasitoids: *Diadegma semiclausum*, *Microplitis mediator*, and *C. glomerata*. Additionally, the volatile responses of plants induced by our treatments were investigated,

Our results show that parasitism, as well as polydnavirus and venom, alter plant-responses in ways that affect subsequent parasitoids, even when the parasitoid targets different hosts. These findings reveal that parasitoid- or even injection component-induced modifications can cascade through plant-mediated interactions, highlighting an underappreciated mechanism shaping multitrophic communities. These modulating effects deserve attention in future studies that investigate the dynamics of plant-arthropod communities.

Rhizosphere endophyte *Trichoderma virens* shapes maize defence and reduces performance of the herbivore *Helicoverpa armigera*

Michael ROSTÁS (Agricultural Entomology, Department of Crop Sciences, University of Göttingen, Germany, Michael.rostas@uni-goettingen.de)

Noor Agha NAWAKHT, Mohammad ALHUSSEIN, Artemio MENDOZA-MENDOZA

Abstract

Plants must continuously adjust their defence responses to cope with diverse biotic challenges in agroecosystems. Beneficial root colonizing fungi such as *Trichoderma virens* can modulate both direct and indirect plant defences. Here, we investigated how endophytic colonization by *T. virens* and its terpenoid deficient *vir4* knockout mutant influence maize (*Zea mays*) interactions with the herbivore *Helicoverpa armigera*. Caterpillars feeding on maize colonized by the wild type strain gained significantly less weight, indicating enhanced direct resistance dependent on the *vir4* gene cluster. Untargeted and targeted metabolomic analyses showed that root colonization by the wild type, but not the mutant, led to the accumulation of two fungal sesquiterpenoids, heptelidic acid and hydroheptelidic acid, in maize roots, with only hydroheptelidic acid detected systemically in leaves. Incorporation of heptelidic acid into artificial diet caused antibiotic effects on *H. armigera* larvae, whereas hydroheptelidic acid showed no detectable activity and was thus excluded as the causative factor for reduced herbivory on wild type colonized plants. Root colonization by the wild type strain also induced distinct shifts in the maize shoot metabolome compared with the *vir4* mutant, which were further amplified by herbivory. Several phenylpropanoid metabolites with putative defensive functions were strongly upregulated. Although colonization moderately altered the composition of herbivore induced plant volatiles, total volatile emissions and the olfactory attraction of the predatory bug *Macrolophus pygmaeus* remained unaffected. Together, our results show that enhanced maize resistance to herbivory arises primarily from endophyte induced reprogramming of plant defence metabolism rather than from direct effects of fungal derived compounds on the leaf feeding insect.

Companion planting oilseed rape with faba bean rewires plant chemistry and impacts multi-trophic-interactions

Léa BOLIS (Agroscope / University of Neuchâtel, Lea.bolis@unine.ch)

Ivan HILTPOLD, Sergio RASMANN

Abstract

Associative cropping of oilseed rape (*Brassica napus*) with faba bean (*Vicia faba*), traditionally used for weed control and nitrogen supply, has recently been shown to help reduce pest pressure from the cabbage stem flea beetle (CSFB, *Psylliodes chrysocephala*), an important pest of oilseed rape. The mechanisms underlying these pest-regulating effects remain poorly understood and are likely multifactorial. Recent laboratory and field studies revealed shifts in defense metabolites of associated oilseed rape and faba bean plants as compared to sole crops, driving pest behavior and associated host location mechanisms. Moreover, the presence of faba bean was shown to enhance parasitism rates of CSFB larvae, impacting pest pressure through the regulation and support of multi-trophic interactions. Together, these findings shed light on the complex chemical and behavioral processes driving pest dynamics in diversified oilseed rape fields.

Effect of residual streams from black soldier fly farming on single, sequential or simultaneous herbivory by chewing and phloem-feeding insects

MARIA ROSARIA CHIANESE (University of Naples Federico II, Department of Agriculture, Portici, Italy, Mariarosaria.chianese@unina.it)

GABRIELE BOLLETTA, ILARIA DI LELIO, MARCO GEBIOLA, FRANCESCO PENNACCHIO, ERIK H. POELMAN

Abstract

The industrial farming of the black soldier fly, *Hermetia illucens*, to produce feed ingredients results also in side streams, such as frass, pupal exuviae and dead adult bodies. These byproducts, given their chitin content, could also be used as biostimulant of plant growth or resistance to insect attack. This study investigates how these residual streams from black soldier flies (BSF) influence plant growth and defence responses to insect herbivores under single or dual attack in *Brassica oleracea*.

Plants were grown in soils receiving either mineral NPK fertilizer only (control) or NPK supplemented with BSF frass, exuviae, or adults in powder form. At the eight-leaf stage, plants were exposed to single, sequential, or simultaneous herbivory by two specialist herbivores with distinct feeding modes: the chewing caterpillar *Pieris brassicae* and the phloem-feeding aphid *Brevicoryne brassicae*. We quantified plant growth and biomass, herbivore performance (development, weight, and fecundity), and expression of key genes associated with defence pathways regulated by jasmonic acid (JA) and salicylic acid (SA).

BSF-derived products enhanced early vegetative growth, with exuviae and adult residues producing taller plants than the control. Herbivory reduced plant biomass, particularly under sequential aphid–caterpillar attack. Notably, frass and adult carcasses increased plant tolerance under sequential herbivory, allowing plants to maintain higher fresh and dry biomass. Herbivore responses were treatment-specific: pupal exuviae enhanced caterpillar growth and pupal mass following prior aphid infestation, while frass primarily promoted plant tolerance without increasing caterpillar-induced biomass loss. Aphid performance showed strong fertilizer–herbivory interactions, with frass, exuviae, and adults differentially modulating aphid population growth depending on prior or concurrent caterpillar feeding.

Overall, BSF-derived residual streams differentially shaped plant defence responses and herbivore performance, acting not only as biostimulants but also modifying JA-SA defence dynamics and plant tolerance, with practical implications for sustainable agriculture.

Insect Long-Distance Dispersal: Mechanisms, Impacts, and Responses to Global Change

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Abstract

Each year, quadrillions of insects disperse over long distances across continents and oceans, connecting ecosystems worldwide. Long-distance dispersal (LDD) represents one of the most critical yet poorly understood aspects of insect ecology, with profound implications for biodiversity conservation, ecosystem functioning, and pest management. This presentation synthesizes how recent breakthrough discoveries are revolutionizing our understanding of how insects overcome geographical barriers through LDD and respond to rapidly changing environments. We explore the ecological and evolutionary implications of LDD, including its role in colonization, species range expansion, and disease vector dynamics. We describe how recent methodological advances including isotope geolocation, pollen metabarcoding, vertical and meteorological radar, and niche and atmospheric dispersal modeling have enabled, for the first time, the reconstruction of insect LDD events and the unveiling of surprising dispersal mechanisms that challenge traditional assumptions about insect movement ecology. We examine how global change is fundamentally altering insect dispersal patterns and the ecological consequences of these alterations. Finally, we highlight critical knowledge gaps and research priorities, including the need for mechanistic models linking climate variables to dispersal capacity, integration of spatial and temporal approaches, and development of climate-informed conservation and pest management strategies.

Cotton bollworm (*Helicoverpa armigera*) has become a threat to maize crops in southeast Romania

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Lidia CANĂ, Maria TOADER, Sebastian BRUMĂ, Cristina RADU, Paula-Lucelia PINTILIE, Luxița RÎȘNOVEANU

Abstract

Cotton bollworm (*Helicoverpa armigera*) is a polyphagous pest that can produce higher economic damage to maize, soybean, or cotton worldwide except the North American continent. In Romania till ten years ago was considered a minor pest. We are monitoring the population of this pest in south-east Romania, using pheromone traps from 2020 to 2024, and we study the behavior of nine maize hybrids from different maturity groups to this pest attack in 2024. We analyze the maize hybrids' yield for total aflatoxins (B1 + B2 + G1 + G2) level. The monitoring and field assessments were made in south-east Romania, Călărași County, at the NARDI Fundulea. During the monitoring period, from 2020 to 2024, air temperature was higher than average in the summer months while rainfall was below average, except in June 2021. Total captured moths in the traps were 246 in 2020, 406 in 2021, 5064 in 2022, 1024 in 2023, and 4145 in 2024. In the middle of July 2022, the average captured moths per trap were 483.3; in the middle of September, it was 589.0 catches. In 2024, in the last 10 days of July, the average captured moths per trap were 311.7, in the last 10 days of August, it was 358.0, while in the middle of September, it was 362.3. In 2024, at the beginning of August, the attack incidence of corn earworm on maize hybrids ranged from 43.75 to 53.75 %, and on 13 September, it was 100 % at all hybrids. This is the first report from southeast Romania that mentioned a higher population of cotton bollworm in the late summer and beginning of autumn, and the first report that mentioned high pest attacks on maize cobs in September. In 2024, the aflatoxin was higher than maximum limits (Reg. EC 1881/2006) at all maize hybrids.

Assessing the dispersal of *Monochamus galloprovincialis*, the vector of the invasive pinewood nematode, in a mosaic of land-covers in southwestern France

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Hervé JACTEL, Inge VAN HALDER, Jean-Baptiste RIVOAL, Christelle ROBINET

Abstract

The pine wood nematode (PWN), *Bursaphelenchus xylophilus*, is an invasive plant pest responsible for pine wilt disease. Originally from North America, it has spread to Asia and Europe and was detected for the first time in France in November 2025. In Europe, the longhorn beetle *Monochamus galloprovincialis* is the only known vector of PWN. Although previous studies have estimated the dispersal capacity of *M. galloprovincialis* in homogeneous landscapes composed of pine stands, little is known about its movement in heterogeneous landscapes that include multiple forest and non-forest land covers.

We developed an individual-based model (IBM) calibrated with a mark–release–recapture dataset collected in France in 2018 to estimate key parameters of beetle's dispersal behaviour, including flight difficulty and habitat preferences among major land-cover types, and the detection radius governing its response to adjacent land-covers. Model predictions were evaluated using an independent dataset from France in 2023, representing a landscape with different proportions and spatial arrangements of broadleaves, mixed forest, clear-cuts, and pine stands.

Preliminary results indicate contrasting movement responses across land-cover types and highlight the importance of landscape heterogeneity in determining dispersal trajectories. We applied this model to assess the potential spread of the pinewood nematode from the new infested site in France, in order to support surveillance prioritization.

This modelling framework provides a basis for predicting the potential spread trajectory of vector beetles of PWN following PWN's introduction into a new area and can support early-stage management and surveillance planning.

Modelling tools supporting analysis and management of *Popillia japonica* populations

Anna SIMONETTO (Università degli Studi di Brescia, Anna.simonetto@unibs.it)

Iris BERNARDINELLI, Alessandro BIANCHI, Rita BONFANTI, Mariangela CIAMPITTI, Ruggero COLLA, Eric GRANGE, Paola GOTTA, Federica MIGLIORINI, Davide VENANZIO, Gianni GILIOLI

Abstract

Popillia japonica Newman is an invasive pest of major economic and ecological concern, whose ongoing spread in Europe has highlighted the need for reliable tools to support monitoring and management strategies. Initially confined to Northern Italy, *P. japonica* is now recorded in Austria, Slovenia, Germany, Portugal (Azores), and Switzerland. Since 2018, the University of Brescia has been developing a composite modelling approach to improve understanding and prediction of the dynamics of this invasive pest.

The analysis of data from the outbreak in Lombardy (2015-2019) allowed the development of a phenological model, a larval niche model, and a spread model. The *P. japonica* phenology was described using a stage-structured physiologically-based model with nonlinear temperature-dependent functions, including diapause termination. An ecological niche model was applied to estimate the probability of larval presence by integrating land use, soil characteristics, meteorological variables, and infestation history. The dynamics of local population growth and spatial spread were investigated through a reaction–diffusion model.

The phenological model was calibrated and validated using extensive time series (2020-2024) from several Italian regions, ensuring its robustness. The local growth and the spread models were calibrated using data on the spread of *P. japonica* in Lombardy.

By integrating biological knowledge, large amount of sampling data, and spatially explicit modelling approaches, this work offers a replicable quantitative approach to support the design of efficient monitoring strategies, and the planning of control measures. The result of this extensive work is made available to relevant stakeholder by an online DSS allowing to estimate phenological dynamics according to meteorological data and context information.

Adaptive management for *Coenagrion castellani* (Odonata: Coenagrionidae) conservation: Insights from long-term monitoring in agricultural landscape

Gianandrea LA PORTA (University of Perugia, Gianandrea.laporta@unipg.it)

Matteo PALLOTTINI, Silvana PIERSANTI, Manuela REBORA

Abstract

Despite internationally and nationally set goals and environmental policies, insect biodiversity continues to decline, with a significant increase in the number of threatened species. The Habitats Directive and Natura 2000 network represent the primary framework for species conservation across Europe. LifeIMAGINE Umbria (LIFE19 IPE/IT/000015) is a project through which the European Commission is funding the protection and restoration of the environment and reversing the biodiversity loss in the Italian Umbria region. The project focuses on several threatened habitats and species, including the endemic damselfly *Coenagrion castellani*. Since 2017 *C. castellani* populations have been investigated during the flight season in small freshwater bodies running through intensively farmed lowlands, areas that are commonly overlooked by both the Water Framework Directive and biodiversity research programs. Multiple aspects of the biology and ecology of this declining damselfly are being monitored, including sex ratio, home range, routine movement, dispersal, survival, and capture probability. Over 9 years, a total of 5698 adult individuals were marked (1436 females and 4262 males), showing that recaptured individuals had a low vagility, with a high proportion of individuals exhibiting philopatric behavior. The LifeIMAGINE project aims to assess the conservation status of the species in the area, identifying population trends, and analyze how the species interacts with the farming management practices. Through its activities, the project has been instrumental in developing guidelines and a management plan for drainage ditch maintenance in colonized areas. These establish critical measures and evidence-based practices that provide a foundation for effective in-situ conservation of this threatened damselfly.

Rapid Spread and Expansion of *Rachiplusia nu* (Lepidoptera: Noctuidae) in Brazilian Soybean Fields

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Abstract

Climate change, species invasion, and pest outbreaks are among the top concerns for biodiversity in the near future, with direct effects on sustainable food production. The ongoing climatic shifts may drive adaptation and distribution expansion of insects, particularly for pest species, threatening tropical crops such as soybean in Brazil. Recently, the southern soybean pest *Rachiplusia nu* was reported in different Brazilian regions. The lack of records outside southern Brazil in extensive soybean surveys and the scarcity of historical records do not allow clear conclusions about expansion. Thus, we aimed to investigate the occurrence and distribution of *R. nu* over the years, seeking evidence of expansion through an extensive survey conducted from 2019 to 2024 across all Brazilian soybean areas. The dataset included season, regions, soybean technology (Bt-Cry1Ac-soybean; non-Bt-soybean), and presence history in the previous year, grouped by regional scale. A mixed model with a step-up approach was applied, incorporating zero inflation, spatial technology interactions, and random intercepts and slopes. The results suggest a straightforward expansion process, with increasing occurrence over the years and decreasing structural zeros. The expansion began in the southern regions, moved through the central areas, and reached the northern and northeastern regions, indicating environmental adaptation. Regions differed in their suitability, as indicated by the marginal effects. The difference in growth rates could reflect an underlying adaptive process or differences in the sizes of the founder populations. Bt soybean technology has acted as a barrier to local invasion, as the species first arrived in RR soybean, and Bt fields showed substantially lower occurrence. Bt technology also showed stronger density dependence relative to non-Bt, suggesting that local adaptation is required before establishment. Overall, these findings support the hypothesis of species expansion and climatic adaptation across Brazil and may serve as a model for similar demographic events in pest species.

Interaction nestedness mediates network assembly and affects resulting diversity in host-parasitoid microcosms

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Jan HRCEK

Abstract

Understanding how diversity is maintained in ecological networks is one of the key questions in ecology. Network structure is thought to have strong effects but disentangling trait-based and species identity-based effects from structural effects is often hard. Here we used sensitivity data to simulate small networks based on known interactions in our *Drosophila*-parasitoid system. From this data, we chose species assemblages from a defined pool of species with strong differences in predicted nestedness and modularity to build experimentally and observe in a microcosm setup. Our results show that species richness is lower for networks with a higher predicted nestedness after two months. Additionally, variability in species composition was already lower for networks with a higher predicted nestedness after one month. These results suggest that the constraints added by the highly nested original structure influenced the network assembly. Stronger constraints lead to similar responses and reduces the possibilities for networks to respond to changes such as species loss or interaction rewiring.

Drivers of population dynamics of bark beetles under climate change relating to sustainable forest management

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Ana SEIFERT BARBA, Nikica OGRIS

Abstract

In recent decades, changing climate conditions have put increasing pressure on forests, making them more prone to bark beetle outbreaks. Large-scale disturbances such as windthrows and droughts have become more frequent and intense, while less common disturbances from the opposite end of the spectrum, such as ice storms, also occur. One of the most important and valuable tree species in Central Europe is the Norway spruce, which is highly vulnerable to attacks by the European spruce bark beetle (*Ips typographus*). Bark beetle outbreaks are particularly influenced by factors such as increased spruce density, the occurrence of abiotic disturbances, forest management practices, altitude, and soil properties. These abiotic disturbances, combined with unsustainable forest management, can significantly increase the potential intensity of outbreaks. The greater the disturbance intensity, the higher the likelihood of repeated outbreaks in the same area in subsequent years. Therefore, understanding the drivers behind these outbreak patterns is crucial.

One of the countries that has been strongly affected by climate change is Slovenia. Slovenia is a small but heterogeneous country that has experienced several abiotic disturbances in recent decades. In addition, it possesses a unique 30-year database of sanitary felling of Norway spruce due to bark beetle infestations, recorded at the forest subcompartment level. Altogether, this makes Slovenia an excellent case study to understand drivers of bark beetle outbreak and model the population dynamics. We calculated the temporal autocorrelation of sanitary felling in Slovenia and modelled this autocorrelation under different forest management types and disturbance regimes. The results will be discussed in relation to disturbance types driven by climate change and forest management practices.

Multiple linear regression models for predicting the 1st and 3rd nymphal stages of the American grapevine leafhopper (*Scaphoideus titanus*) in Austria

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Gudrun STRAUSS

Abstract

The American grapevine leafhopper (*Scaphoideus titanus*) transmits the economically important grapevine yellows disease flavescence dorée in Europe. Since its introduction in Austria, the leafhopper spread across various wine-growing regions. To determine population size and distribution, a time-consuming monitoring program is currently in place. Forecasting models can be helpful in improving the planning of monitoring and control measures. In this context, prediction models to forecast the first seasonal occurrence of the 1st and 3rd nymphal stages of *S. titanus* were generated by applying stepwise multiple linear regression (MLR) analysis. The prediction models were calibrated and validated using monitoring data (2013 to 2024) from 13 monitoring sites in 3 federal provinces in Austria. The generated prediction models consist of variables derived from daily measurements of mean and/or maximum air temperature and precipitation. The validation of the generated MLR models displayed an R^2 of 0.87 and 0.78, and RMSE of 2.30 and 2.92 for the prediction of the first seasonal occurrence of the 1st and 3rd nymphal stages of *S. titanus*, respectively. Predicting the 3rd nymphal stage proved more difficult, likely due to additional development-influencing factors (e.g., biotic interactions) that were not included in the MLR model. In addition, the MLR models were calibrated for a large area (southern Styria to northeastern Lower Austria), encompassing diverse site conditions (e.g., sea level, sun exposure, soil composition, microclimate). These differences complicated the generation of highly accurate prediction models. Nevertheless, the models achieved high to good accuracy, with 93% of 1st nymphal stage predictions and 78% of 3rd nymphal stage predictions (2013-2025) within the optimal prediction range (± 4 days deviation between observed and predicted occurrence). To further enhance prediction accuracy, it is important to regularly update the models with datasets from years with extreme weather events.

A new vision of modelling in IPM: general optimisation problems

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Emanuele GARONE

Abstract

Integrated pest management can be supported by mathematical models, as they are promising tools to foresee the evolution of the infestations and to plan opportune strategies. Over the years, many models have been proposed to describe the biology of many species, but their implementation is still scarce. We wonder why their application is still limited. Our recent studies pointed out that a model describing the interactions in an agroecosystem is not enough, as i) it is almost impossible to estimate the initial conditions (initial abundance and time zero for the infestation), ii) the effect of treatments is usually not accounted by the models, and iii) the intervention thresholds are usually defined empirically from biological studies. This study introduces a new concept and a new vision in modelling terrestrial arthropods for agroecosystems and ecosystems management purposes. According to this concept, the IPM process can be seen as an optimisation problem composed of a multitrophic model and of a mathematical description of the control actions (inputs), of the constraints (e.g., regulation, technical aspects), and of the costs and revenues. Moreover, the scheme can be updated based on field monitoring, using state-estimation techniques. According to this new vision, agroecosystems and ecosystems can be seen as dynamic systems where we can regulate the inputs to obtain the desired output. Through optimisation, we provide the minimal inputs at the optimal time to maximise the output. This new vision combines entomology with applied mathematics, metrology, and optimal control, building bridges among different scientific communities.

Automatic traps foster the monitoring and prediction of bark beetle swarming

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Abstract

Pest insects, such as bark beetles, are typically monitored using pheromone traps emptied at regular intervals to assess infestation risk. However, this system involves multiple drawbacks like substantial costs, limited spatial coverage, and delayed data availability. To overcome these shortcomings, we developed and implemented an automatic pheromone trap for continuous, high-resolution monitoring of swarming activity in the three economically important bark beetle species *Ips typographus*, *Pityogenes chalcographus*, and *Pityokteines curvidens*. The system automatically records and transmits real-time data on swarming intensity along with climatic parameters, considerably reducing operational costs and delivering timely, reliable information for forest managers. Data from three years across multiple sites along an elevation gradient in Southwest Germany were further used to calibrate predictive swarming models with temperature, global radiation, day of year, pheromone release, and study site as predictors. Temperature emerged as the dominant driver of swarming intensity, while other factors contributed to finer-scale temporal and spatial variation. The resulting models reliably predict relative swarming intensity at the stand level, though absolute trap catches still require local calibration. Integrating automated trap data into digital forest health tools enables area-wide, near real-time assessments of bark beetle activity and infestation risk. Such systems not only eliminate the need for manual trap servicing but also enhance outbreak forecasting and early intervention capabilities. Combined with additional information on stand structure, drought, or past infestations, these models represent a major step toward the digitalization of pest monitoring, thereby offering an efficient and scalable solution for proactive bark beetle management, supporting targeted and timely management actions to mitigate eruptive outbreaks.

The role of climate and trophic resource availability in predicting the establishment of *Spodoptera frugiperda* populations in Europe

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Abstract

The fall armyworm (*Spodoptera frugiperda*) is an invasive alien species of major agricultural concern and is currently regulated as a Union quarantine priority pest in the European Union. This highly polyphagous species is capable of long-distance migratory flights and has rapidly expanded from the Americas to Africa, Asia and Oceania, causing severe crop losses. More recently, it has been detected in Europe, with populations apparently established in some parts of Greece and Cyprus, whereas populations reported from Romania are officially considered transient. Current assessments of its potential establishment in Europe largely rely on climate variables, rarely incorporating the explicit presence and seasonal availability of host plants, despite their central role in determining establishment success for phytophagous invasive species.

We implemented a continent-wide, physiologically based demographic model for *S. frugiperda* to estimate its potential for establishment across Europe. The model integrates temperature-dependent development, mortality, and fecundity rates, while explicitly accounting for spatiotemporal host plant availability. Temperature inputs were obtained from a multi-year, high-resolution hourly climate reanalysis (ERA5_Land, 2010–2024 period, 0.1° grid resolution), whereas host availability was represented by combining spatial information on crop and habitat distributions with a satellite-derived plant phenology index capturing intra-annual vegetation dynamics.

Population dynamics were simulated independently for each grid cell across Europe, with potential establishment defined as the ability of a population successfully producing viable offspring with a likelihood of continued survival, including during the winter. Our results indicate that incorporating host plant availability refines the estimation of potential establishment areas. These estimates, informed by both climatic factors and host availability, can improve the planning of risk-based surveillance and support preparedness measures aimed at mitigating the impacts of future *S. frugiperda* incursions across Europe.

Science to practice: The Austrian Bark Beetle Dashboard supports forest management in a warming climate based on established and novel model approaches

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Sigrid NETHERER

Abstract

Outbreaks of the European spruce bark beetle (*Ips typographus*) have increased across Europe due to climate change and pose major challenges for forestry. Over the past decade, Austria has experienced two bark beetle outbreaks of unprecedented intensity. The first one was mainly triggered by prolonged drought in northern Austria at altitudes below 600 m. In contrast, the second one emerged as a consequence of extensive abiotic damage over three consecutive years in southern Austria at high altitudes above 1000 m. This situation demonstrates that bark beetle outbreaks increasingly challenge forest management in both secondary spruce forests at lower elevations and near-natural spruce forests at montane to subalpine altitudes. These outbreaks highlight the strong demand for operational risk assessment and early warning systems to improve pro-active bark beetle management and preserve Austria's forests for the future.

To provide forestry with accessible and spatially explicit information, we launched the Bark Beetle Dashboard as a joint project between BOKU University and the Austrian Research Centre for Forests, in May 2024. This map server synthesises over two decades of bark beetle research, offering valuable support for *I. typographus* management in the form of several maps with high spatial and temporal resolution, covering the whole of Austria. The dashboard currently provides the daily updated *I. typographus* development status, the current water supply, as well as the susceptibility of forests to bark beetle disturbance, and bark beetle damage of preceding years. The recent AI-driven advances in remote sensing-based detection of tree species and forest disturbances push forward the ongoing development of machine learning-based disturbance probability models with a spatial resolution of 10 metres, which enable one-year disturbance predictions in the future. The Bark Beetle Dashboard demonstrates how scientific knowledge can be transferred into practice and provides a robust foundation for incorporating new findings.

New data on *Simulium maculatum* Meigen in southern Kazakhstan: biogeography, bionomics

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Abstract

New data on *Simulium maculatum* Meigen in southern Kazakhstan: biogeography, bionomics

The study of the species composition and distribution of black flies (Diptera: Simuliidae) in southern Kazakhstan has become relevant due to an unprecedented increase in their numbers. Mass reproduction of black flies in southern Kazakhstan were first observed in 2012 and coincided with the start of operation of the large hydrological facility - the Koksarai counter-regulator on the Syrdarya River. Prior to this period, black flies were present along the Syrdarya but occurred in low numbers and did not cause significant harm. The presence of *S. maculatum* as the dominant hematophagous species in southern Kazakhstan is reported for the first time, which is confirmed by both morphological and molecular-genetic analyses. The diagnostic features of the larva, pupa, and imago are described in detail, including the structure of the larval head capsule, pupal cocoon, and genitals of both sexes. Species identification was performed using the morphological keys of Rubtsov and Yankovsky, and taxonomic classification was confirmed using the structure proposed by Adler. Molecular confirmation of *S. maculatum* was performed through DNA analysis. The species was found upstream and downstream of the Syrdarya River from the Koksarai counter-regulator, with a gradual decrease in the number of aquatic stages to complete absence as the distance from the hydraulic structure increased.

Black flies are disease carriers, active and aggressive blood-sucking insects of mammals and humans. In connection with the increasing black fly population, alongside studies of species composition and distribution, the problem of regulating their numbers has become a pressing issue. During 2023–2025, extermination measures have been implemented. Technologies for the application of a bacterial preparation based on *Bacillus thuringiensis* var. *israelensis* were developed, achieving a certain level of effectiveness (as evidenced by a reduction in larval density).

Gaining insight on the off season biology of the olive fruit fly paves the way for developing and implementing novel control approaches

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Polychronis REMPOULAKIS, John VONTAS

Abstract

We delved into the seasonal biology of the olive fly (*Bactrocera oleae*), a predominantly monophagous pest of the esteemed crop, olives by reviewing recent and older literature. Our focus was on the less extensively studied off-season (winter and spring) phenology of this pest. We assert that the spring generation plays a pivotal role in the subsequent population growth of the pest. While winter severity influences the survival patterns of the overwintering generation and the density of the founding population in spring, the abundance of breeding resources in spring (remaining fruit on trees) is crucial for the development of the spring generation, thereby significantly impacting population growth later in the season. We present a model that captures the interactions between olive flies and olive fruit during spring and elucidates the cyclic patterns observed in the population dynamics of the fly across successive years. Additionally, we introduce novel approaches to the off-season management of olive fly, which presents a sound and environmentally friendly strategy for controlling this devastating pest.

Guidelines for modelling invasive species distributions: the case study of *Drosophila suzukii*'s continued expansion in a warming climate

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Michael ØRSTED

Abstract

Climate change is rapidly causing the redistribution of many species' ranges, impacting species communities but potentially also our societies. This is especially evident in invasive insects, which often threaten native species, agriculture or human health. To estimate potential distribution changes of such insects, species distribution models (SDM) are an often-used tool. However, there is no standard procedure for modeling invasive insects.

As a case study, we focused on the invasive fruit fly, *Drosophila suzukii*, which is now established in most continents with major economic consequences for the fruit and berry production industry. We combined updated occurrence records (n=3569 expanding the known distribution), with bioclimatic predictors in a MaxEnt binary classifier algorithm. We designed the model specifically for invasive species (iSDM) in terms of background point selection and binarizing model predictions. Using envelope-models across multiple global circulation models (GCMs) and shared socio-economic pathways (SSPs), we also predicted the potential future distribution of *D. suzukii* 2041-2060 and 2061-2080.

We found that our iSDMs predict the current distribution of *D. suzukii* with high reliability and predicted suitable habitats in high-latitude areas which were previously considered low-risk zones. The future distribution showed clear spatial and temporal patterns predicting a continued poleward expansion and range retractions closer to the Equator through time. This expansion seem consistent with recent records in Scandinavia, Canada, Argentina and lately the Faroe Islands.

Our study highlights that specifically tailoring SDMs for invasive species should be considered best practice, instead of relying on default settings and common practice from non-invasive SDM. This will in turn improve the precision of predictions on invasive species distribution both in the current and future climate. This could make SDM a more reliable tool for the management of invasive species and potentially help mitigate the effects of these insects on society.

A probabilistic formalism linking multiple equilibria and biodiversity in ecological models

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Abstract

Ecological communities do not always settle into a single predictable configuration. Models such as Lotka-Volterra or replicator dynamics often predict several possible stable states. Slightly different initial conditions may then lead to different configurations: one state where only a few species persist, and another where many coexist. This phenomenon, known as multistability, is central for understanding robustness, species coexistence, and sudden shifts in diversity. Yet, standard practice typically treats the equilibria obtained from different systems collectively losing information about how many stable states can arise within the same ecological scenario and how diverse these states are.

We introduce a system-level probabilistic formalism that captures this hidden structure and could be applied to a wide range of models, drawing inspiration from hurdle and zero-inflated models. Each ecological system is viewed as generating a distribution over its possible stable outcomes. This allows us to quantify jointly whether such equilibria exist, how many does the system admit, and how biodiverse these states are. This unified perspective reveals patterns that remain invisible when equilibria are analyzed individually or pooled across systems.

Our framework offers a new way for studying the robustness of community structure, the likelihood of alternative outcomes under small changes in initial conditions, and the potential for shifts between states of low and high diversity in entomology and beyond.

A coupled plant–insect model for the asparagus beetle *Crioceris asparagi*

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Daniele BEVACQUA, Davide REDANA

Abstract

Crioceris asparagi is a specialist herbivore of asparagus whose **biology** and **population dynamics** remain insufficiently understood. By feeding on the fern during the growing season, larvae and adults affect photosynthetic assimilation and can substantially reduce growth in the following years. Although some studies exist, **major aspects of asparagus beetle ecology and of its interactions with crop management practices remain unclear**. Our objective is to achieve a clearer understanding of this insect's population dynamics in relation to the perennial plant's growth and reserve–allocation processes, particularly given that the timing of fern emergence can be modulated by extending or shortening the spear-harvesting period.

Depending on climate and cultivation strategies, growers may harvest part or all of the early spears before allowing the remaining stems to develop into fern. This biomass is **essential for the beetle**, which completes its development on it, **and for the plant**, which relies on the fern for photosynthesis and the accumulation of carbohydrate reserves that sustain spear production in the next season. Consequently, asparagus phenology influences the development and reproduction of *C. asparagi*, while herbivory by the beetle can reduce fern biomass and compromise reserve accumulation, potentially lowering subsequent growth.

To investigate these **reciprocal effects**, we build on an existing mathematical model of fern growth and carbon reserve dynamics in *Asparagus officinalis* and **develop a population dynamics model** of *Crioceris asparagi* based on available scientific knowledge. Coupling these two components enables **the exploration of feedbacks** between plant carbon dynamics and herbivore populations under different harvesting regimes and environmental conditions.

This integrated approach **improves our understanding of plant–insect interactions** in perennial crops, **highlights key knowledge gaps**, and **provides a framework for evaluating management strategies** aimed at reducing damage while promoting **more sustainable** production.

A model describing population dynamics of *Philaenus spumarius* (Hemiptera: Aphrophoridae)

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Anna SIMONETTO, Enrico BERTOLDI, Paola GERVASIO, Andrea DE FRANCESCO, Crescenza DONGIOVANNI, Vincenzo CAVALIERI, Gianni GILIOLI

Abstract

The meadow spittlebug, *Philaenus spumarius*, is considered the main vector of *Xylella fastidiosa* (*Xf*) in European outbreaks, an invasive bacterial plant pathogen that poses a serious threat to numerous economically important crops. Management options targeting *P. spumarius* populations are one of the primary strategies to mitigate the spread of *Xf* outbreaks, and therefore quantitative tools capable of accurately representing vector phenology and abundance are essential to support surveillance and guide the timing of control interventions. We developed a stage-structured, physiologically based demographic model (PBDM) to simulate the population dynamics of *P. spumarius*. The model is formulated as a system of Kolmogorov partial differential equations that track population density across chronological time and physiological age. Five developmental stages are represented: eggs, early nymphs (N1–N2), late nymphs (N3–N5), pre-reproductive adults, and reproductive adults. Transitions between stages are driven by stage-specific, temperature-dependent development functions, whereas mortality incorporates intrinsic (temperature-related) and extrinsic (e.g., competition) components. Egg diapause and female ovarian parapause are explicitly modelled as environmentally regulated processes, and fecundity is described by an age-dependent function. Biodemographic parameters were estimated from literature and monitoring data collected in northern and southern Italy. Model performance was evaluated through validation against independent field datasets. The calibrated model provided consistent biological estimates of key parameters and reproduced major patterns of observed population dynamics. In particular, it accurately predicted the timing of the N3–N5 peak and the onset and peak of adult stage, critical periods for effective vector control. The incorporation of mechanistic physiological responses to environmental conditions allows the model to simulate population dynamics across diverse climates at fine spatial and temporal resolutions. When integrated into *Xf* epidemiological frameworks, this PBDM provides a valuable tool to support vector surveillance and monitoring, guide intervention timing, and optimize Integrated Pest Management (IPM) strategies across Europe.

Comparaison of a generic lepidoptera model with digital traps monitoring for 4 major's lepidopteran in grapes, apples and ear for 5 years of counting in Europe.

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Abstract

This study investigates the flight dynamics of four major lepidopteran pests in Europe — *Lobesia botrana*, *Cryptoblabes gnidiella*, *Cydia pomonella*, and *Grapholita molesta* — by combining a generic phenological model with five years of data from digital pheromone traps. The model, based on degree-day accumulation and species-specific biological parameters, simulates generational succession and predicts flight periods. Continuous records from digital traps provide a detailed view of intra- and interannual variations, revealing the influence of local climatic conditions and microclimates on the timing and intensity of flight peaks. The analysis highlights consistent patterns in flight cycles, as well as shifts driven by thermal variability and pest pressure. These findings demonstrate the value of coupling modelling and automated monitoring to better understand pest phenology and optimize intervention timing in integrated pest management strategies.

Diversity and population dynamics of some predatory spiders from district Loralai, Balochistan, Pakistan.

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Abstract

A complete survey was carried out in four distinct of District Loralai, Baluchistan, Pakistan. Spiders were collected by using different methods such as pitfall traps, hand picking, beat sheet and sweep netting. Collectively a total of 13,894 specimens representing 50 species, 41 genera and 18 families of predatory spiders were recorded. Lycosidae was the most diverse and abundant family contributing 20% of total species richness ($n=12$) followed by Salticidae (11%; $n=4$) while Theraphosidae and Euagridae were least abundant. Menhinick's index indicated the highest species richness in Kili Zengiwal (0.6512), while Margalef's index showed the highest richness in Kach Ahmaqzai (5.334). Shannon-Weiner index recorded the highest diversity of predatory spiders in Kach Ahmaqzai (3.465), whereas Simpson's index emphasised a dominating report as highest value in Kili Zengiwal (0.9635). Pielou's evenness index identified Barnema as the site with the highest species evenness (0.9032). Spider abundance was highest in July while lowest in May and September. There was a positive association between environmental factors and functional spider density particularly with minimum temperature in each locality i.e. Kach Ahmaqzai (0.612**), Kili Sagar (0.621**), Kili Zengiwal (0.626**) and Barnema (0.690**) while other factors have not strong influence on predatory spiders. Landscape diversity and remoteness from urban areas played a key role in determining spider species richness while altitude negatively impacts species richness (-0.0025 , $p=0.025^*$) and abundance (-0.0027 , $p<0.05$). These findings provide valuable insight into diversity, distribution and environmental associations of predatory spiders that highlighted their ecological potential as biocontrol agents from Baluchistan, Pakistan.

The Stylet Cuticle as a Molecular Interface Driving Aphid-Mediated Plant Virus Spread

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Yu FU, Emma ACHARD, Bastien CAYROL, Sophie LE BLAYE, Stefano COLELLA

Abstract

Aphids are among the most frequent and economically important vectors of plant viruses worldwide. The majority of aphid-vectoring viruses are transmitted through a non-circulative, stylet-borne mechanism, in which virions or virion-helper complexes are transiently retained on specific receptors exposed on the cuticle of the maxillary stylets. Early studies showed that aphid stylets are not biochemically homogeneous structures. Using integrated omics, advanced microscopy, synchrotron X-ray microtomography studies and 3D imaging, our research uncovered the dynamics of synthesis of stylets and revealed that their surface is spatially functionalized into discrete micro-territories, most notably the acrostyle, a nanostructured domain at the stylet tip specialized for molecular interactions.

We demonstrated that the functionalization relies on the selective surface exposure of cuticular proteins from the CPR (RR-1) family, termed stylins, whose domains emerge at the cuticle-environment interface and confer molecular recognition properties to a specific region of the cuticle. Stylin-01 was identified as a candidate receptor for Cauliflower mosaic virus (CaMV) and later functionally validated using a CRISPR-Cas9 knockout aphid line, which impaired CaMV retention and transmission, definitively establishing Stylin-01 as the major CaMV receptor. Partial functional compensation by other stylins further supports a modular receptor platform at the acrostyle.

Current work extends this model to potyviruses, using Turnip mosaic virus to examine how helper-dependent viruses exploit the acrostyle for transmission. Beyond virus retention, the acrostyle also interacts with aphid salivary effectors. Together, these findings establish the acrostyle as a multifunctional interaction hub, where CPR-based surface functionalization enables interactions with both endogenous salivary effectors and diverse viral ligands. Deciphering the molecular properties of this interacting platform opens new perspectives for vector-targeted strategies.

Host Plant Species and *Ca. Arsenophonus* phytopathogenicus Infection Shape Performance and Behaviour of *Pentastiridius leporinus*

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Abstract

Pentastiridius leporinus (Hemiptera: Cixiidae) has recently emerged as a major agricultural pest in Europe, a trend facilitated by sugar beet–winter wheat rotations that ensure continuous host availability. This planthopper is the principal vector of *Candidatus Arsenophonus phytopathogenicus* (CAp), the causal agent of the disease “syndrome basses richesses”. However, the effects of host plant selection and bacterial infection on its performance remain insufficiently understood. We posited that the performance of *P. leporinus* differs between its ancestral host (reed grass) and more recently exploited crop hosts (sugar beet, wheat, and potato), and that CAp infection modulates plant–insect interactions. To test these assumptions, we quantified adult longevity, oviposition performance and choice, nymphal survival, and olfactory responses on the above-mentioned plants. Additionally, we tested the suitability of a potential non-host, latex-producing crop (*Taraxacum kok-saghyz*, under consideration for cultivation in regions heavily infested by *P. leporinus*). We also assessed insect responses to CAp-free versus CAp-infected sugar beet. Sugar beet supported significantly greater adult longevity (30 days) and fecundity (100 eggs per female) than other plants (12 days and 30 eggs, respectively). Nevertheless, females showed no consistent oviposition preference when sugar beet was paired with another tested plants, suggesting spill-over effects associated with the presence of sugar beet. Nymphs were attracted to root volatiles from all plant species, but adult emergence occurred predominantly on sugar beet. Dual-choice assays revealed that both adult females and third-instar nymphs significantly preferred CAp-infected over uninfected sugar beet. *Taraxacum* spp. permitted only marginal survival, negligible oviposition, minimal nymphal emergence, and no detectable CAp transmission, as confirmed by qPCR. These findings identify sugar beet as the most suitable host sustaining *P. leporinus* and demonstrate that CAp infection enhances host attractiveness. They also indicate that cultivating *T. kok-saghyz* in regions with high *P. leporinus* pressure could represent viable alternative to sugar beet.

Interactions between *Bemisia tabaci* and the first whitefly-transmitted polerovirus

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Carmit ZIV, Benaya ZINI

Abstract

Poleroviruses (family Luteoviridae) are phloem-limited, positive-sense RNA plant viruses that are traditionally transmitted exclusively by aphids. We previously identified an unusual polerovirus infecting bell pepper (*Capsicum annuum*) that breaks this paradigm by being transmitted by whiteflies. This virus induces typical polerovirus symptoms in pepper, including vein yellowing, leaf rolling, and fruit discoloration. It was named Pepper whitefly-borne vein yellows virus (PeWBVYV) and is transmitted specifically by *Bemisia tabaci* Middle East–Asia Minor 1 (MEAM1), but not by the Mediterranean (MED) species. Genome sequencing revealed that PeWBVYV has a recombinant structure. Its 5′ genomic region shares more than 95% sequence identity with the aphid-transmitted Pepper vein yellows virus (PeVYV) from Israel, whereas the 3′ region is related to African eggplant yellows virus (AeYV). PeWBVYV is persistently transmitted by *B. tabaci* MEAM1 and exhibits a competitive advantage over PeVYV in pepper plants. Since its emergence in the Jordan Valley, PeWBVYV has completely displaced PeVYV in this region, although it has not yet become widespread in other major pepper-growing areas of Israel. To investigate virus transmission, disease development, and the association between infection and fruit discoloration, we conducted extensive field surveys complemented by controlled laboratory experiments. Field data indicate that disease incidence and severity are influenced by multiple interacting factors, including environmental conditions, pepper cultivar, plant physiological status, whitefly population density, and virus inoculum pressure. Despite high transmission efficiency and disease prevalence under field conditions, laboratory transmission assays showed relatively low efficiency, limiting the ability to isolate individual determinants of virus spread. These results highlight the complexity of PeWBVYV epidemiology and underscore the need for further studies on its interactions with host plants, vectors, and environmental factors.

Plant virus mediates endosymbiont effects on aphid-parasitoid interactions

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Consuelo DE MORAES, Mark MESCHER

Abstract

Aphid-vectored plant viruses often modify host plant and vector traits to enhance transmission, with subsequent effects on aphid vector resistance or susceptibility to parasitoid wasps. These effects can be further influenced by aphid-associated endosymbiotic bacteria (endosymbionts), which can also mediate aphid-parasitoid interactions. Despite their frequent co-occurrence and the employment of parasitoids as biocontrol agents, how the interactions between plant viruses and endosymbionts influence aphid-parasitoid dynamics remains largely unexplored. Here, we investigate the effects of pea enation mosaic virus (PEMV) and diverse facultative endosymbionts on interactions between pea aphids (*Acyrtosiphon pisum*, genotype LSR1) and parasitoid wasps (*Aphidius ervi*). In laboratory assays, groups of aphids with varying virus and endosymbiont combinations were exposed to female parasitoids, and we recorded parasitism outcomes and traits of aphids that survived the attack. Our results indicate that the pea aphid genotype LSR1 is highly susceptible to parasitoid attack, with most facultative endosymbionts providing only minor survivorship improvements. Nevertheless, the presence of PEMV induced a range of effects on these interactions. In aphids harboring *Regiella insecticola* strain R5.15, PEMV was associated with reduced mummification and lower parasitoid emergence from mummies compared with virus-free counterparts. By contrast, in aphids harboring *Hamiltonella defensa*, PEMV revealed strong effects on post-attack traits: surviving aphids on PEMV plants were significantly more likely to develop wings, and they showed higher cumulative fecundity and cumulative survival than their virus-free counterparts. These results highlight that the plant virus modulates endosymbiont effects on interactions between a susceptible pea aphid line and its parasitoid, suggesting potentially important implications of viral infection and microbial symbionts for trophic ecology. More broadly, our findings indicate that virus presence can reshape symbiont-dependent outcomes of parasitoid attack, with consequences for dispersal, host-parasitoid dynamics, and the effectiveness of parasitoid-based biocontrol in pathosystems where vectors harbor facultative symbionts.

Host susceptibility and recalcitrance to the vector and/or virus affects the outcome of vector fitness and vector-virus interactions in an aphid-RNA virus pathosystem

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Abstract

Hemipteran vector and virus interactions often are studied on individual plant hosts that are susceptible to the virus and/or vector. The fidelity of such interactions is regularly discussed in the context of virus persistence within the vector, but not in the context multiple (alternate) hosts with varying levels of susceptibility to the vector and/or virus. Using a series of ecological experiments and Omics approaches, we attempted to address the above-stated concept in the cotton aphid-cotton leafroll dwarf virus (CLRDV) pathosystem with cotton and three alternate hosts. Cotton aphid (*Aphis gossypii*)-transmitted CLRDV is an RNA virus that belongs to the genus Polerovirus. CLRDV was recently introduced into the United States, and CLRDV infection induced symptoms range from none to severe (often with multiple symptoms).

We found that besides cotton, CLRDV can infect other commonly found Malvaceae hosts in the landscape viz., hibiscus, prickly sida, and okra. Investigation revealed that each of the hosts had varying levels of susceptibility to the virus predominantly and to a degree to the vector. The virus induced symptoms and virus accumulation levels differed between the primary (cotton) and alternate hosts and between alternate hosts.

Annotated transcriptomes from cotton and alternate hosts revealed that genes associated with plant development, photosynthesis, defense, and vector fitness influencing compounds were differentially expressed following CLRDV infection and varied with host. Aphids feeding on those plants also had differentially expressed genes pertaining to virus acquisition, signal transduction, immune systems, and fitness, and varied with host. Consequently, fitness and biology studies indicated that differential gene expression in hosts differently influenced aphid fitness and biological parameters, reiterating that host plant's vector and/or virus susceptibility or recalcitrance could be the key determinant of vector-virus interaction outcomes. These results also will be compared and discussed with that of another hemipteran-DNA virus pathosystem.

Xylella fastidiosa and the transmission capability of insect vectors between plants of agricultural and silvicultural interest in Switzerland

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Francesca DENNERT, Alice PESSINA, Denise ALTENBACH, Laure APOTHÉLOZ-PERRET-GENTIL, Stéphane HAGMANN, Attilio RIZZOLI, Valentin QUELOZ, Ramona MAGGINI

Abstract

Xylella fastidiosa is an extremely harmful plant pathogen with potentially significant economic, social and environmental impacts. Native to the Americas, it has already established in southern Europe, and it is categorized as a priority quarantine organism in Switzerland and the EU. With a proactive approach towards a possible introduction of the bacterium in Switzerland, this project is aimed to assess the capability of a selection of insect species commonly present in Switzerland to acquire and transmit *X. fastidiosa* (several subspecies) to woody plants of agricultural and silvicultural interest. Acquisition and transmission experiments have been carried out in biosecurity level 3 facilities at WSL (Birmensdorf, Switzerland) with insect vectors *Philaenus spumarius*, *Aphrophora alni* and *Cicadella viridis*. The target plants include agricultural species (*Vitis vinifera*, *Prunus armeniaca*) and silvicultural species (*Fagus sylvatica*, *Quercus robur*) of interest for the Swiss landscape, as well as shrub species (*Rubus fruticosus*, *Corylus avellana*) that bridge and occur in both ecosystems. Two types of acquisition systems have been tested; namely from artificially inoculated plants and from artificial diet. The results of our research will answer fundamental questions about *X. fastidiosa* epidemiology and identify possible pathways of spreading of the bacterium across the Swiss landscape. Moreover, these findings will support its early detection by improving targeted surveillance, contribute to containing its propagation and, ultimately, limit the economic losses in cultivated crops and the impacts on forest ecosystem services.

HOST PLANT ASSOCIATION AS A DRIVER OF GENETIC DIVERGENCE IN *CACOPSYLLA MELANONEURA* (HEMIPTERA, PSYLLOIDEA, PSYLLIDAE).

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Abstract

Apple proliferation (AP) is a severe disease in European apple cultivation, caused by the bacterial pathogen ‘*Candidatus Phytoplasma mali*’. The insect vectors of ‘Ca. P. mali’ are the apple psyllids *Cacopsylla melanoneura* and *C. picta*. The former species is associated with both apple and hawthorn trees, and in regions where *C. picta* is absent, it acts as the sole vector for the spread of ‘Ca. P. mali’ in apple orchards. Laboratory experiments suggest that populations developing on apple trees are ecologically different from those on hawthorn. The goal of our study is to identify the genetic basis of the different reproductive host preferences in *C. melanoneura* and to define evolutionarily significant units. To achieve this, we first generated a reference nuclear genome of *C. melanoneura* using a combination of long- and short-read technologies. Based on our newly generated genome, we investigated the genetic variants associated with host preferences in sympatric wild populations collected from apple and hawthorn trees across Europe (Austria, Italy, Germany, the Czech Republic, Romania, and Serbia). Mitochondrial data suggest that *C. melanoneura* represents a species complex with at least two cryptic lineages, although no morphological differences have been found so far, while nuclear SNPs support the presence of two genetically distinct groups of individuals with different host preferences across Europe. These findings will also be useful for monitoring the spread of ‘Ca. P. mali’ vectors in Europe and for gaining insights into the genetic basis of reproductive host preferences in *C. melanoneura*.

#12378

INSECT VECTORS: Vectors of plant pathogens 1

02/07/2026 at 12:30, Chinon

High-resolution 3D imaging insights into the biomechanics of xylem sap ingestion by leafhoppers

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Elizabeth CLARK

Abstract

We used synchrotron-based X-ray micro-CT imaging to generate 3D images and digital reconstructions of key internal features of the feeding complex of xylem sap-feeding insects. In addition to revising details of pre-cibarial valve operations and muscle attachments, we have been able to use associated techniques to study cibarial filling during ingestion and the frequency and angles of cibarial diaphragm movement as insects ingest sap. Our results show that volumes ingested are variable, and that insects variations in diaphragm muscles contraction provide mechanical flexibility in this process.

Co-acquisition and transmission of two *Liberibacter* by the potato psyllid

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Tafim HRITHIK

Abstract

The potato psyllid, *Bactericera cockerelli*, transmits two haplotypes of the bacterial plant pathogen ‘*Candidatus Liberibacter solanacearum*’, LsoA and LsoB. While previous studies have examined the acquisition and transmission of individual Lso haplotypes, in this study, we investigated the dynamics of LsoA and LsoB co-acquisition and co-transmission by *B. cockerelli*. We quantified the total and haplotype-specific Lso titers in psyllid guts after different acquisition access periods. Additionally, we conducted sequential inoculation of tomato plants using psyllids that had undergone a 7-day acquisition access period on double-infected plants. We also evaluated the expression of psyllid genes differentially regulated by each haplotype upon acquisition. Our results showed that the co-acquisition of these haplotypes affects their accumulation, their transmission as well as the psyllid responses elicited upon acquisition. These findings provide valuable insights to improve our understanding of the biology of Lso acquisition and transmission, and the potential role of co-infection as a driver of disease epidemiology.

NGS-Based Screening of *Bemisia tabaci* for Plant Virus Threats and Insecticide Resistance

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Abstract

The whitefly *Bemisia tabaci* is a major agricultural pest, responsible for crop losses exceeding one billion euros annually. It feeds on plant phloem and acts as an efficient vector of numerous detrimental plant viruses. Within the European Union (EU), *B. tabaci* is regulated as a quarantine pest when detected on non-EU plant imports. Although *B. tabaci* is reported to be present in Belgium, the extent to which non-EU *B. tabaci* populations pose phytosanitary risks to Belgian greenhouse crops and ornamentals has remained unclear. Between 2021 and 2024, more than 50 *B. tabaci* populations were intercepted at Belgian entry points on plant material originating outside the EU, while additional populations were collected from crops and ornamental plants within the EU. PCR assays and next generation sequencing (NGS) were used to identify whitefly biotypes, characterize viral communities, and detect mutations associated with insecticide resistance. Results revealed two predominant biotypes and a diverse array of plant viruses, including poleroviruses and criniviruses not previously reported in the EU. Both EU and non-EU *B. tabaci* populations carried known and novel resistance-associated mutations, likely complicating control strategies. This study strengthens our understanding of *B. tabaci*-related risks and provides a basis for targeted strategies to protect Belgian—and EU—crops from emerging viral threats.

Biological control of *Xylella fastidiosa* vectors by *Verrallia aucta* (Diptera: Pipunculidae) in Spain: survey of prevalence, host and parasitism rate.

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Natalia MOLINA ESPINEL, Martin GODEFROID

Abstract

Xylella fastidiosa (*Xf*), an invasive insect-borne plant pathogenic bacteria, is one of the main threats to Mediterranean agriculture as it affects some of the most important crops in this region like olive, almond or grapevine. As there is not curative treatment for *Xf*, control mainly relies on reducing vector population and removal of infected plants. In Europe spittlebugs from suborder Auchenorrhyncha have been described as *Xf* vectors. The biology of spittlebugs is widely studied however there are still gaps of knowledge on their natural enemies. The endoparasitoid *Verrallia aucta* Fallén 1817 (Diptera, Pipunculidae) regulates densities of *Xf* vectors. While several studies have shown its control potential in Scotland or Italy, the distribution, host range and prevalence of *V. aucta* was poorly studied in Spain.

The objective of this study was to fill this gap of knowledge. Five species of spittlebugs were collected from 9 areas in peninsular Spain and molecularly screened for the detection of *V. aucta* parasitism. In total 702 spittlebugs were analysed finding parasitism in all the places sampled. The highest parasitism rate was observed in *Neophilaenus lineatus* (44%) and *Neophilaenus campestris* (27%), followed by *Philaenus spumarius* (16%) and very low in case of *Lepyronia coleoptrata* (1%), first time reported. No parasitism was observed in case of *Cercopis intermedia*. When *P. spumarius* and *N. campestris* were present on same place we observed a higher parasitism rate for the later one. We are currently investigating the potential genetic differences in *V. aucta* based on the infected host.

Using video-phenotyping to detect antixenosis traits affecting aphid behavior and virus transmission in sugar beet

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Gabin MARDOC, Aurélie MARMONIER, Héloïse LESAGE, Anne-Marie CORTESERO, Fabienne MAUPAS, Audrey FABAREZ, Véronique BRAULT

Abstract

Understanding how plant traits shape vector behaviour is central to the ecology of plant–virus interactions. Following the ban of neonicotinoids in France, identifying resistance mechanisms that disrupt insect vectors, especially *Myzus persicae*, the main vector species responsible for sugar beet yellows, has become a priority for sustainable crop protection. Our research aimed to identify antixenosis-associated traits in sugar beet cultivars to reduce the likelihood of viral transmission. We first developed a high-throughput video-phenotyping tool to quantify aphid (locomotory) behaviour on leaf discs. Screening 96 cultivars revealed strong behavioural contrasts: on several genotypes, aphid immobility decreased up to 2.75-fold while travelled distance increased up to ninefold, indicating difficulties in settling. Based on these observations, six contrasting cultivars were selected for deeper behavioural analyses. Contrary to our initial hypothesis that video-tracking could act as high-throughput proxy of electropenetrography (EPG), EPG recordings and virus transmission assays did not show consistent differences among cultivars. These discrepancies suggest that early probing and phloem ingestion are not the primary processes affected by the underlying plant traits. In contrast, two-choice assays between the selected cultivars strongly matched the video-tracking outcomes: aphids consistently avoided cultivars previously identified as “unfavourable” based on locomotion activity. Taken together, these findings indicate that video-tracking captures broader behavioural responses such as vector orientation, leaf surface exploration, and settling propensity rather than fine-scale feeding events. This highlights another dimension of plant-mediated resistance acting at the pre-feeding stage, which could contribute to reducing vector pressure independently of virus acquisition or inoculation efficiency. Overall, our work demonstrates the ecological relevance of high-throughput video-phenotyping to detect antixenosis traits affecting early aphid–plant interactions, offering a promising tool for breeding sugar beet cultivars that disrupt vector behaviour and may help mitigate virus spread in the field.

High-throughput and Sanger sequencing based Gut Content Analysis of *Xylella fastidiosa* vector *Philaenus spumarius*

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Elena GONELLA, Alberto ALMA

Abstract

Philaenus spumarius is a ubiquitous and highly polyphagous spittlebug, main vector of *Xylella fastidiosa* in Apulia Region. Given adults dispersal from olive trees during the summer, the identification of alternative host plants is crucial to identify possible sources for pathogen inoculation. The aim of this study was to conduct the first high-throughput sequencing Gut Content Analysis (GCA) on *P. spumarius* adults and compare the outcomes with two Sanger sequencing-based approaches. Adult insects were sampled from olive trees during the summer season of 2021 in two olive-growing areas with diverging environmental features, namely Apulia (Southern Italy) and Lombardy (Northern Italy). Illumina-based GCA revealed a significant reduction of *Olea* sequences from July to September in both sites, confirming the dispersal behaviour described in monitoring studies. More than 30 plant families were identified from insects collected in both regions. Excluding Oleaceae, the most abundant family in Apulia was Asteraceae and the most abundant genus was *Picris* throughout the season. In Lombardy the most abundant families were Oleaceae and Fagaceae in July and Asteraceae and Urticaceae in August; the most abundant genera were *Olea* and *Castanea* in July and *Artemisia*, *Centaurea* and *Urtica* in August. Two different Sanger-based GCA strategies were assessed, a nested PCR targeting the trnL intron and a PCR targeting ITS2. Despite the high concentration of *Olea* DNA, in both cases *Olea* sequences were seldomly retrieved, while other feeding host were distinguishable. Trials with *Olea* DNA mixed with other plant families confirmed a better amplification of Asteraceae and Fabaceae DNA for trnL marker, while from ITS2 marker no *Olea* sequence was obtained from mixed DNA. These results suggest that the application of GCA by Sanger sequencing on adults found infected with *X. fastidiosa* could support the identification of plant reservoirs for pathogen infection, by highlighting the feeding sources other than olive.

Applied biotremology for vector insect control: New frontiers in plant protection

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Abstract

Biotremology, the study of vibrational communication in living organisms, is opening new horizons for sustainable pest management. Many insect vectors of plant pathogens, such as leafhoppers and planthoppers, rely on substrate-borne vibrations for intraspecific communication, particularly mate finding. Their chordotonal organs are highly sensitive to mechanical cues, making vibrational signaling their primary sensory channel and, at the same time, a critical vulnerability.

Among available approaches, the transmission of disruptive vibrational signals (DVS) into host plants has reached a precommercial stage, with promising trials currently underway in Northern Italy. DVS can interfere with mating communication and feeding behavior, offering a novel, eco-friendly tool for disease control. By altering probing and ingestion patterns, key steps for pathogen acquisition and inoculation, vibrational interference has the potential to reduce vector competence and limit phytoplasma transmission.

Turning this biological principle into effective field strategies requires technological innovation. Recent advances in sensors, actuators, and signal processing now enable precise delivery of interference signals in both laboratory and field conditions. Current research in precision agriculture platforms aims at developing real-time monitoring: accelerometer-based detection of species-specific signals, combined with machine learning algorithms, enables automated pest alerts and targeted interventions, minimizing non-target effects and ensuring ecological sustainability.

Another vibration-based solution is the use of species- and sex-specific vibrational lures to create new traps for species currently monitored by sweeping nets or colored sticky panels, reducing bycatch compared to broad-spectrum methods. These strategies are particularly relevant for perennial crops, where chemical control is limited and disease pressure can be high. Applied biotremology thus represents a multidisciplinary frontier combining physics, biology, and engineering to develop eco-innovative solutions for crop health. Synergies with semiochemical and biological control methods are expected. By disrupting both communication and feeding while enabling real-time monitoring, biotremology transforms vector management into a proactive, sustainable approach for plant protection.

Suitability of different Brassicaceae species as non-host plants for interrupting the life cycle of the sugar beet pest *Pentastiridius leporinus*

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Abstract

The polyphagous planthopper *Pentastiridius leporinus* (Hemiptera: Cixiidae) is a vector of two phloem-restricted bacteria associated with the Syndrome des Basses Richesses (SBR) disease in sugar beet. First observed in the 1990s in France, SBR has recently spread to Switzerland and Germany, where it now represents the main threat to sugar beet production, and also to potato and vegetable crops. In Central Europe, common agricultural practice consists of sowing sugar beet in the spring, harvesting it in early fall, then growing winter wheat until next summer. However, this crop rotation system creates ideal conditions for *P. leporinus*, enabling nymphs to feed on sugar beet roots then shift to wheat roots once the beet crop is harvested. Adults emerge in summer and migrate to a sugar beet field to lay eggs. Previous studies have shown that leaving fields bare fallow after sugar beet harvest can drastically reduce planthopper populations, but this practice poses drawbacks such as elevated erosion risk. To identify alternative non-host plants that could replace winter wheat in crop rotations, we assessed the suitability of 7 Brassicaceae cover crop species for *P. leporinus*. Three-week-old plants grown in 5-L pots were infested with 2nd-instar *P. leporinus* nymphs. The first adults emerged at 11 weeks post-infestation (wpi), and emergence was recorded weekly until 22 wpi. At this point, the remaining nymphs were counted and their life stage determined. Relative to wheat controls (57% survival at 22 wpi), survival on all Brassicaceae species was significantly lower, and two species (*Raphanus sativus* var. *longipinnatus* and *Brassica rapa* var. *silvestris*) supported no nymphal survival. Root glucosinolate profiles were also analyzed to evaluate potential effects on feeding behavior and survival. Our findings highlight the promise of Brassicaceae cover crops as a strategy to suppress *P. leporinus* populations and reduce disease pressure in sugar beet production systems.

Dual Impact, Single Strategy: RNAi for Vector–Virus Knockdown

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Abstract

Virus-induced gene silencing (VIGS) and spray-induced gene silencing (SIGS) are emerging as powerful approaches for dissecting gene function and developing next-generation pest management tools. We are deploying a novel independently mobile RNA (iRNA) vector to target four essential genes in western flower thrips (WFT) and five genes in tomato spotted wilt virus (TSWV), a globally important pathogen transmitted exclusively by WFT. Using this platform, iRNA constructs achieved up to 92% knockdown of WFT target genes in a context-specific manner, resulting in significant mortality when delivered through tomato hosts. Early experiments also show substantial reductions in WFT fitness and TSWV transmission, driven by iRNA-mediated silencing of both vector and viral genes. In parallel, we are developing a complementary dsRNA-based strategy targeting critical fitness-related genes in greenbug aphids. Data on gene knockdown efficiency, aphid performance, and mortality outcomes will be presented. Collectively, these findings underscore the promise of RNAi-based technologies as precise, adaptable, and sustainable pest management strategies—capable of simultaneously suppressing insect vectors and the pathogens they transmit.

Silencing the vectors: RNA interference is a flexible platform for functional genomics, transmission disruption and innovative pest control

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Abstract

RNA interference (RNAi) emerged as versatile tool to investigate gene function and design next-generation strategies against insect vectors of plant pathogens. In recent years, we applied RNAi across multiple economically relevant insect species in Europe, including the spittlebug *Philaenus spumarius*, a vector of *Xylella fastidiosa* in olive and grapevine, as well as the leafhoppers *Scaphoideus titanus* and *Euscelidius variegatus*, which are field and laboratory vectors of the grapevine flavescence dorée phytoplasma. To broaden the applicability of RNAi to vectors occurring in other biogeographic regions, additional experiments were extended to *Macrosteles quadrilineatus* and *M. quadripunctulatus*, vectors of ‘*Candidatus* Phytoplasma asteris’ in America and Europe respectively. We evaluated different RNAi delivery protocols to optimize silencing efficiency and enhance the general applicability of the approach. While direct microinjection of double-stranded RNA (dsRNA) proved to be highly reliable for functional gene characterization, feeding-based strategies, including petiole absorption, provided delivery methods suitable for semi-field applications. Genes with key physiological roles, namely actin, ATP synthase β , vATPase, hexokinase, different subunits of the 26S proteasome, natterin-like and legumain, showed significant and reproducible knockdown upon dsRNA treatment. Silencing of these targets resulted in decreased survival and fertility, or reduced pathogen acquisition, highlighting pathways of interest for vector control. In *S. titanus* and *E. variegatus*, RNAi of ATP synthase β , legumain and natterin-like genes revealed molecular functions linked to vector competence for FD phytoplasma. In *P. spumarius*, dsRNA uptake through petiole absorption offers a promising route for suppression of *X. fastidiosa* spread. Reduced fertility in *M. quadripunctulatus* upon silencing of ATP synthase β was consistent with results observed in other species, confirming the broad applicability of RNAi for conserved gene functions across Auchenorrhyncha. Our findings demonstrate that RNAi provides a species-transferrable platform for functional genomics in non-model insects and pave the way for innovative, targeted, and sustainable pest management.

Identifying pea genes conferring resistance to aphid-transmitted Pea Enation Mosaic Virus

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Maiwenn LE FLOCH, Stéphanie MORLIÈRE, Stéphanie ROBIN, Sylvain GUILLOT, Julie JAQUIÉRY, Martin DRUCKER, Jean-Christophe SIMON, Marie-Laure PILET-NAYEL, Akiko SUGIO

Abstract

The incidence of insect-borne viral diseases in crops is increasing in Europe due to pesticide bans, recurrent emergences of insecticide resistance and global warming. Pea (*Pisum sativum*) is an important protein source but is threatened by aphid-borne viral diseases, causing up to 90% yield loss. One of the most predominant pea viruses in France is PEMV (pea enation mosaic virus). PEMV is a symbiosis of two RNA viruses (PEMV1 = enamovirus, PEMV2 = umbravirus) and is transmitted by aphid in a persistent and circulative manner: the virus circulates in the aphid body, accumulates in salivary glands and is reinjected into plants with saliva. PEMV1 is required for aphid-mediated transmission, and PEMV2 is required for systemic infection in plants. The main vector of PEMV is the pea aphid, *Acyrtosiphon pisum*, a major parasite of peas. PEMV resistance locus En is deployed in commercial *P. sativum* varieties, but En gene has not been characterised or cloned. It is theoretically targets the virus and not the vector aphid, but its mechanism of action is unknown. In this study, PEMV resistance in 244 genetically diverse pea accessions including En carrying genotypes were assessed by inoculating the viruses by *A. pisum*, measuring plant growth, monitoring symptom development and quantifying PEMV-derived RNAs. Our results suggest the presence of a pea locus, likely En, that functions against the replication of PEMV1 but not PEMV2. We then carried out a genome-wide association study (GWAS) to identify the pea genes involved in PEMV resistance or susceptibility. The genetic architecture of PEMV resistance and the mechanism of action of pea resistance against aphid-transmitted PEMV will be discussed.

Improving the Management of Cereal Aphids and Barley Yellow Dwarf Virus in Irish Winter Barley

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Abstract

Aphids reduce grain yield and quality in cereal crops via direct feeding and vectoring viruses. The most economically important aphid vectored virus in Irish cereals is barley yellow dwarf virus (BYDV), which can cause yield reductions of 5 t/ha. Managing aphids is increasingly challenging due to reduced insecticide availability, insecticide resistance, and a lack of robust insecticide application thresholds. Navigating these challenges requires an increased understanding of aphid and BYDV epidemiology in Ireland, as well as robust monitoring programmes that account for both spatial and temporal distribution of aphids.

From 2022 to 2025 we conducted a nationwide aphid monitoring programme in Irish winter and spring barley. Our primary objectives were to determine which BYDV species were present in Irish crops, and which aphid species were responsible for vectoring them. We tested 565 leaf samples from barley crops and 484 individual aphids for BYDV from fields across Ireland.

Our second aim was to validate two monitoring tools—in-field pan traps and in-field aphid searches—as BYDV risk indicators in Ireland. In spring barley, 28 growers placed pan traps in 48 fields throughout the growing season. All 265 BYDV-vectoring aphids caught in pan traps were identified to species and tested for BYDV. Additionally, each field was visited twice during the growing season to search for aphids; all 354 aphids found were tested for BYDV. The BYDV species present in the aphids caught in the two monitoring tools was compared to the BYDV species present in the fields, to validate the use of each monitoring tool as a BYDV pressure indicator.

This programme established the first comprehensive dataset on BYDV species and aphid vector populations in Irish barley. The validation of monitoring tools has helped determine if these monitoring methods can assist in making BYDV integrated pest management decisions in the future.

Spring soil applications of *Metarhizium brunneum* show potential to control *Bactrocera oleae* and reduce *Auchenorrhyncha* populations

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Islam BOUKETTA, Enrique QUESADA-MORAGA

Abstract

Soil application of EAMa 01/58-Su strain of the entomopathogenic fungus (EPF) *Metarhizium brunneum* targeting last instar larvae of olive fruit fly (OFF) beneath the tree canopy has been previously showed to be an effective alternative to chemicals in terms of efficacy and security for environment and human health. However, within an integrated pest management (IPM) strategy, soil application of this multifunctional EPF strain could provide added values to both olive crop production and protection. This study delves into the efficacy of such soil treatments during Spring to target both emerging OFF adults and *Auchenorrhyncha* (Hemiptera) populations, known potential vectors of *Xylella fastidiosa* Wells. For that, three year wide-area field study was carried out within 40 hectares of olive orchards located in Alcolea (Cordoba), southern Spain. The results obtained from the study showcased promising outcomes, with the fungal strain demonstrating noteworthy effectiveness in pest control. Specifically, the application of the *M. brunneum* EAMa 01/58-Su strain resulted in a considerable 40% decrease in the OFF population when compared to untreated controls. Moreover, there was a significant reduction of over 50% in the natural populations of *Auchenorrhyncha* insects. The fungal inoculum reached basal levels approximately four months post- treatments setting at 3.74×10^3 conidia per g of soil. These findings underscore the potential of the EPF *M. brunneum* (EAMa 01/58-Su strain) as a viable component of IPM strategy in olive orchards, offering a sustainable alternative to conventional pesticide approaches. Moreover, the observed decline in *Auchenorrhyncha* populations suggests a broader ecological benefit by potential mitigating the spread of *X. fastidiosa*, a significant concern in the region.

How do tissues sense their size to tailor their dynamics during development?

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Abstract

How biological systems adjust their properties to size has fascinated biologists for decades. Yet, we still lack a clear understanding of how size is sensed and translated into the morphogenetic processes that shape developing organs. Using *Drosophila* as a model system, I will present new insights into how epithelial tissues measure their size during development. By combining experimental perturbations with theoretical modeling, I show that scaling of genetic patterning with animal size enhances force production to drive tissue displacement. However, genetic patterning alone is not sufficient to ensure proportional scaling of tissue velocities across all sizes. Instead, robust scaling emerges within a crossover regime of tissue mechanical properties that is tuned to the physiological range of animal sizes. Together, these findings uncover previously unrecognized principles—and inherent limits—of developmental scaling, revealing how genetic patterning and tissue mechanics cooperate to adapt collective cell flows to organismal size.

Evolution of a novel left-right asymmetry through co-option of an ancestral tissue remodeling process

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Abstract

Left-right asymmetries have repeatedly evolved in diverse animals and affect the position, shape or size of specific organs. How novel left-right asymmetries arise remains unknown. We examine *Drosophila pachea*, where asymmetric genitalia lobes and a right-sided copulation posture evolved in the past 3-6 million years. Although asymmetric lobes are only found in *D. pachea*, distinct asymmetries and right-sided mating postures are also observed in closely related sister species. We investigate the development and character evolution of asymmetric genitalia and assess the co-evolution of one-sided copulation behavior and asymmetric male genitalia morphology. Male genitalia differentiate during metamorphosis and *D. pachea* asymmetric lobes grow during a 360° clockwise rotation of male genitalia, a conserved and widespread developmental process in flies. Using drug application and a CRISPR-induced *MyoID* mutant, we altered genitalia rotation and found that asymmetric lobe sizes depend on genitalia rotation completion, while the sidedness of lobe asymmetry is determined by the rotation direction. However, males with reversed genital asymmetry still mate in the typical right-sided posture, indicating that right-sided behavior is not determined by asymmetric male genitalia. Now, we aim to identify genes underlying asymmetric tissue growth in *D. pachea*. For this, we use diverse approaches to study left-right differential gene expression. We also develop functional genetic tools for this species to impair gene function in developing genitalia. Overall, a novel genitalia asymmetry has evolved through the co-option of a pre-existing tissue remodeling process. Tissue rotation represents a new mechanism, through which a bilateral organ can acquire a left-right size asymmetry.

Allometric Growth of Organs During Springtail Postnatal Development

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Alexey POLILOV

Abstract

Understanding patterns of morphological scaling is fundamental to evolutionary biology, particularly in explaining body size evolution. The study of growth allometry in ancient hexapods, such as springtails (Collembola), is especially crucial for reconstructing the evolutionary trajectories of arthropod miniaturization. However, the absence of comprehensive data on ontogenetic organ size changes in these organisms has severely constrained meaningful comparisons with other arthropod lineages. Here, we perform the first quantitative analysis of internal organ allometry throughout postembryonic development in the springtail *Hypogastrura assimilis* (Hexapoda: Collembola). We show that the relative volume of the digestive, excretory and muscular systems remains constant during growth (isometric scaling). In contrast, the central nervous system (CNS) and reproductive system scale allometrically. The relative CNS volume is highest in first-instar juveniles (19% of body volume), significantly exceeding that typical of adult hexapods but resembling values found in first-instar larvae and nymphs of microinsects. Concurrently, the neuropil volume in this species is lower than in other hexapods. This pattern provides a key comparative dataset, bridging the gap between insects and their early-diverging hexapod relatives. These findings reveal the specific pattern of allometric growth in springtails and offers a framework for studying the evolution of body size regulation in arthropods, particularly the strategies for organ size adjustment under miniaturization.

This study was supported by the Russian Science Foundation (project no. 25-64-00002).

The PIWI pathway in the oogenesis of the cockroach *Blattella germanica*

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Abstract

Piwi-interacting RNAs (piRNAs) are small non-coding RNAs that were initially identified for their role in counteracting transposable elements, which is part of an evolutionarily conserved mechanism that helps to maintain genomic stability. Beyond this classical role, piRNAs have been implicated in regulating coding genes and influencing gene expression, expanding their functional repertoire.

In this context, we investigate the function of piRNAs during insect oogenesis, using the cockroach *Blattella germanica* as an experimental model. This cockroach possesses panoistic ovaries, an example of the reproductive biology in basal insects. We have identified the components of the PIWI pathway in the ovaries and analyzed their expression throughout the gonadotropic cycle. To study the corresponding functions, we employed RNA interference (RNAi) to deplete PIWI proteins and examined the resulting phenotypes.

Furthermore, we have identified piRNAs expressed in nymphs and adult ovaries, with a subset highly expressed at specific stages of the gonadotropic cycle, coinciding with hormonal signals and changes in the ovarian cell program. Our results suggest that piRNAs may influence cockroach oogenesis by modulating the expression of genes involved in the process. To test this hypothesis, we used antisense oligonucleotides (ASO) to deplete the expression of specific piRNAs and examine the resulting molecular and morphological phenotypes.

Overall, our research provides new insights into the functional significance of piRNAs in insect reproduction, highlighting their potential as versatile regulators.

Resistance to Vip3A toxin from *Bacillus thuringiensis* as a probe for the activation of chitin synthase 2 in peritrophic matrix synthesis

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Zhenxing LIU, Chongyu LIAO, Luming ZOU, Minghui JIN, Peng WANG, Bruce E. TABASHNIK, Yutao XIAO

Abstract

Insects possess two chitin synthases: CHS1 is responsible for the chitin in the exoskeleton and CHS2 makes the chitin in the peritrophic matrix (PM), the fibrous net enclosing the food in the midgut. When the peritrophic matrix (PM) is absent from the midgut of *Spodoptera frugiperda*, the larvae are highly resistant to the Vip3A toxin from *Bacillus thuringiensis* (Liu et al. 2024, PLoS Biology 22:e 3002704). Elimination of the PM in this case is due to a naturally-occurring mutant that eliminates the C-terminal extracellular domain C7 of chitin synthase 2 (CHS2), responsible for PM synthesis. This domain has been shown to be important for switching on CHS2 activity, modulated by binding to a chymotrypsin-like protease (CTLTP1, Broehan et al. 2007, J Exp Biol 210: 3636). Therefore we are investigating how this interaction modulates CHS2 activation by creating CRISPR/Cas9 mutations in C7 and elsewhere in the CHS2 protein, as well as CTLTP1. Heterologous expression of chitin synthases in insect cells has proven to be extremely difficult and this alternative approach may provide a solution. Comparable mutations in CHS1 would be lethal, but CHS2 knockouts are viable in the laboratory, despite complete absence of the PM.

A changing hierarchy of environmental time cues guide development of the migratory pest moth *Loxostege sticticalis*

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Zun XU, Yiyang ZHANG, Hui QIU, Jingxian ZHOU, Fajun CHEN, Xingfu JIANG, Abhishek CHATTERJEE, Guijun WAN

Abstract

Insects use environmental cycling cues to align developmental progression. In holometabolous insects, the progression from larva to adulthood entails decision points, i.e., larval diapause and pupal eclosion, that engage circadian timing mechanisms. What environmental time cues dynamically interact to regulate these developmental checkpoints lying at the intersection of the orthogonal timing systems, remains elusive. We used the seasonally migratory insect *Loxostege sticticalis* to disentangle the influence of photoperiod regimes and temperature conditions at distinct checkpoints of larval growth and metamorphosis. We here employed sensory conflict paradigms to reveal that the relative dominance of these cues' changes over ontogeny. Our results confirm that diapause is induced primarily by the photoperiod during early larval development, rather than by the day-night thermoperiod. In contrast, the circadian clock-controlled adult eclosion, normally locked to the first hour of the daybreak, is jointly controlled by light and temperature cycles. An increase in the constant temperature advanced the peak timing of daily eclosion. On the other hand, the interval timing mechanism regulating the duration of the eclosion event is tuned specifically by the night temperatures. Together, light dominates early developmental decisions, but temperature gains weight at later stages. This shifting hierarchy provides a mechanistic framework for understanding phenological plasticity. Since the timing of eclosion presents a window of increased vulnerability for this pest insect, our results could help to optimize the daily timing of pest management intervention under variable thermal and light conditions.

Functional genetics in the cricket *Gryllus bimaculatus*: characterization of an ancient histone variant absent in *Drosophila*

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Emmanuel GONZALEZ-SQALLI, Matthieu CARON

Abstract

MacroH2A is the most atypical histone variant described so far, being three times larger than canonical H2A due to the presence of a 25kDa nonhistone domain at its C-terminus, known as the macrodomain. Most efforts to unravel its role have been carried out in vertebrate models such as mice, zebrafish, and cell lines; nevertheless, its precise molecular function remains poorly understood. Despite this uncertainty, macroH2A has been linked to a large variety of processes, such as embryo development, cellular differentiation, lipid metabolism, and nuclear and nucleolar organization.

Due to its absence in *Drosophila melanogaster* and *Caenorhabditis elegans*, macroH2A was until recently thought to be a vertebrate-specific histone. However, recent studies have proved that it is an ancient histone present in invertebrates and even in some protists. Regarding insects, macroH2A was lost in the superorder holometabola but is present in apterous and hemimetabolous insects.

Here, we will present our results on the functional characterization of macroH2A in the cricket *Gryllus bimaculatus*, an hemimetabolous, orthopteran model insect. Unlike vertebrates, which carry two macroH2A genes encoding three isoforms, the cricket genome contains a single gene. Using CRISPR-based approaches, we generated a tagged allele at the endogenous locus to follow the distribution of Gb-macroH2A in vivo, particularly in the male germline and during embryonic development. Additionally, we obtained two mutant alleles to study its function: a full knock-out, and a tagged allele lacking linker and macrodomain.

Stikingly, despite ~500 million years of divergence, macroH2A appears to have conserved not only its gene architecture, but also its spatio-temporal distribution, nuclear localization, and core function in genome protection. These results bridge classical cytogenetics in orthopteran insects and contemporary functional genetics, repositioning *Gryllus* as a powerful, fully editable model insect.

Evolution of developmental programs shaping the insect brain

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Abstract

The nervous system is composed of a wide diversity of neuronal cell types arranged into complex circuits that support a broad range of behaviors. Neuronal identity and specialization are established during development, and a key mechanism underlying this diversity is the temporal patterning of neural stem cells. Through this process, distinct transcription factors are sequentially expressed in progenitor cells over time, thereby specifying the identities of neurons generated at particular developmental stages. Although multiple temporal transcription factor series have been described across species and within different neural tissues of the same organism, the evolutionary origins of these series remain largely unresolved.

Advances in single-cell mRNA sequencing have transformed our ability to analyze gene expression at cellular resolution. In the optic lobe of *Drosophila melanogaster*, this approach has not only confirmed known temporal transcription factors but has also uncovered previously unrecognized ones, providing a powerful framework that can be extended to other species. Here, we apply single-cell mRNA sequencing to investigate temporal transcription factors involved in optic lobe development across a diverse set of insect species spanning a broad phylogenetic range. Computational predictions generated from *in silico* analyses are experimentally validated using fluorescent *in situ* hybridization (FISH).

By reconstructing the temporal transcription factor series in each species and comparing them with the well-characterized series in *Drosophila melanogaster*, we identify a conserved temporal ground plan. At the same time, our comparative analysis reveals striking species-specific variations, including the loss and gain of distinct temporal windows. Together, these findings demonstrate both conserved and divergent features of temporal transcriptional programs across species and enable the reconstruction of the evolutionary history of a complex gene regulatory network underlying neuronal diversity. This integrative approach transcends species-specific studies, offering broader insights into the mechanisms driving neuronal development and evolutionary diversification.

The role of host-parasitoid interactions in dormancy induction of endoparasitic braconid wasp larvae

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Christa SCHAFELLNER

Abstract

The parasitic wasp *Glyptapanteles porthetriae* (Hymenoptera: Braconidae), a key natural enemy of the oak forest pest *Lymantria dispar* (Lepidoptera: Erebididae), relies on alternative host species to enable overwintering of its endoparasitic larvae. As in many koinobiont endoparasitoids, winter dormancy is pivotal in temperate regions yet remains poorly understood due to complex host-parasitoid interactions. For *G. porthetriae*, both the identity of overwintering hosts and the cues that induce dormancy remain largely unknown. We investigated the development and dormancy induction of *G. porthetriae* in three host species with distinct dormancy syndromes: *Orgyia antiqua* (Lepidoptera: Erebididae; facultative embryonic diapause), *Lasiocampa quercus* (Lepidoptera: Lasiocampidae; facultative pupal diapause), and *L. dispar* (obligate embryonic diapause). In the former two species, diapause is induced during larval development, whereas *L. dispar* larvae are insensitive to photoperiodic cues that induce diapause. Parasitized larvae and unparasitized controls were reared under long- or short-day photoperiods at 20 °C and under regimes simulating natural autumn conditions. We monitored developmental progress, respiratory activity, and selected metabolites in hemolymph and body tissues (sugars, cyclitols, glycogen, proteins, lipids). In *L. dispar*, neither the host nor the parasitoid showed evidence of dormancy induction under any treatment. In contrast, parasitized larvae of *O. antiqua* and *L. quercus* exhibited pronounced photoperiodic responses, with a 3-6-fold prolongation of endoparasitic development under long-day conditions, accompanied by significant suppression of host development relative to unparasitized controls. Metabolic shifts included elevated hemolymph carbohydrate levels, glycogen accumulation in the fat body, and reduced respiratory activity. Together, these results indicate that photoperiodic sensitivity in the host larva is an essential prerequisite for dormancy induction in the endoparasitic larvae of *G. porthetriae*.

Spatio-temporal characterization of markers distinguishing sexual and asexual embryonic ovaries in the pea aphid

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Abstract

Aphids are considered major crop pests. These damages are notably due to of the peculiarity of their reproduction during their annual life cycle. Aphids indeed switch from an asexual mode of reproduction, which allows them to rapidly colonize the environment in spring and summer, to a sexual mode of reproduction in autumn, producing overwintering eggs. This reproductive mode switch is associated with a shift from the production of asexual to sexual females. This project aims at understanding the cellular mechanisms involved in the differentiation of these two female morphs during embryogenesis and to identify specific cell identity markers for the sexual and asexual embryonic ovaries.

So far, no specific markers for sexual or asexual females during the embryonic stages have been identified yet. To fill this gap, we compared the spatio-temporal expression pattern of candidate genes in sexual and asexual embryonic ovaries by in situ hybridization. We already identified four genes which appear to be specifically expressed in asexual ovaries (in germ cells and/or somatic cells), in early or late embryos. Based on these encouraging results, we implemented a laser capture microdissection (LCM) approach to collect ultra-low amount of mRNAs (<10ng) from ovarian tissues of asexual and sexual embryos in the aim of identifying novel markers. RNA-Seq was performed on these samples to identify differentially expressed genes (DEGs) between asexual or sexual embryonic ovaries. Four highly expressed DEGs have been identified. They will be validated by HCR-ISH to confirm their role as cell-identity markers, based on their specific expression patterns in asexual or sexual ovaries.

Functional Insights into Honey Bee Apolipophorin-1 Revealed by Its Interactome Analysis

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Jana HURYCHOVÁ, James B. BURRITT, Pavel DOBEŠ

Abstract

Apolipophorin-1 (Apolp1) belongs to the large lipid transfer protein superfamily. This group of insect proteins is known for its role in the transport of lipids and other hydrophobic compounds, but there is an increasing amount of evidence suggesting that they have other functions, e.g. participation in the immune system or redox homeostasis. Despite its regular appearance in honey bee omics study datasets, and its sharing of several conserved domains with the highly studied, multifunctional protein vitellogenin, honey bee Apolp1 remains severely understudied.

In our research, we explored the conserved domains of Apolp1, monitored its seasonal variations, and localised it in several tissue types using in-house monoclonal antibodies. We also employed immunoprecipitation, followed by tandem mass spectrometry, to identify its protein interactors.

Our results revealed a distinct expression pattern for Apolp1 that was negatively correlated with that of the key regulatory protein vitellogenin. This suggests that Apolp1 may play a pivotal role in the seasonal adaptations of honey bees. Interactome analysis identified 183 interacting proteins that participate in various biological processes, suggesting that Apolp1 has a plethora of roles beyond lipid metabolism. These results provide new hypotheses that we plan to corroborate using confocal microscopy and in vivo knock-down experiments.

This research is supported by the Ministry of Agriculture of the Czech Republic (project no. QK21010088) in collaboration with the CEITEC Proteomics Core Facility, part of the CHSB, Instruct-CZ Centre, supported by the Ministry of Education, Youth and Sports of the Czech Republic (project no. LM2023042).

Genetic mechanisms mediating energy homeostasis during the summer and winter diapause of two leaf beetles

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Abstract

Most insects enter a dormancy phase, referred to as diapause, to survive harsh seasonal conditions, including cold winters and hot, dry summers. Diapause is tightly regulated at hormonal and genetic levels and induces physiological alterations, including metabolic suppression, to tolerate food scarcity and reduce desiccation risk. Although hormonal changes during insect diapause are well characterized, the genetic mechanisms underlying metabolic regulation remain poorly understood. Here, we investigated the genetic mechanisms underlying metabolic regulation during diapause in two leaf beetle pests, namely *Psylliodes chrysocephala*, the cabbage stem flea beetle, and *Leptinotarsa decemlineata*, the Colorado potato beetle. In *P. chrysocephala*, we examined how microRNAs are differentially expressed to regulate target gene mRNAs through degradation and translational inhibition, thereby suppressing metabolism and feeding behavior during obligatory summer diapause. Functional studies showed that this regulation enhances resilience to hot and dry summer conditions. In *L. decemlineata*, we investigated how lipid metabolism genes such as ACCase and FAS ensure triacylglycerol accumulation during the preparatory phase for facultative winter diapause. Functional studies showed that knockdown of these genes inhibits triacylglycerol (TAG) accumulation and prolongs the preparatory phase, suggesting nutrition-dependent dynamic changes in diapause decisions. Finally, we contrast the genetic mechanisms underlying metabolic regulation in these two leaf beetles with distinct diapause strategies, obligatory summer diapause versus facultative winter diapause. The occurrence of diapause at the adult stage in both species and their close relatedness facilitate direct comparison. This comparison reveals how diverse diapause behaviors converge and differ in energy homeostasis strategies at the molecular level.

Translating GLP Signaling into Insect Physiology: Probing Metabolic Control in the Colorado Potato Beetle

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Abstract

Glucagon-like peptide (GLP) receptor agonists are widely used in human medicine to modulate insulin signaling, energy balance, and body weight, yet their functional relevance in insects remains entirely unexplored. Here, we introduce the Colorado potato beetle, *Leptinotarsa decemlineata*, as a comparative model to investigate GLP-driven metabolic regulation within an insect physiological framework.

Building on established knowledge of insulin-like peptides and adipokinetic hormone signaling in this species, this study examines whether pharmacological GLP agonists can interfere with conserved metabolic pathways governing growth, nutrient allocation, and developmental progression. Using a controlled injection-based delivery approach to ensure endocrine-level exposure, we assess GLP-induced modulation of insulin signaling components, body weight dynamics, carbohydrate and lipid metabolism, and developmental timing. Complementary feeding-based applications are explored as a secondary strategy to evaluate translational feasibility and peptide stability.

By integrating endocrine manipulation with metabolic and developmental readouts, this work aims to establish a novel conceptual bridge between mammalian incretin biology and insect metabolic physiology. Beyond advancing fundamental understanding of hormonal control in insects, the study highlights the potential of insect systems as tractable models for dissecting evolutionarily conserved mechanisms of energy homeostasis and for exploring innovative, metabolism-targeted pest management strategies.

Fat synthesis, host size and habitat type in natural populations of parasitoid wasps.

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Mathilde SCHEIFLER, Suzanne SCHEIFLER, Bertanne VISSER

Abstract

Phenotypic plasticity, the ability to express different phenotypes from one genetic background, is an essential mechanism for organisms to cope with rapid changes in their environment. The evolution of phenotypic plasticity itself is, however, not well understood, particularly in natural populations. During my PhD project I aim to provide insights into natural variation in fatty acid synthesis, a key metabolic trait for all animals. Previous work already revealed that the amber wasp *Leptopilina heterotoma* shows phenotypic plasticity of fatty acid synthesis, but we do not yet know how natural environments shape plastic responses. Amber wasps are generalist parasitoids that can develop in more than 10 different *Drosophila* species. Wasps are further expected to switch host species regularly due to spatial variation in host quality and community composition. In turn, host species largely vary in size, and fat content is tightly correlated with size in arthropods. I hypothesize that habitat type influences host community composition and host size. To test this, I have collected hosts and parasitoids during the summer of 2021 from 5 woodlands and 5 orchards in Belgium. Emerged females were then allowed to feed for 7 days with or without stable isotopes for tracing into the fatty acid fraction using SCI/MS. My preliminary data reveal that host size indeed differs between woodlands and orchards, with a higher variation in host size in woodlands. I further showed that females from woodlands use larger hosts and are themselves larger, suggesting that females choose bigger hosts when available. Data on fatty acid synthesis is currently being gathered and will lead to important insights into the environmental conditions leading to variation in wasp fatty acid synthesis in nature.

The fondness of leaf beetles for symbionts and their digestive enzymes

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Abstract

Beetles that feed on the nutritionally imbalanced and recalcitrant tissues of living plants comprise one-quarter of all herbivorous insect species. Plant cell wall-degrading enzymes (PCWDEs) are key adaptations for beetle herbivores, enabling them to break down the fastidious polymers in the cell wall and grant access to the nutritious cell content. While largely absent from the non-herbivorous ancestors of beetles, such PCWDEs were occasionally acquired via horizontal gene transfer (HGT) or by associations with specialized symbionts. However, the macroevolutionary dynamics of PCWDEs and their impact on evolutionary transitions in herbivorous insects remained poorly understood. Through genomic and transcriptomic analyses of leaf beetles and their symbionts in combination with the characterization of enzymes from both parties, we show that multiple independent events of microbe-to-beetle HGT and digestive symbioses lead to convergent evolutionary innovations. Enzymatic assays further indicate that these events significantly expanded the beetles' digestive repertoire in a beetle-symbiont complementary manner. Our results exemplify how recurring HGT and symbiont acquisition catalyzed digestive and nutritional adaptations to herbivory and thereby contributed to the evolutionary success of a megadiverse insect taxon.

Can cockroaches eat everything? Differential utilization of cellulose and chitin in the American cockroach

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Abstract

Cellulose and chitin are the two most abundant polysaccharides on Earth. The American cockroach (*Periplaneta americana*), an extreme generalist omnivore, thrives on a wide range of diets; however, its capacity to metabolize structural polysaccharides such as cellulose and chitin remains poorly understood. We fed cockroaches ^{13}C -labeled cellulose and chitin to assess their metabolic capacity and the tissue-level allocation of these polysaccharides across sexes and life stages. Our results show that *P. americana* metabolized chitin at a significantly higher rate than cellulose and incorporated carbon derived exclusively from chitin into body tissues. This incorporation exhibited clear sex- and life stage-specific patterns: nymphs allocated more chitin-derived carbon to muscle tissue, whereas females incorporated more into the fat body and reproductive tissues.

These findings provide in vivo evidence that *P. americana* can metabolize both cellulose and chitin, while revealing a pronounced bias toward chitin utilization. More broadly, this study advances our understanding of nutrient allocation strategies in generalist insects and offers evolutionary insight into the digestive capacities of Blattodea, highlighting their adaptive ability to use structurally complex dietary components.

Unexpected nutritional symbiosis: microbial partners sustain nitrogen metabolism in the mosquito *Aedes albopictus* despite nitrogen-rich diets.

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Abstract

Insects rely on nutrients such as vitamins, sterols, and nitrogenous compounds for growth, reproduction, and survival. To cope with nitrogen imbalances, several species have established symbiotic associations with microorganisms that complement their nutrition. While these interactions are well documented in insects feeding on nitrogen-poor resources such as sap, they may appear counterintuitive in omnivorous or hematophagous species consuming nitrogen-rich diets. The Asian tiger mosquito shifts from an omnivorous larval diet to occasional blood meals that enhance adult female oogenesis. We previously identified two eukaryotic microorganisms exhibiting mutualistic traits at mosquito life stages requiring substantial assimilation of nitrogenous molecules: the yeast *Rhodotorula mucilaginosa*, which enhances larval growth, and the protist *Ascogregarina taiwanensis*, which promotes female oogenesis^{1,2}. We disentangled their contribution to nitrogen metabolism throughout mosquito development. Using stable isotope (¹⁵N)-labeled substrates, Nuclear Magnetic Resonance, and Elemental Analyzer-Isotope Ratio Mass Spectrometry, we unraveled differences in metabolic fluxes between mosquitoes associated with and those deprived of their symbionts. In larvae, *R. mucilaginosa* supports development by supplying aromatic amino acids such as tyrosine. Protein digestion and assimilation are improved, and 48.6 percent more ¹⁵N-nitrogen is incorporated into the cuticle. Finally, nitrogenous wastes from tissue renewal are more efficiently recycled during molting. Throughout female oogenesis, *As. taiwanensis* facilitates blood protein digestion and enriches essential amino acids for egg production, including valine. In total, 28.5 percent more ¹⁵N-nitrogen from blood was allocated to mosquito eggs from females associated with the symbiont. This study deepens our understanding of symbiont-mediated contributions to insect physiology through a mechanistic approach. It challenges the conventional view of symbiosis by showing that mutualistic nutritional interactions can arise even when diets are nitrogen-rich.

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Sweetness, metabolic value, and feeding decisions in the whitefly *Bemisia tabaci*

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Arshed REAM, Ofer AIDLIN-HARARI, Shai MORIN

Abstract

Recently, we identified a sucrose-sensitive gustatory receptor, BtGR1, in the phloem-feeding whitefly *Bemisia tabaci* and found that it is expressed both in head and gut tissues. This led us to hypothesize that *B. tabaci* integrates sweet taste signals detected by gustatory receptors in the mouthparts with internal evaluation of sugar value in the alimentary canal. This integration should enable the insect to distinguish sugars that support metabolism from those that do not, thereby regulating feeding motivation, meal duration, and longer-term dietary preferences. To test this model, we combined behavioral, physiological, and molecular approaches. Using artificial diets, we present adult whiteflies with phloem-relevant sugars and additional sugars spanning a range of perceived sweetness and predicted metabolic value. We conduct short- and long-term choice assays, alongside no-choice assays with quantitative measures of intake, honeydew excretion, and survival, to classify sugars into four functional categories: sweet/non-sweet × nutritive/non-nutritive. We then link predicted metabolic value to actual utilization by measuring CO₂ emission and ¹³C enrichment after feeding on labeled sugars, distinguishing sugars that are poorly metabolized from those that contribute to energy balance. Finally, we use RNAi-mediated silencing of BtGR1 to assess its contribution to sugar choice and intake. Preliminary results reveal a clear dissociation between perceived sweetness and nutritional value. Sugars that generate a strong sweet taste signal promote high initial acceptance and sustained intake when they also deliver reliable metabolic benefit. In contrast, some sugars taste sweet yet show weaker, longer-term support of feeding, consistent with internal feedback overriding initial taste cues. Conversely, other sugars evoke little or no sweet taste response but still support feeding and survival, indicating nutritive value. Together, these findings suggest that BtGR1-expressing tissues in the head and gut might act as nutrient sensors integrating taste information with energetic state to shape feeding decisions in *B. tabaci*.

The Hidden Sweet Tooth of the Black Soldier Fly (*Hermetia illucens*)

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Tasnim GUEDES, Mouhamadou Moustapha GUEYE, Meroua FOUGHAR, Jessica JOGUE-LACDO, Pierre-Olivier MAQUART, Frédéric MARION-POLL, Jonathan FILÉE

Abstract

The black soldier fly *Hermetia illucens* (BSF) is increasingly studied for its ability to convert organic waste into protein, offering solutions for waste valorisation and livestock feeding. While egg production depends on adult performance, the biology of adult BSF remains poorly understood. In particular, several lines of evidence suggest that the adult flies are able to feed and benefit from sugar supplementation of their water source. However, the feeding behaviour involving sugar detection, have never been studied so far.

We tested whether adult BSF can detect and prefer sugar by using binary-choice behavioural assays, proboscis extension response tests, scanning electron microscopy, and electrophysiological recordings from labial sensilla. These experiments were complemented by an analysis of the gustatory receptor (GR) gene repertoire and its expression, with a focus on sugar-responsive receptors.

Tests show adults detect and consume sucrose, with stronger female responses. Genome analysis identified 28 GRs – a surprisingly small number for a generalist fly – including only three putative sugar-specific GRs homologous to those of the eight known sugar GRs in *Drosophila*. Moreover, one of these GRs show a general high level of expression including in the head and in the antennae whereas the two others display tissue-specific patterns of expression. We also identify a high number of GR pseudogenes, including four putative sugar receptor pseudogenes, indicating multiple gene loss events and substantial reduction of the GR repertoire compared to other dipteras sharing a similar ecological niche.

We conclude that although BSF possesses a reduced set of GR genes, including only three putative sugar-responsive GRs, adults have retained a strong sensitivity to sugars. We also believe that the experimental test developed in this study laid the foundation for a better understanding of the feeding behaviour of this important insect species for the agro-ecological transition.

Novel transcriptional regulators facilitate insect survival under hypoxia

Keyan ZHU-SALZMAN (Texas A&M University, Ksalzman@tamu.edu)

Abstract

Oxygen (O₂) plays an essential role in aerobic organisms, including terrestrial insects. Under hypoxic stress, many insect species cease feeding and growing. However, those living in hypoxic habitats have developed certain levels of tolerance to hypoxia and can recover from hours to weeks of exposure to hypoxia. Cowpea bruchid (*Callosobruchus maculatus*) 4th instar larvae, for example, exhibit very high tolerance to hypoxia. To better understand the molecular mechanism enabling insects to cope with low O₂ stress, we performed RNA-seq to identify hypoxia-responsive genes in midguts. Subsequently, we determined potential common cis-elements in the promoters of hypoxia-induced and -repressed genes, respectively. Selected elements were subjected to gel-shift and transient transfection assays to confirm their cis-regulatory function. Of these putative common cis-elements, AREB6 appeared to regulate the expression of CmLPCAT and CmScylla, two hypoxia-induced genes. CmZFH, the putative AREB6-binding protein, was hypoxia-inducible. Transient expression of CmZFH in *Drosophila* S2 cells activated CmLPCAT and CmScylla, and their induction was likely through interaction of CmZFH with AREB6. Binding to AREB6 was further confirmed by bacterially expressed CmZFH recombinant protein. Deletion analyses indicated that the N-terminal zinc-finger cluster of CmZFH was the key AREB6-binding domain. Through in silico and experimental exploration, we discovered novel transcriptional regulatory components associated with gene expression dynamics under hypoxia that facilitated insect survival.

Linking tissue- and development-specific amino acid profiles to genome-scale metabolic model in the parthenogenetic and symbiotic pea aphid

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Karen GAGET, Garance LAPETOULE, Isabelle RAHIOUI, Pedro DA SILVA, Federica CALEVRO, Hubert CHARLES, Léo GERLIN

Abstract

Aphids are crop pest insects feeding exclusively on phloem sap, an unbalanced diet rich in carbohydrates but poor in some essential amino acids. These missing compounds are supplied by the obligate endosymbiotic bacterium *Buchnera aphidicola*. Yet, amino acid requirements are expected to shift throughout the development of the insect, especially because adult aphids undergo intense parthenogenetic reproduction. Although numerous studies have deciphered the symbiotic metabolism of amino acids in aphids, little is known about how these requirements evolve during the insect development and parthenogenesis. In addition, few studies have explored the connection between these requirements and phloem sap inflows. In this study, we used HPLC to quantify amino acid composition of different tissues, including embryonic chains, across life stages of the pea aphid *Acyrtosiphon pisum*. We demonstrate that each tissue displays a specific amino acid profile, with its own developmental dynamics. For instance, embryos contain high level of free aspartate, whose proportion decreases with aphid age, while carcass exhibits high, but gradually decreasing throughout development, proportion of free tryptophan. To further explore amino acid allocation, we built the first genome-scale metabolic model of *A. pisum*, comprising more than 1,000 manually curated reactions. We integrated our quantifications of amino acids into the model as numerical constraints, and simulated fluxes across the whole metabolism. This approach revealed that limiting symbiotic supplies drastically alters some amino acid fluxes. It also enabled us to determine which nutritionally acquired amino acids are critical at certain development stages and in specific tissues. Overall, our study demonstrates how phloem-derived nutrients, especially amino acids, shape the reproductive and symbiotic capacities of the pea aphid. Moreover, our metabolic model provides a predictive framework for further studies on metabolism and resource allocation in a symbiotic insect.

#12618

EVOLUTIONARY GENETICS: Eco-evolutionary dynamics of host-microbiome interactions

02/07/2026 at 16:30, Loches

The bacterial march to endosymbiosis: on-ramps and off-ramps

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Abstract

Host-associated bacteria are found across the tree of life and can have crucial influences on the performance of their hosts. Despite the clear importance of such intimate host-microbe associations for individual hosts, it remains a mystery how and when these associations establish, and how these may impact host evolution and adaptation. This knowledge gap is partly due to the lack of theoretical frameworks that capture the evolutionary dynamics of host-microbiome systems. I explore to what extent the foundation for such frameworks lies in existing evolutionary theory. For this talk, I merge insights from classical population genetics, quantitative genetics and evolutionary ecology to highlight three key drivers that shape the fate of a host-microbe association: Host life history, chance and ecological context. By seeking general principles emerging from broad features of host and microbe, and benefiting from the wealth of theory existing in the field of evolutionary biology, this work paves the way for future empirical tests to unravel the origin, function and evolution of the vast ubiquity of the host-microbe associations surrounding us.

A Partnership in Flux: Unraveling Symbiont Dynamics Across the Psyllid Tree of Life

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Erika CORRETTO, Liliya Štarhová SERBINA, Michael GERTH, Martin KALTENPOTH, Hannes SCHULER

Abstract

Sap-feeding insects commonly harbor one or more obligate bacterial symbionts to compensate for nutritional deficiencies in their diet. Associations with multiple symbiotic partners are highly dynamic, forming a continuum ranging from a single obligate symbiont with one or more facultative secondary symbionts to an association with multiple obligate primary symbionts. Although primary symbiont replacement is relatively rare, the acquisition, replacement and loss of co-primary symbionts appear to be frequent. Despite the prevalence of these symbiont shifts in sap-feeding insects, their evolutionary origin and underlying prerequisites remain poorly understood. Moreover, it is unclear whether newly acquired symbionts simply compensate for lost functions lost by older associates or instead confer novel metabolic capabilities and fitness benefits to their host.

Psyllids (Hemiptera: Psylloidea) are phloem-feeding insects that have evolved intimate associations with a diverse range of bacterial symbionts. While most psyllid species are free-living, some representatives adopt a gall-forming lifestyle. However, how this ecological lifestyle influences their symbiont community remains largely unexplored.

Here, we use psyllids as a model system to investigate symbionts dynamics and host-symbiont co-divergence. Our study aims to elucidate the evolutionary dynamics of symbionts in psyllids and more broadly, to advance our understanding of insect-microbe interactions.

Experimental Removal of Niche Construction Alters the Pace and Mechanisms of Resistance Evolution

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Abstract

Niche construction is a key eco-evolutionary process whereby organisms modify their environment and thereby influence their evolutionary trajectories through ecological inheritance. Although theory predicts that niche construction can facilitate adaptation, direct empirical evidence remains limited. Red flour beetles (*Tribolium castaneum*) construct their niche by secreting quinone-rich antimicrobial compounds from their stink glands, providing a form of external immunity. Using an experimental evolution approach, we tested how the removal of niche construction—via RNA interference targeting a gene required for stink gland secretion—affects adaptation to the bacterial entomopathogen *Bacillus thuringiensis*. Beetles evolved under pathogen exposure or control conditions in flour conditioned either by intact or strongly reduced stink gland secretions. All pathogen-exposed populations rapidly evolved resistance; however, beetles with intact niche construction acquired resistance earlier, indicating that niche construction initially accelerated adaptation. Transcriptomic analyses revealed pronounced differences in gene expression between selection regimes, demonstrating that the genetic mechanisms underlying resistance depended on niche construction. We extended the experiment for additional generations to examine longer-term dynamics and potential effects on host-associated microbiota and secretion chemistry. Resistance continued to increase under pathogen exposure, while development and fecundity remained stable. Analyses of larval-associated microbiota showed that pathogen adaptation itself did not alter microbial community composition, but populations capable of niche construction exhibited increased microbial diversification. In contrast, chemical profiles of stink gland secretions did not change across selection regimes. Together, our results provide empirical evidence that niche construction facilitates resistance evolution and shapes host–microbe interactions.

Reconstructing the drivers of microbial associations across populations and communities

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Abstract

Insect-associated bacteria and fungi can profoundly influence host physiology, ecology, and evolution. Despite growing interest in insect microbiota, most insights derive from a limited number of model systems, leaving microbial diversity and distribution across natural populations and multi-species communities poorly understood. Marker-gene amplicon studies can address these gaps, but are frequently compromised by host taxonomic uncertainty, large variation in microbial abundance, and contamination from environmental or laboratory sources. These challenges are further exacerbated by the lack of an integrated analytical framework tailored to diverse insect systems.

Here, we present a conceptual and analytical approach for reconstructing the drivers of microbiota composition across large numbers of taxonomically and ecologically diverse insects. By integrating metabarcoding-based characterization of both hosts and their microbial associates, microbiome quantification, and statistical modelling, this framework resolves the effects of insect genotype, population structure, and environmental characteristics, while accounting for confounding variables such as parasitoid interactions. In insect systems such as sap-sucking hemipterans and scuttle flies, we detect major differences among microbial functional categories in their distribution, association stability, and within-host abundance. For example, while putative nutritional symbionts are often fixed within broader host clades, facultative endosymbionts such as *Wolbachia* vary across host genotypes, populations, and sexes, and many other microbes show sporadic occurrence despite broad host taxonomic ranges.

By explicitly accounting for host identity, microbial load, and microbial biology, we obtain substantially deeper biological insight than using traditional amplicon-based community profiling approaches. This workflow provides a scalable foundation for comparative studies of insect–microbe associations across populations and communities.

Immune regulation of the bacterial microbiota of the tiger mosquito in response to interference with de novo production of aromatic amino acids

Mélanie BRETTON (Laboratoire d'Écologie Microbienne, UMR5557, UCBL, INRAE, VetAgroSup, Villeurbanne, France, Melanie.bretton@univ-lyon1.fr)

Pierre ANTONELLI, Edwige MARTIN, Laurent VALLON, Catherine LEGRAS-LACHUER, Claire VALIENTE MORO, Aurélien VIGNERON

Abstract

In their successful colonization of terrestrial environments, insects have developed the ability to thrive on nutritionally unbalanced food sources. Among insect essential nutrients, aromatic amino acids (AAAs) are crucial for their development, immunity, and motricity while often lacking in their diets. These AAAs can be supplied to insects by their associated microorganisms, which can synthesize them via the shikimate pathway. The availability of AAAs fluctuates in the environment, influencing the need for insect to depend to their microbiota. However, it is unclear whether insects can specifically regulate their microbiota for AAAs provisioning. This project used the Asian tiger mosquito *Aedes albopictus* to address this question. This insect undergoes an aquatic and detritivore larval phase with highly variable nutrient availability across habitats. To induce competition between the host and its microbiota, mosquito larvae were exposed to glyphosate, a shikimate pathway inhibitor, making the microbiota auxotrophic for AAAs and competing for their availability in the insect diet. In response to glyphosate exposure, we observed a stage-specific decrease of the bacterial microbiota independent of the inhibitor's action, suggesting activation of local immune processes. RNA-Seq analysis further characterized the insect transcriptional response to glyphosate, revealing the expression of genes encoding Defensins, broad-spectrum antimicrobial peptides. RNAi-mediated silencing of defensin partially restored bacterial microbiota density, validating that microbiota elimination due to glyphosate involves local immunity. This project highlights a direct link between nutrient availability and host-microbiota interactions in the Asian tiger mosquito, suggesting mechanisms governing the intricate dialogue between mosquitoes and their associated microorganisms.

Bees as ecological reservoirs and dispersal agents of fission yeasts

Marie-Amélie PUSSACQ--CAILLET (CEFE - CNRS, Marieameliepussacq@gmail.com)

Ambre NOLY, Jade ZANUTTO, Dominique HELMLINGER, Maryse VANDERPLANCK

Abstract

Bees have an important effect on ecosystems, engaging in continuous interactions with their environment. Microorganisms such as yeasts play ubiquitous roles in these dynamic exchanges, as residents of floral resources, bee gut microbiota, and bee products. Recently, a majority of fission yeast species (*Schizosaccharomyces* spp.) have been isolated from bee food provisions. While little is known about the natural history and evolutionary trajectory of this early divergent clade of Ascomycetes, these observations suggest that bee food provisions serve as an important reservoir of fission yeasts. Intriguingly, neither field surveys nor metagenomics data have identified these species within floral nectar or the honeybee microbiota, prompting us to investigate the mechanism underlying their propagation from the phyllosphere to bee products.

We thus designed an experiment to test whether these species can survive, at least temporarily, in the bee digestive tract upon ingestion. To this aim, three fission yeast species recurrently isolated from honey and pollen bread (*S. pombe*, *S. octosporus* and *S. osmophilus*) were ingested in three different physiological states (proliferation, quiescence and sporulation) by females from two social (*Apis mellifera* and *Bombus terrestris*) and two solitary (*Osmia cornuta* and *O. bicornis*) bee species.

While *S. pombe* survived in the digestive tract of all bee species after 48h, *S. octosporus* and *S. osmophilus* survival appear limited to *Osmia* sp. and *A. mellifera*. Yeast spores survive better overall within bees, while the abdomen is the body part with the highest abundances. The latter suggests random dispersal through dejections, which is currently under investigation. In addition, we observed yeast survival in bee mouthparts, supporting the hypothesis that live yeasts may be transferred through nectar regurgitation during the processing of food resources. We will discuss how this study provides one of the first hint of fission yeast biotics interactions and dispersal.

Socially shared bacterial symbionts shape the seed harvesting behaviour of *Messor* ants

Jie XIE (Ghent University, Department of Biology & Department of Plants and Crops, Jie.xie@ugent.be)

Diego CASTILLO-FRANCO, Maxence JACQUET, Godefroi GIGNOUX, Jonathan ROMIGUIER, Patrick DE CLERCQ, Peter VANDAMME, Nicky WYBOUW

Abstract

The evolution of herbivory is severely constrained in animals due to the unfavorable nutritional and defensive qualities of plants. Of the ~25,000 species of ants, only few lineages have evolved the ability to survive solely on a plant diet. Seed-harvesting *Messor* ants are remarkable because entire colonies can thrive on the highly imbalanced diet of plant seeds. Through exhaustive long-read genotyping of field colonies across the species-rich *Messor* genus, we uncover widespread and complex co-infections of *Weissella* bacteria. Leveraging novel circular genomes and MALDI-TOF mass-spectrometry, we show that these co-infections are formed by a great diversity of *Weissella* species and genotypes. Using experimental colonies, we track *Weissella* transmission and titers across tissues, developmental stages, and castes, revealing a close association with the seed harvesting and feeding behaviour of *Messor*. We further gathered evidence that social interactions mediate the spread of these bacteria in *Messor* colonies. To test for a functional role of some of the unique *Weissella* lineages in the seed harvesting behaviour, several complementary assays were conducted using our genome-sequenced in vitro cultures. Of note, we show that seed preference is contingent on symbiotic inoculation and varies across different *Weissella* lineages, ranging from strong positive to negative effects. Together, our results uncover the complex reciprocal effects of symbiosis on animal herbivory and behaviour.

#10553

PHYSIOLOGY & BIOCHEMISTRY: Insect pathology and immunity 1

02/07/2026 at 10:30, Loches

Insect immunity and antimicrobial resistance

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Abstract

Upon infection insects always deploy cocktails of immune effectors, many of which are antimicrobial peptides. Here I will discuss reasons why cocktails have been the result of natural selection. If these AMP cocktails are adaptive, they can inspire new ways to tackle antimicrobial resistance.

Variation in the duration of the immune protection after priming stimulation among populations of *Tenebrio molitor*

Jordy LARGES (Biogéosciences, UMR 6282 CNRS/Université Bourgogne Europe, Dijon, Jordy.larges@u-bourgogne.fr)

Charlène DEVELAY, Aude BALOURDET, Thierry RIGAUD, Yannick MORET

Abstract

Immune priming refers to an invertebrate individual's ability to improve its immune response following an initial, non-lethal exposure to a pathogen. This form of innate "immune memory" has likely evolved as a result of repetitive challenges by the same pathogens throughout the invertebrate's lifetime. Adults of the mealworm beetle, *Tenebrio molitor*, exhibit interindividual variation in the duration of the immune protection conferred by the priming response to a standard pathogenic challenge. Immune priming incurs fitness costs, which generate trade-offs with other life-history traits and may, therefore, contribute to variation in its expression. Allocating resources to immune priming should depend on the likelihood of future survival and reproduction, which is a function of mortality risks caused by re-infection exposure. Consequently, short-lived individuals may have a low probability of being exposed to repeated infections by the same pathogen, whereas individuals with extended longevity should benefit from investing in immune priming because they are more likely to face re-infection.

This study investigated whether investment in immune priming, estimated as the duration of the immune protection after priming stimulation, is associated with adult longevity among three genetically distinct populations of *T. molitor* that exhibit contrasted life histories. To this end, age-controlled adults from each population were immune-primed 14 days post-eclosion with a standard dose of inactivated *Bacillus cereus* and then subsequently infected with the live bacterium at different time intervals post-priming stimulation (i.e., 30, 45, 60, 75, and 90 days post-injection). Survival was monitored for 15 days following infection to assess the persistence of the protective effect induced by priming. Long-lived insect populations are expected to exhibit sustained late-life protection than short-lived ones.

Insect extracellular vesicles as vectors of RNA Interference: A proteomic and functional perspective

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Iris CALLEWAERT

Abstract

Extracellular vesicles (EVs) play a crucial role in intercellular, interspecies and interkingdom communication, facilitating the exchange of molecular information among diverse cells and organisms. Their ability to transport small RNAs enables them to modulate gene expression in recipient cells via the conserved regulation mechanism of RNA interference (RNAi). This property holds great promise for the development of sustainable, RNAi-based crop protection strategies. However, our knowledge of the molecular composition of insect-derived EVs remains limited.

To address this, we isolated EVs from *Drosophila melanogaster* cells and characterized their proteome, revealing a repertoire of EV-associated proteins. These findings illuminate the intricate molecular and biological processes in which these vesicles are involved. Notably, orthologs of proteins found in human EVs are identified in the insect EV proteome, highlighting the evolutionary conservation of molecular components involved in EV-mediated processes across species.

The ability of EVs to transfer RNA molecules suggests a potential mechanism for systemic RNAi and the horizontal transmission of RNAi signals between insects. We investigated the potential of this interspecies communication at cellular level and elucidated the involvement of EVs in RNAi.

By integrating proteomic data with insights into interspecies RNA transfer, we present a comprehensive view of insect EV functions and provide a foundation for exploring their potential applications in pest control strategies. Overall, our findings highlight the significance of EVs in orchestrating molecular crosstalk within the insect kingdom and open new avenues for research in insect biology and beyond.

Incidence and detection of spore forming bacteria in mass-reared black soldier fly larvae

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Abstract

The larvae of the black soldier fly (*Hermetia illucens*) (BSFL) can grow on a wide range of wastes and byproducts, differing in nutritional composition and pH and representing the optimal growing environment for many microorganisms that might represent a risk for human or animal health. BSFL are known for their capacity to reduce some pathogens. However, their efficacy in eliminating spore-forming bacteria is less well documented. In this study we describe *Paenibacillus thiaminolyticus*, a Gram+ spore-forming bacteria, isolated from symptomatic BSFL in France, and discuss its interactions with the growing media and the host. First, the evaluation of *P. thiaminolyticus* ecology in diet and its persistence in BSFL was evaluated in order to estimate the risk of contamination and pathogens persistence during insect rearing. Then, challenge tests using pathogen inoculation into the diet were performed to assess the virulence of *P. thiaminolyticus* on BSFL growth, survival and eventual capacity to reduce *P. thiaminolyticus*, depending on spores or vegetative form. In laboratory conditions, the infected insects exhibited symptoms such as brownish colour, softening, liquefaction, off flavour, death, decay of the larvae, cannibalistic behaviour, and arrested or delayed development, resulting in reduced larval weight, pupation and adult emergence. However, on the industrial site, symptoms were sometimes more severe, with growth arrest, softening, death, and decay of larvae. During the challenge tests, the presence of the *P. thiaminolyticus* strain in both BSFL and diet was verified with specific molecular detection probes as well as by using fluorescence and antibiotic labeling genetic techniques. This study describes a new spore-forming BSFL pathogen, a *P. thiaminolyticus* strain, and underscores the importance of developing good manufacturing practices (GMP) guidelines and detection methods for spore-forming pathogens in rearing equipment, feeds and larvae to preserve insect health in mass rearing environment.

Malpighian Tubules as an Immune-Active Tissue in the Honey Bee (*Apis mellifera*)

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Abstract

The Malpighian tubules (MTs) of honey bees (*Apis mellifera*) are mainly known for their roles in excretion, detoxification, and osmoregulation. However, their potential contribution to immune defence remains largely unexplored. MTs can be directly targeted by the parasitic amoeba *Malpighamoeba mellificae*, a major pathogen of these organs, suggesting that local immune activity in these tissues may be biologically important.

To investigate whether MTs function as an immune-active tissue, we examined the gene expression and localization of key antimicrobial peptides (AMPs), small and rapidly induced effectors of insect innate immunity. We focused on four honey bee AMPs: apidaecin, abaecin, defensin-1, and hymenoptaecin. Quantitative PCR (qPCR) was used to measure transcript levels, and immunohistochemistry was performed to detect AMP localization *in situ* within MT epithelial cells.

The qPCR analysis revealed that all four AMPs were expressed in MTs, with different patterns suggesting selective upregulation in response to immune stimuli. Immunohistochemical staining confirmed the presence of abaecin, defensin-1, and hymenoptaecin, which were localized in the epithelial cells lining the MTs. Together, these findings show that MTs produce AMPs locally at both the transcript and peptide levels, highlighting their role as an autonomous immune organ, complementing both gut and systemic hemolymph-derived responses.

Our findings demonstrate that MTs function not only in excretion and detoxification but also as an active site of antimicrobial defence. This newly characterized immune function may play a critical role in protecting MTs against pathogens, such as *Malpighamoeba mellificae*, and more broadly, in maintaining gut-associated immunity in honey bees. Understanding local immune mechanisms in MTs may provide new insights for enhancing honey bee health and resilience in both apicultural and ecological contexts.

The grant supported this study by the MŠMT of Czech Republic, grant LUAUS24085.

It takes two to tango – Painless channels and tachykinin-related peptides as modulators of haemocyte activity in mealworm beetles, *Tenebrio molitor* L.

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Abstract

Transient receptor potential channels (TRP channels) are a conserved family of cation channels that participate in cell signalling. Initially, their functions and distribution were associated with the nervous system, but recent findings clearly indicate their role in modulating the activity of non-neuronal cells, including immune cells. Moreover, TRP channels participate in neuropeptide signalling and seem to be a link between the perception of stress stimuli and the modulation of the synthesis and release of neuropeptides involved in stress responses, such as tachykinins. Interestingly, neuropeptides are compounds that orchestrate all physiological processes as well as immune mechanisms. Therefore, TRP channels and neuropeptides are closely connected in the modulation of immune cell activity. However, in insect immunomodulatory role of TRP channels and their relationships with neuropeptides are poorly understood. Based on the structural and functional homology between TRP channels and neuropeptides in insects and vertebrates, we assume that similar relationships can be also observed in insects.

Our research conducted on mealworm beetles (*Tenebrio molitor*) confirmed the role of both components: TRP channels (by Painless channel example) and tachykinin-related peptides (TKRP), in the regulation of haemocyte activity. These findings were confirmed not only by injection of Painless activator and Tenmo-TRP-7 (one of the TKRPs identified in *T. molitor*) but also via dsRNA-based knockdown. Furthermore, we revealed that the knockdown of *Painless* influences the expression level of the genes encoding the TKRP precursor (*TKRP*) and receptor (*TKRPR*). On the other hand, knockdown of *TKRP* and *TKRPR* affected the expression of *Painless*.

The obtained results clearly indicate the presence of dependencies between insect TRP channels and tachykinin-related peptides like those observed in vertebrates. Therefore, the presented results allow us to better understand evolutionary dependencies in the regulation of immune cells in invertebrates and vertebrates.

The research was partially supported by OPUS 2021/41/B/NZ9/01054 (National Science Centre).

Eco-immunology: An integrated approach of the interactions between nutrition, immunity, symbionts and infection

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Abstract

Nutrition is critical to immune defence and resistance to pathogens, with consequences that affect not only the health, welfare and reproductive success of individual organisms, but also have profound ecological and evolutionary implications. The research in my team focuses in better understanding the network of interactions that defines the relationships between nutrition, immunity, infection, and microbiota to provide a more comprehensive understanding of the key determinants of the outcome of host–pathogen interactions. In this seminar I will talk about my fundamental and applied work on flies, beetles and bees. I will demonstrate how basic research in nutrition, immunology and symbiosis can lead to biosecurity applications through, for instance, the use of probiotics in bees and development of control methods for hive beetles using symbionts volatiles.

Fickle things: Mosquito virome dynamics under spatial and temporal factors

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Anamarija BUTKOVIC, Lionel FRANGEUL, Hervé BLANC, Aurélien GIBAUD, Annabelle HENRION-LACRITICK, Rohit CHITALE, Sébastien BOYER, Jean-Bernard DUCHEMIN, Philippe DUSSART, Romain GIROD, Nina GRAU, Carine NGOAGOUNI, Maria-Carla SALEH

Abstract

Mosquito vectors are often known for the viruses they transmit, but their viral microbiota comprise much more. These virus communities are part of a meta-ecosystem that engages in positive or negative interactions with co-infecting mosquito-borne viruses. Thus, understanding the spatio-temporal dynamics of viromes helps us predict the emergence and transmission potential of mosquito-borne viruses. However, longitudinal virome data are scarce. In this work, we sought to quantify the relative contributions of the host and ecological factors that shape mosquito virome diversity and composition. To this end, we performed a metatranscriptomic analysis to characterise the virome of 15 mosquito species sampled seasonally over two years from countries representing South American, African, and Southeast Asian geographies. We reveal that, while host species largely determine virus community diversity, community composition varies heterogeneously across host species and virus families. Overall, mosquito viromes are highly dynamic, with spatial factors influencing composition more strongly than temporal factors. Certain host phylogenies, notably *Culex* mosquitoes, are more frequently associated with generalist viruses. Altogether, this work highlights the nuances in which evolutionary and ecological drivers influence mosquito virome dynamics. The trends we observed provoke new questions necessary to translate surveillance data into actionable preparedness efforts against mosquito-borne viral diseases.

Formicine ant venoms as external immune defence trait

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Abstract

Secretions delivered by an organism to its environment can play a major role in mediating the interaction of these organisms with the microbes surrounding them. These secretions can improve an organism's survival acting as an externalized immune defense trait. Although external immune defence in the form of such secretions can be found in many different taxa, the extension of immune defence to the environment is well documented for exocrine gland secretions in social insects.

Ants from the subfamily Formicinae are famous for the formic acid contained in their venom gland secretion. Research of the last decade has revealed that their venom gland secretion is not only a weapon used for attack as well as defence, but that it is used to prevent disease spread by manipulating microbes in the nest, food resources and on group members.

Here I present new evidence into the evolutionary pressures that shape the maintenance and expression of formicine venom gland secretion as external immune defence trait, supporting the view that external immune defence has likely been favoured in social insects. Moreover, I present evidence that the use of the venom gland secretion as external immune defence trait is not restricted to formicine ants but likely broadly present in Hymenoptera. Finally, I present evidence that the venom gland secretion of formicine ants contains much more than just formic acid, highlighting an arsenal of so far undescribed, evolutionary novel antimicrobial components.

RISC-bound small RNA-seq elucidates dsRNA processing and guide siRNA strand selection

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Abstract

RNA interference (RNAi) has emerged as an environmentally friendly pest control strategy. RNAi-based pest control relies on the delivery of double-stranded RNA (dsRNA) complementary to essential pest genes. Insect Dicer-2 processes dsRNA into small interfering RNA (siRNA) duplexes, and if the antisense is selected as the guide strand, it directs the RNA-induced silencing complex (RISC) to cleave target mRNA. We previously showed that considering siRNA features during dsRNA design can improve insecticidal efficacy. However, the processing of different dsRNAs into distinct siRNA pools in vivo remains poorly understood, which limits the potential of dsRNA sequence optimization. In this study, we generated a comprehensive dataset of RISC-bound siRNAs derived from 34 insecticidal dsRNAs injected into *Tribolium castaneum*. Analysis of this dataset revealed that dsRNA termini generally generated fewer sense than antisense siRNA strands, while internal regions generated both strands in similar abundances. We also tested the processive cleavage model that assumes Dicer-2 cuts dsRNA in regular 21-nt frames based on the previous in vitro studies. Injection of dsRNAs differing only by a few terminal base pairs showed no effect on RISC-bound siRNA peaks, suggesting that it is not a reliable model for improving dsRNA designs. We next examined factors influencing guide strand selection or retention by RISC. Correlation analysis suggested that GC% differences between the terminal 1-5 paired nucleotides of siRNA duplexes influence the strand selection, which can be exploited to improve the antisense-to-sense strand ratio incorporated into RISC. Targeting protein coding, rather than 3' untranslated, regions of the mRNA and a lack of self-folding structures were also associated with higher antisense-to-sense ratios in RISC. Overall, this study reveals insights into how exogenously delivered dsRNA sequence determines the final pool of RISC-bound siRNAs in an insect pest in vivo, and the findings may allow us to refine dsRNA optimization strategies.

Blade-running: An efficient yet simple behavior to potentially combat summit disease in ants

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Abstract

Social insect colonies are prime targets for parasites due to high host density and frequent interactions that facilitate transmission. Some pathogens induce "summit disease," manipulating infected hosts to climb vegetation before death, thereby optimizing spore dispersal from elevated positions. In ants, previous observations suggested that early corpse removal might reduce transmission success of summit-disease pathogens such as *Pandora* fungi. We experimentally tested whether corpse disposal represents an effective prophylactic mechanism by simulating summit disease using fresh uninfected ant corpses and dummies affixed to grass blades near a large nest complex. Ants rapidly detected and removed corpses, with removal efficiency highest for those positioned close to nest margins. Our results suggest that corpse removal functions as a general hygienic behavior rather than a pathogen-specific response, providing broad protection against diverse pathogens including—but not limited to—those causing summit disease. This non-specific prophylactic strategy may represent an evolutionarily stable defense mechanism in social insects facing multiple pathogen threats.

Molecular mechanisms and evolution of a hemolymph neurotoxin in the Colorado Potato Beetle

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Abstract

Many insects harbour toxins in their hemolymph that are lethal to their predators, but not to themselves. However, the underlying genetic mechanisms and evolutionary drivers enabling toxin production and auto-resistance remain largely unknown. The Colorado potato beetle (*Leptinotarsa decemlineata*) is a notorious agricultural pest renowned for its remarkable resilience to environmental stresses and lack of natural enemies – traits likely linked to the production of leptinotarsin, a potent neurotoxin present in its hemolymph. Upon injection, leptinotarsin induces a sustained influx of calcium ions, triggering neurotransmitter release from presynaptic terminals and causing lethality in insects and vertebrates. Notably, this toxin is present across all life stages, suggesting an essential but uncharacterized biological role. While its neurotoxic effects are well-documented, the genetic basis of leptinotarsin biosynthesis and the beetle's self-tolerance mechanisms remain unresolved, raising critical questions about how toxin-rich organisms evolve precise regulatory pathways to avoid autotoxicity.

To address this, we combined transcriptomic, proteomic, and functional genomic approaches to identify leptinotarsin-associated genes. Hemolymph toxicity was first confirmed via injection assays in adult *Drosophila melanogaster*, establishing a robust bioassay system to quantify leptinotarsin's lethal effects. Toxic hemolymph components were then isolated by fast protein liquid chromatography (FPLC), and characterized using shotgun proteomics. Our findings challenge previous hypotheses suggesting leptinotarsin evolved from juvenile hormone esterase. Instead, we found novel candidate genes linked to toxin production. Preliminary results implicate voltage-gated calcium channels as toxin targets, potentially explaining autoresistance.

We established RNA interference (RNAi) feeding assays to target candidate genes, with subsequent injection of RNAi-treated beetle hemolymph into *Drosophila melanogaster* to confirm reduced lethality and identify toxin-producing genes. Together, our work establishes the first genetic framework for leptinotarsin biosynthesis and advances our understanding of the evolutionary mechanisms of novel hemolymph toxins in insects.

Changes in transcriptomic profiles of wild and lab flies during an infection with a natural pathogen.

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Abstract

Insect model organisms have proven powerful tools to understand the biology of infections and host-pathogen interactions. The immune pathways of *Drosophila melanogaster* in particular have been extensively studied.

However, how representative is the response to an infection of domesticated insect lines of the response of their wild counterparts remains unclear.

We performed RNAseq of wild caught *D. melanogaster* as well as flies of a line established in the lab, 6 hours after an infection by *Providencia burhodogranariae*, a bacteria previously isolated from wild *Drosophila*. Our samples consisted of individually processed flies, allowing us to capture the variation in their transcriptomic profiles. In parallel, we tested the virulence of *P. burhodogranariae* by assaying the load it achieved in the flies of different conditions, as well as their survival.

We found that while the bacterial loads achieved by *P. burhodogranariae* in wild and lab flies were similar, wild flies had a poorer survival than lab flies when kept in laboratory conditions. As expected, domestication resulted in major changes in the transcriptomic profiles of the flies. By comparison, wounding and the infection had a smaller effect on the transcriptomic profile, although we did find a differential expression of immune genes in wounded and infected flies compared to control.

Our results suggest that a few immune genes plus a change in resources allocation might be responsible for differences in survival between wild and domesticated flies.

Invasion of the body snatchers: Leveraging zombie-making strategies of entomopathogenic fungi to understand insect behaviour

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Abstract

The evolutionary arms race between parasites and hosts can culminate into complex extended phenotypes that benefit disease progression and transmission. Many entomopathogenic fungal species seem to have developed this strategy. The fungus-adaptive changes in behaviour as seen in *Ophiocordyceps*-infected carpenter ants are a prime example. These “zombie ants” demonstrate a suite of behaviours that are thought to circumvent the social immune responses of the colony. Subsequently, the hijacked ant attaches itself at an elevated position that benefits fungal spore development and dispersal. The precise mechanisms underlying these, and other, parasite extended phenotypes are largely unknown. Filling this knowledge gap would improve our molecular level understanding of insect behaviour and could lead to novel pest control strategies.

To unravel the molecular underpinnings of fungal manipulation of insect host behaviour, we have developed “zombie ants” into an integrative model system. Combined fungal culturing and lab infections with behavioural assays and multi-omics unveiled several fungal effector proteins and their putative ant host targets underlying manipulated behaviours. To determine the function of presumed fungal “manipulation” effectors, the host behaviours they elicit, and the host pathways that underly those phenotypes, we are currently, for the first time, integrating functional genetics. With this approach, we found that *Ophiocordyceps* secretes a novel cysteine-rich peptide that binds to insect scramblases, thereby inducing aberrant odour-related behaviours. Moreover, we discovered that fungal indole diterpenes cause tremors in ant hosts and affect locomotion and grooming behaviours. Additionally, we found that the molecular circadian clock of the ant is likely involved. These results represent some of the first molecular insights into parasitic hijacking of insect behaviour.

Honeybees vs. wild bees in context

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Abstract

Honeybees have increasingly been suggested to drive declines of wild bees via competition for food and pathogen transmission. This has already resulted in respective non-evidence-based policy making.

However, a sweeping opposition of “honeybees” to “wild bees” is not correct because: 1) only two species of the genus *Apis* are managed: western honeybees (*Apis mellifera*) and eastern honeybees (*Apis cerana*) and 2) most eastern and western honeybee colonies globally are wild and occur in their native range. Accordingly, wild native honey bees deserve the same protection as any other wild bees. Therefore, the term “honey bees” is wrong in this context and conservation of wild honey bees should be advocated more strongly in the ongoing public debate.

Irrespective of potential competition for resources and pathogen transmission between bee species, the key drivers for the ongoing global insect decline are pesticides, habitat destruction, invasive species and climate change. We here argue that research efforts and conservation policies should focus on the main drivers. The current focus on interactions between bees is distracting attention and resources from the main stressors and is thus detrimental for the conservation of all insects.

It seems high time to act now accordingly. We therefore propose that interactions between bees need to be communicated to the public urgently in a more appropriate fashion to limit counterproductive policy decision making. Further, sustainable solutions for key drivers will benefit all insects resulting in a win-win situation for managed and wild species.

Reduced-risk pesticides cause multiple disorders on individuals and colonies of bumble bees

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Abstract

There is increasing recognition that prolonged exposure to pesticides deemed “bee-safe,” including biopesticides, herbicides, and fungicides, may still impair pollinators. In this study, we evaluated the individual- and colony-level effects of four pesticide types on *Bombus terrestris* using an integrative approach. Workers were chronically exposed via oral ingestion to either uncontaminated honey syrup (control) or syrup containing the neonicotinoid acetamiprid (ACE), the herbicide glyphosate (GLY), the fungicide metalaxyl-M (MET), or the biopesticide sweet orange essential oil (OEO). All pesticide treatments induced sublethal effects in both individuals and colonies, whereas lethal effects emerged only in OEO-treated colonies, likely due to the higher concentration used. Colonies exposed to pesticides showed reduced mass gain (ACE, OEO, GLY), lower food consumption (all treatments), and decreased egg production (all treatments). At the individual level, food ingestion was negatively affected by OEO exposure. Worker walking behavior was influenced by both colony-level pesticide exposure and social isolation during individual assays. Overall, our findings show that chronic exposure to pesticides widely regarded as safe can still compromise bumble bee health, reinforcing concerns about their role in pollinator declines and emphasizing the need to account for social context when evaluating pesticide toxicity in social insects.

Climate change: Conservation measures are required to prevent the loss of genetic diversity of honey bees

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Grace MCCORMACK, Norman CARRECK

Abstract

Variability is a requirement for evolutionary success, never more urgent for biodiversity, given the current context of climate change. Natural variability in honey bee morphological, behavioural and genetic traits has allowed adaptation of native subspecies to a diversity of temperature and other environmental conditions. Such natural diversity shows that the species possesses sufficient plasticity and genetic variability to allow the development of populations suited to new environmental conditions that are emerging. In recent decades, however, the genetic diversity of honey bees has been reduced due to commercial beekeeping favouring a very limited range of genotypes. Conservation measures are therefore required to prevent the loss of the genetic diversity of honey bees and preserve ecotypes that are so valuable for the world's biodiversity.

Multilevel immune disruption in honey bees by parasites and viruses

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Abstract

Honey bees (*Apis mellifera*) are key pollinators in both natural ecosystems and agriculture, but their health is increasingly compromised by multiple interacting stressors. Biotic and abiotic challenges can disrupt immune function, leading to increased susceptibility to disease, elevated mortality, and colony losses. The honey bee immune system plays a central role not only in pathogen defense but also in maintaining gut microbial homeostasis by discriminating between beneficial symbionts and opportunistic microbes. Here, we provide a tentative model to describe how major biotic stressors, *Varroa destructor* and associated Deformed Wing Virus (DWV) redirect host physiology and metabolism, generating a complex immunosuppression syndrome. Using transcriptomics and RNA interference to dissect *Varroa* salivary components, alongside proteomics and metagenomics to characterize DWV replication and pathogenesis, we have shown that these stressors concur in the disruption of metabolic balance and immune signaling, associated with a gut dysbiosis which further contributes to the overall reduction of immune defence barriers. The proposed model tries to summarize how this multifaceted immunosuppressive syndrome by a parasite/pathogen association undermines honey bee health and can be aggravated by interacting stress agents. This provides the basis for the development of further functional studies and to design novel sustainable strategies to strengthen pollinator resilience in modern agricultural landscapes.

Population genomics of the invasive yellow-legged hornet *Vespa velutina nigrithorax* in Europe

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Abstract

The yellow-legged hornet (*Vespa velutina nigrithorax*) is a social Hymenoptera native to Asia and an invasive species in Europe, where it was first detected in France in 2004. Since then, the species has spread across the continent, invading France, Italy, Spain, or Portugal. Here, we further unveil the invasion genomics of *V. velutina* in Europe by surveying populations using single-nucleotide polymorphisms (SNPs). Population structure (sNMF) and relationship (DAPC) analyses revealed that invasive populations present strong clustering patterns with a unique genetic cluster, in contrast with previous studies based on short tandem repeats (STRs). All populations showed similar allelic richness, an excess of heterozygous individuals ($FIS < 0$), and bottleneck signals (Tajima's $D > 0$). Moreover, relative migration analyses revealed asymmetrical gene flow among populations, indicating that France constitutes the primary genetic source in continental European populations. Overall, this study provides further insights into the invasion genomics of *V. velutina* in Europe, which can aid in developing strategies to manage this major threat to ecosystems and beekeeping.

AI BeeGuard: SafeGUARDing honeyBEEs from invasive hornets through a multi-approach with Artificial Intelligence

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Abstract

Biological invasions constitute a major threat to biodiversity and ecosystem functioning and generate significant economic impacts. Invasive predatory hornets exemplify this problem, as their spread has severely affected apiculture and has led to increasing management expenditures for public authorities. Although the yellow-legged hornet (*Vespa velutina nigrithorax*) has received growing scientific attention, key gaps remain regarding optimal strategies for its surveillance and control. Furthermore, research on other recently introduced hornet species in Europe, such as *V. orientalis* and *V. bicolor*, is still scarce despite its urgent relevance.

In this contribution, we provide an overview of the global status of non-native hornet species and introduce the AI BeeGuard project. Of the 22 recognized species within the genus *Vespa*, five are currently established outside their native ranges (*V. velutina*, *V. orientalis*, *V. tropica*, *V. bicolor* and *V. crabro*). In addition, four other species (*V. mandarinia*, *V. affinis*, *V. simillima* and *V. soror*) have been detected in several countries.

The AI BeeGuard project addresses these emerging challenges by focusing, for the first time in Europe, on the recently detected species *V. bicolor* and *V. orientalis*, while also improving monitoring and management approaches for invasive hornets, including *V. velutina*. Specifically, the project aims to:

- (1) investigate the origin, genetic diversity, and ecological traits of *V. orientalis* and *V. bicolor*, as well as their impacts on beekeeping activities;
- (2) develop innovative tools for the detection and long-term monitoring of invasive hornets (*V. velutina*, *V. orientalis* and *V. bicolor*), combining non-invasive automated technologies (computer vision and optical sensors) with a mobile application (iHORNET) designed for beekeepers to report and monitor spatio-temporal patterns and;
- (3) assess control and mitigation measures to reduce hornet impacts, including the use of tubular muzzles to protect honeybee colonies and the preparation of a best-practices management guide for beekeepers and public managers.

A Multidisciplinary Strategy for Invasive Species Management: Can the Expansion of the Small Hive Beetle (*Aethina tumida*) Be Stopped?

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Michela BERTOLA

Abstract

The small hive beetle (*Aethina tumida*, SHB) is an invasive parasite and predator capable of causing severe losses in beekeeping industry worldwide. Following its first detection in southern Italy in September 2014, Italy implemented a structured, coordinated, and multidisciplinary response to contain its spread. This intervention was supported by a solid regulatory framework, as SHB is an EU and WOAHP listed disease with predefined control measures that allowed authorities to activate official protocols immediately. Containment efforts were further strengthened by the fact that the parasite affects managed honey bee colonies, whose movements are traceable through a national registry facilitating rapid identification of at-risk apiaries and supported efficient implementation of control actions.

The response integrated emergency measures, including intensive surveillance, destruction of infested apiaries, creation of protection and surveillance zones, and deployment of sentinel nuclei, with the establishment of a consolidated monitoring and reporting network. National surveillance was simultaneously reinforced beyond the outbreak areas to ensure prompt detection of any new incursions.

Beekeepers played a crucial role by strengthening voluntary monitoring, supported by compensation schemes that encouraged timely reporting. Institutional activities such as laboratory diagnostics, standardized data collection, and targeted information campaigns further reinforced the system. Between 2014 and 2017, more than 9,000 colonies from 164 apiaries and 46 sentinel nuclei were destroyed. As the epidemiological situation evolved, the strategy transitioned from attempted eradication to long-term containment. This coordinated framework successfully restricted SHB presence to Calabria and, sporadically, to parts of Sicily, with only two outbreaks recorded in 2014 and 2019.

A third outbreak detected in northeastern Sicily in October 2024 prompted immediate activation of all planned measures, demonstrating system preparedness and resilience. The Italian experience shows that containing an invasive parasite is achievable only through regulatory foundations, structured actions, robust surveillance and reporting network, and strong collaboration among all stakeholders.

CONTRIBUTIONS OF CHEMICAL ECOLOGY TO A BETTER UNDERSTANDING OF SOCIAL IMMUNITY IN THE HONEY BEE

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Abstract

Despite their high susceptibility to invasions and disease spread, many social animals such as the honey bee have evolved mechanisms that allow effective defence at the group level. These collective strategies play a role at society level that parallels that of an immune system, and the social immunity they confer provide the basis for colony resistance to pathogens and parasites, such as varroa and other diseases. How compromised individuals are accurately diagnosed, and how the collective actions of bees undertaking the immune strategies are regulated at colony level pose many unsolved challenges. It is however known that chemical communication, which plays a central role in homeostasis maintenance within colonies, also plays a key role in host-parasite interactions and in defence against pathogens in general. We will present the current knowledge on the contribution of chemical ecology to social immunity, as well as our latest findings on the mechanisms of hygiene against varroa parasitised brood. This presentation will highlight the input of an in-depth understanding of host defence mechanisms to provide essential tools not only to predict, but also to mitigate against consequences of invasive species events.

Sperm storage in males of the buff-tailed bumblebee (*Bombus terrestris*)

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Abstract

Sperm cells typically undergo functional decline with age. However, social Hymenoptera queens are well known for their remarkable ability to maintain high quality sperm throughout their life, which can last for several decades in some species. Here, we show a comparable phenomenon in males of the buff-tailed bumblebee (*Bombus terrestris*). Sperm quality remains high throughout male lifespan, despite male survival declining with age. By combining multi-omics profiling (long-read epigenomic sequencing and untargeted proteomics) and flow cytometry, we show that sperm cells lack canonical hallmarks of aging. Long-term colony monitoring demonstrates that the duration of sperm storage by males before mating does not affect colony growth or productivity. Together, these findings show that *B. terrestris* males maintain high quality sperm throughout their life, sustaining their reproductive fitness regardless of age.

From tree beekeeping heritage to biodiversity: log hives as nesting resources for social Hymenoptera in managed montane forests

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Abstract

Tree cavities are increasingly limited in managed forests, constraining nesting opportunities for cavity-dependent species such as the Western honey bee (*Apis mellifera*) and cavity-nesting wasps (Vespidae). In Eastern and Central Europe, traditional forest beekeeping has left a cultural legacy of log hives—hollowed tree trunks that now persist as surrogate cavities. These structures provide an opportunity to assess how cavity availability shapes the distribution of social insects in managed landscapes.

We investigated the occurrence of *A. mellifera* and wasps, including the European hornet (*Vespa crabro*), in approximately 1,000 log hives across montane forests of the Sudety Mountains (south-western Poland). Using repeated surveys (2019–2025) and high-resolution data on forest composition and microclimate, we modeled species occurrence across multiple spatial scales while accounting for spatial clustering and interannual variation.

The occurrence of all species was positively associated with broadleaf forest cover and local tree species diversity, whereas vertical cavity occupancy was strongly associated with temperature conditions. Honeybee occupancy probability declined from approximately 25% at low elevations (400 m asl) to less than 5% above 650 m. Habitat effects were most pronounced at intermediate spatial scales (several hundred meters), indicating that surrogate nesting site suitability depends on the surrounding forest matrix rather than on cavity availability alone. Log hives functioned as persistent surrogate cavities, facilitating occupancy in otherwise cavity-poor managed stands.

Our findings demonstrate that cultural forest legacies meaningfully influence the distribution of social Hymenoptera in production forests. Maintaining traditional log hives alongside structurally diverse forests may offer a low-cost option to support cavity-nesting insects in managed montane landscapes.

Genetic diversity of the Ivorian honeybee, *Apis mellifera adansonii*, and implications for sustainable food systems in Africa

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Abstract

L'abeille domestique (*Apis mellifera*) joue un rôle crucial dans la sécurité alimentaire, la réduction de la pauvreté et la résilience des agroécosystèmes. En Côte d'Ivoire, l'intégration des ruches dans les cultures maraîchères suscite un intérêt particulier comme solution à la baisse des rendements et de la qualité de la production. Elle contribue également à sensibiliser les maraîchers au problème des pesticides. Dans ce contexte, la présente étude, menée dans le cadre du programme TSARA visant à développer des systèmes alimentaires durables en Afrique et en Europe, a pour objectif de caractériser la diversité génétique des populations locales d'abeilles domestiques afin de comprendre leurs capacités d'adaptation. Pour ce faire, nous avons collecté des abeilles domestiques dans cinq zones agroécologiques du pays, en complétant nos enquêtes de terrain auprès des apiculteurs. Malgré quelques publications suggérant une plus grande résistance ou tolérance au varroa chez les populations africaines, nous avons constaté une prévalence significative de ce parasite. Les échantillons ont été séquencés à l'aide de la technologie Illumina (lectures courtes). Les analyses de diversité et de structure des populations ont été réalisées à partir de SNP autosomiques, ainsi que par l'analyse d'assemblages complets de novo de l'ADN mitochondrial. Cette approche a été privilégiée par rapport à l'alignement conventionnel des lectures sur une séquence de référence, ce dernier induisant des taux d'erreur élevés dus à la présence d'insertions d'ADN mitochondrial nucléaire (NUMT). Les premiers résultats indiquent que la population d'abeilles ivoiriennes appartient à la lignée africaine A et forme un groupe distinct des autres lignées mondiales. Ceci souligne l'existence d'un patrimoine génétique local intact, susceptible de contribuer à une résistance naturelle aux parasites et aux variations environnementales. Les résultats de cette étude ouvriront la voie à l'amélioration des pratiques apicoles, au renforcement de la résilience des agroécosystèmes et au soutien du développement durable en Côte d'Ivoire. Cette étude constitue également un bon exemple de coopération européenne et subsaharienne, incluant des aspects aussi variés que le travail de terrain, avec des enquêtes auprès des apiculteurs et des analyses bioinformatiques.

An Individual-based model to assess the efficiency of pollination ecosystem services

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Paola GERVASIO, Giorgio SPERANDIO, Fani HATJINA, Anna SIMONETTO, Gianni GILIOLI

Abstract

Managed honeybee colonies and wild pollinators are key providers of pollination services in both natural and agricultural ecosystems. The efficiency of these services emerges from complex interactions among pollinator population dynamics, landscape-level resource availability, and interspecific competition. Most models developed to examine pollination services, address pollination in isolation, limiting the ability to capture feedback between colony dynamics, landscape structure and dynamics, competition between pollinators.

The Individual-based model presented here couples honeybee colony dynamics with a spatially explicit and dynamically evolving landscape, linking resource availability, foraging behaviour, and pollination demand. The landscape is represented as a mosaic of cells characterized by land-use type and floral resource supply, with nectar and pollen availability modified by pollinator visitation. Pollination demand is defined at cell level and satisfied through pollinator activity, linking colony behaviour and ecosystem service provision.

Intraspecific competition among managed colonies is accounted for by allowing multiple hives within an apiary to exploit shared landscape resources, while internal colony dynamics are represented through a single average hive. A simplified module for wild pollinators is also included, representing trait-based assemblages that consume floral resources and contribute to pollination demand satisfaction, thereby introducing interspecific competition. Hive dynamics are driven exclusively by environmental conditions and resource availability, without explicit dependence on calendar time, enabling application across climatic contexts with differing degrees of seasonality.

The framework is designed to explore alternative scenarios combining landscape structure, apiary density, and management choices, and to quantify their implications for both apiary productivity and pollination service provision. In particular, it enables investigation of the relationship between total apiary productivity and the number of hives, while accounting for the satisfaction of landscape-level pollination demand. As such, the model provides a tool to address the dual challenge of maximizing beekeeper productivity while ensuring adequate pollination services for agricultural systems.

Understanding bee microbiome diversity: contributions of behavior, host phylogeny, and climate

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Johan EKROOS, Anne DUPLOUY

Abstract

The assembly of the microbial communities associated with bee species are strongly affected by environmental, ecological and evolutionary aspects of their hosts. The relative importance of these variables and their interactions in shaping bee microbiome globally remain unclear. In our study, we collect global public 16S rRNA amplicon sequencing data and their curated associated metadata to disentangle the importance of climate, host phylogeny and behavioral traits on structuring bee-associated microbial communities. We hypothesize that: (a) phylogeny directly structure gut bacterial communities, with the evolution of host nesting and social behavior having a strong effect in the structuring; and (b) climatic variables act as environmental filters that also structure microbial assemblies independently of host phylogenetic relationships, through homogenizing selection of β -diversity within climatic regions, and differential selection of environmentally-sensitive bacterial taxa. Our study contribute to the evaluation of how environmental and host-associated factors shape bee microbiome assemblies, informing microbiome-based approaches for wild bee conservation, management, and food security.

The alarm pheromone could be used for a pheromone-based trap to control the invasive Yellow-legged hornet?

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Mélissa HAOUZI, Claire MARCOUT

Abstract

In social insects, alarm pheromones are particularly useful to protect the colony, by inducing nestmates recruitment and defensive behaviours when they are exposed to a danger. The chemical composition of these pheromones can vary depending on factors such as caste, colonial origin, and the age of individuals. Studying the alarm pheromone composition in invasive species is essential for identifying attractive compounds that could be used in the development of effective pheromone-based traps. Additionally, understanding how the chemical profile of this signal changes throughout the insect's life cycle could enhance the design of such applications. We showed that the composition of the alarm pheromone can vary in the invasive hornet *Vespa velutina* according to the caste, the colony, the task of workers and their age. In spite of its variability, workers, whatever their colonial origine, can be attracted by the pheromone blend, demonstrating its putative use in a trap to control the invasive population.

Funerary archaeoentomology: a discipline to investigate biodiversity, local extinction and new arrivals

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Giuseppina CARTA

Abstract

Archeoentomology, a subfield of environmental archaeology, studies insects and other arthropods to help reconstruct past events, climates, and landscapes. Funerary archaeoentomology, defined by Huchet (1996), examines arthropods associated with human remains or with elements of funerary practices, such as offerings.

Recent Italian research spans roughly 5,000 years and diverse contexts. Samples include remains from Sardinian necropolises, Egyptian mummies in Italian museums, votive offerings, and mummified or skeletonized bodies of rulers, saints, and ordinary people. Over 80% of studies focus on modern-era burials—particularly crypts beneath churches and World War I soldier interments. Across contexts, the dominant insect orders recovered are Diptera and Coleoptera; among arachnids, mites are the most significant group.

Reported findings encompass local extinctions (e.g., *Phormia regina*, Calliphoridae), introductions of potential new species (e.g., *Hermetia illucens*, Stratiomyidae), human and animal ectoparasites (Siphonaptera, Psocodea), and pests of food and wood (Curculionidae, Ptinidae, Dermestidae, Cleridae, Tenebrionidae). Distribution patterns of various flies (Phoridae, Muscidae, Fanniidae, Calliphoridae, Sarcophagidae) are also discussed. With robust historical documentation and reliable dating, this body of work enables temporal analysis of entomofaunal change in relation to human activity, trade, and travel.

Scarab Chronicles: Reconstructing Neolithic Pastoralism and Coastal Resource Management through Beetle Remains in South-Western France

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Jean-Bernard HUCHET, Florence VERDIN

Abstract

Erosion along the French Atlantic coastline exposes previously unknown archaeological sites, while simultaneously threatening this fragile heritage with irreversible loss. At the archaeological site of l'Amélie (Soulac-sur-Mer, Gironde), waterlogged and anoxic sediments have preserved insect remains in exceptional condition. An archaeoentomological study undertaken during doctoral research identified 250 taxa, whose remarkable diversity and narrow ecological specialisation provide unprecedented insights into coastal environments and human practices from the Neolithic to Antiquity in south-western France.

A rich assemblage of dung beetles offers robust evidence of livestock farming, revealing spatial and temporal variations in grazing intensity. High proportions of dung-associated taxa in a Middle Neolithic well indicate substantial herds as early as 5500 years ago, providing the first evidence of coastal livestock farming in Neolithic France and highlighting a pivotal stage in the emergence of sedentary lifeways. Lower proportions in other contexts suggest more limited grazing, possibly constrained by saline water availability. The diversity and abundance of aquatic and riparian beetles point to a water-rich landscape used for animal watering, while pasture-associated species indicate open environments favourable to agropastoral practices. Differences between freshwater- and saline-associated taxa helped position archaeological structures within the former tidal regime and clarified their function (wells, salt production). The discovery of the stored-product pest *Sitophilus granarius* (L., 1758) in the oldest structure (4300 BC) represents the earliest occurrence in western France, providing evidence of long-distance exchange networks already active six millennia ago. Finally, comparisons between fossil and modern entomofaunas from the Gironde region reveal long-term biodiversity shifts shaped by climate and human activity.

These findings demonstrate the potential of archaeoentomology and statistical approaches to explore multi-millennial interactions between humans, animals, and coastal ecosystems. This innovative study along the French coastline provides new insights into the lifeways of estuarine societies and contributes to the preservation of endangered archaeological heritage.

In archeoentomology, sedimentary DNA sheds light on soft-bodied arthropods absent from classical insect remains

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Marina QUEREJETA, Simon DUPONT, Karine MUSSET, Christophe BRESSAC

Abstract

Archeoentomology is a discipline that studies insect remains preserved in archaeological deposits to reconstruct human practices and paleoenvironments. This discipline relies on the most robust groups, such as dipteran pupae or beetle fragments, because soft-bodied arthropods decompose too quickly to allow for identification. This preservation limitation inevitably restricts our view of the diversity of insects in the past. Here, we present the potential of ancient sedimentary DNA (sedaDNA) to overcome this limitation by reconstructing insect communities from two archaeological wells excavated at two distinct Gallo-Roman sites in France. To assess the complementarity of metabarcoding with conventional approaches, we directly compared DNA data with morphological identifications obtained in the same contexts.

The joint study of the two approaches reveals differences between archaeological contexts, whether in terms of local environmental conditions or the use of each site during its occupation. The most striking result comes from sedaDNA: most of the taxa detected belong to soft-bodied groups that almost never appear in conventional assemblages. In contrast, sclerotized insects, which generally dominate archeoentomological samples, particularly beetles, are only marginally represented in the DNA sequences. Despite these differences in taxonomic resolution, the two approaches converge and highlight the influence of ancient agricultural activities on the composition of insect communities associated with the two sites.

Overall, our findings indicate that sedimentary DNA expands the taxonomic range accessible to archeoentomology, revealing groups that would otherwise remain invisible in the archaeological record. By combining molecular and morphological results, we gain a more complete picture of past ecosystems. This combined approach not only refines our understanding of ancient environments but also offers new ways to explore how interactions between insects and human activities have shaped landscapes over time.

Landscape Reconstruction from Roman Pit Fauna at Marcon (Venice, Italy): The Contribution of Archaeoentomology

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Michael MONZON

Abstract

Reconstructing past landscapes requires the integration of multiple lines of evidence, among which entomological proxies can play a crucial role. An archaeological excavation carried out in 2000 at the Zuccarello Estate in Marcon, Venice (North-eastern Italy) uncovered the remains of a Roman pit dated to 2000 ± 40 BP. The pit yielded a large assemblage of faunal remains in an excellent state of preservation. The analysis of the animal remains allowed for a landscape reconstruction of the site that indicated open spaces with woodlands, wetlands, and limited human impacts. While this zoological assemblage was thoroughly investigated, the entomological remains from the pit were set aside for future analysis. The present contribution reports the current results of an archaeoentomology analysis of these subfossil entomofaunal remains. We aimed to replicate a landscape reconstruction using the entomofaunal assemblage from the site. The goal of our investigation was to use the insects as proxies for understanding landscape resources and any anthropogenic impacts during the Roman Period in Marcon. We used Minimum Number of Individuals (MNI) to represent observed abundances based on the most frequent non-repeating body plate (sclerite) per diagnosed taxon group. Beetles (Coleoptera) comprised almost the entire assemblage, but Diptera puparia were also present. The identified insect taxa provide additional nuance for reconstructing the local paleoenvironment. Specifically, the ground beetles *Pterostichus* cf. *melanarius* and *Chlaenius* cf. *nigricornis* both indicate wetlands, with the former also known to exploit ruderal or garden environments. Other beetle families present were Curculionidae, Elateridae, Staphylinidae and Dermestidae. By integrating entomological data with previously published zoological evidence, this study offers a complementary reconstruction of the environmental setting of the Zuccarello site during the Roman period. These results highlight the utility of insect remains as indicators of past environments and demonstrate the importance of revisiting archaeological collections for multidisciplinary analyses.

When the Past Still Buzzes: Unravelling the Secrets of a Fifth-Century Tree Hive

Bartłomiej MOLASY (Jagiellonian University, Faculty of Biology, Bartlomiej.molasy@doctoral.uj.edu.pl)

Michał KOLASA, Adam TOFILSKI, Artur GÓRECKI, Michał FILIPIAK, Andrzej OLEKSA, Marek KRAPIEC, Michael HOFREITER

Abstract

Interactions between humans and the western honey bee (*Apis mellifera*) have deep historical roots. Yet, while the development of beekeeping practices is well documented, the bees that accompanied past human societies remain largely unknown. In forested regions of Central and Eastern Europe, honey bees were traditionally managed in man-made tree cavities, a form of forest beekeeping known as tree beekeeping. Here, we report the discovery of an exceptionally well-preserved honey bee colony recovered from a tree hive, dated to approximately 1,500 years before present.

The find represents both a cultural artefact and a biological archive. Using an interdisciplinary approach, we reconstructed the history of the tree hive from a living tree growing in a primeval forest of present-day south-eastern Poland, through its intentional modification for forest beekeeping, to its preservation in waterlogged riverine deposits. Radiocarbon dating of the wood and bees, combined with palynological analysis of pollen preserved in the combs, independently confirms the age of both the tree hive and the colony.

Analysis of beebread from the colony enabled reconstruction of the bees' diet and allowed us to estimate the season in which the colony collapsed. Moreover, geometric morphometric analysis of wing venation was used to assess the subspecies affiliation of the recovered individuals, providing rare insight into the identity of honey bees managed by the local Slavic tribes. In parallel, efforts are currently underway to retrieve genetic information from the preserved specimens.

By directly linking archaeological evidence, ecological reconstruction, and bee morphology, this study demonstrates how insights from the past can help safeguard the future. The genomic and phenotypic footprint of historical, locally adapted honey bee populations offer valuable guidance for contemporary conservation efforts, supporting the protection of native honey bee biodiversity in an era of rapid environmental change and increasing genetic homogenisation.

Archaeoentomological Investigation of Santa Maria Maggiore Crypt in Vercelli (Northern Italy)

Giuseppina CARTA (Department of Earth, Environment and Life Sciences (DISTAV), University of Genoa, Italy, Giuseppina.carta@edu.unige.it)

Marta LICATA, Roberta FUSCO, Stefano VANIN

Abstract

Funerary archaeoentomology applies the principles and methods of forensic entomology to archaeological contexts, particularly funerary settings, providing valuable insights into post-mortem processes, burial conditions, and the environmental context of interments. The study of entomological remains can reveal key aspects of burials, including seasonal timing of death, pre-burial exposure, post-mortem relocations, and the use of wooden coffins or offerings, while the presence or absence of specific taxa may indicate the application of repellent substances or environmental constraints.

In this study, the insect fauna associated with burials in the crypt of the Church of Santa Maria Maggiore in Vercelli, Northern Italy (18th – early 19th Cent) was analyzed. Sediment and associated materials were collected from the burial contexts, oven-dried, sieved through multiple mesh sizes, and examined under a stereomicroscope. Specimens were identified to the lowest possible taxonomic level using dichotomous keys and a laboratory reference collection.

The assemblage was dominated by Diptera puparia, particularly from the Muscidae and Phoridae families, taxa characteristic of bodies buried in hypogean or confined environments. Adult Coleoptera were also recovered, including xylophagous and molt-feeding species (Curculionidae, Mycetophagidae, Ptinidae) that interacted with wooden coffins, and decomposer-associated taxa (Cleridae, Histeridae) linked to the breakdown of organic matter. Additional insects, including Tineidae Lepidoptera specimen, associated with clothing, offerings, or the surrounding environment, were also detected among the samples.

These results demonstrate that funerary archaeoentomology provides a multi-dimensional view of burial microenvironments, revealing interactions between insects, corpses, and human funerary practices. The study highlights the potential of insect assemblages to inform on historical burial conditions, post-mortem dynamics, and environmental factors affecting decomposition in hypogean contexts, contributing to a broader understanding of past funerary behavior and local biodiversity.

Archaeoentomological Analysis and Canonical Recognition of the Blessed Body of Maria Vittoria De Fornari Strata (Genoa, Northern Italy)

Giuseppina CARTA (Department of Earth, Environment and Life Sciences (DISTAV), University of Genoa, Italy, Giuseppina.carta@edu.unige.it)

Ezio FULCHERI, Stefano VANIN

Abstract

The body of Blessed Maria Vittoria De Fornari Strata (1562–1588) was examined following its transfer in 2025 to the conventual church of the Daughters of Our Lady on Mount Calvary in Genoa (Italy). Blessed person in Christianity is someone who has been officially recognized by the Church for leading a life of extraordinary virtue and holiness, and who is believed to be in Heaven, interceding for believers.

Macroscopic inspection revealed clear traces of past insect activity, primarily in the form of perforations consistent with dipteran larval feeding. Despite these traces, the overall quantity of entomological remains was limited, reflecting continuous care, cleaning, and monitoring typical for a venerated body.

Entomological analysis focused on isolating and identifying all recovered remains. Diptera puparia were the most abundant specimens, particularly *Hydrotaea* sp. (Muscidae) and Phoridae, taxa typically associated with decomposition in enclosed environments. Their presence suggests that the body was not exposed during the early stages of decay and was likely placed quickly within a coffin or protective container. Among Coleoptera, *Anobium punctatum* (Ptinidae) were interpreted as associated with wooden elements of the coffin or display case rather than the body itself. Additionally, Lepidoptera Tineidae (*Tineola* sp.) were recovered, consistent with keratin-rich substrates such as hair, desiccated skin, and textiles of animal origin, suggesting the possible persistence of clothing or other textile elements.

This case study highlights the value of funerary archaeoentomology in venerated contexts, demonstrating its potential to reconstruct post-mortem processes, environmental conditions, and conservation history. In combination with historical and palaeopathological analyses, these entomological data provide independent evidence on the interactions between insects, preservation practices, and microenvironmental stability. This study thus contributes to both the understanding of a specific devotional context and the broader methodological framework for studying and preserving sacred human remains.

Describing wasp species well or describing them quickly?

Gavin BROAD (Natural History Museum, G.broad@nhm.ac.uk)

Abstract

At a time when we are losing biodiversity all too quickly, and there are hundreds of thousands of undescribed parasitoid wasp species, proponents of minimalist species descriptions have argued that we should be describing species rapidly, based only on DNA barcodes and some photographs. Is this a useful approach? Simultaneously, other species are being described and delimited with an ever-increasing wealth of morphological, ecological and genetic data. Can this maximalist approach be employed at scale? I will demonstrate that minimalist methods are not necessarily faster than traditional taxonomy, and that minimalist species descriptions conflate methods with results.

Describing many newly discovered organisms is clearly very important, but it's equally important to accurately delimit species within supposedly better-known faunas. Bestowing a name on a species doesn't necessarily help us protect that species or give us insight into its ecology. However, through integrative taxonomy, historically 'difficult' groups of parasitoid wasps, such as *Netelia* (nocturnal ichneumonid wasps), can become model organisms for comparative genomics, mapping species ranges, detecting change in population structure, regional variation in ecology, etc. We have the potential to both document poorly known biotas and untangle centuries of taxonomic confusion in 'better known' faunas, but who will be doing this work?

DNA-based species delimitation and description of dark taxa using Cecidomyiidae as a model group

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Niina KILJUNEN, Marko MUTANEN

Abstract

Interest towards biodiversity has increased during the last decades. It has become clear how much we lack information on true species diversity. Currently, less than 2 million species have been described, while estimations on how many there are still to be found vary heavily. Based on results obtained from DNA-based species delimitation tools, the commonly referred estimate of 8.7 M species is likely underestimating the total biodiversity – even while we are in the progress of losing it.

Gall midges (Diptera: Cecidomyiidae) are a hyperdiverse and ubiquitous, but on a global scale inadequately studied insect family. So far, less than 7000 species have been described. DNA-barcode based estimations suggest the number of gall midge species being around 1.8 million. Discovering and describing all these species using morphotaxonomic practices is unrealistic, both by being highly time consuming, and due to the lack of experts in the area.

In our work, we aim to develop a solution for delimiting and describing gall midge species. Our delimitation is based on the universally used mitochondrial barcode indexes (BINs), supported and refined by nuclear markers. By including select nuclear markers, we aim to both investigate the robustness of mitochondrial barcodes as species proxies in Cecidomyiidae, as well as develop a highly confident species delimitation method. Our end goal is to facilitate the definition of species through a sequencing and bioinformatics pipeline, speeding up the process.

Preliminary results based on ca. 12 thousand specimens suggests nuclear markers largely support BINs as species proxies, while also hinting towards certain evolutionary processes, such as the presence of hybridization and mitochondrial introgression.

A computational framework for continually expanding the Tree of Life from barcode data

Nicolas CHAZOT (Swedish University of Agricultural Sciences, Nicolas.chazot@slu.se)

Johanna ORSHOLM, Fredrik RONQUIST, Brendan FURNEAUX, Tomas ROSLIN

Abstract

Building the Tree of Life is one of the greatest endeavors in evolutionary biology yet hampered by the slow process of species discovery and classification, the need of information for establishing evolutionary relationships and methodological limitations. Here we present a new computational framework designed to harness the large amounts of barcode sequences available and offer an immediate solution for populating the Tree of Life and provide ecologists with robust phylogenetic frameworks. Barcoding and metabarcoding are nowadays fast, cheap and popular tools for ecologists and taxonomists to delimitate and identify species, thus characterizing species assemblages with great efficacy. These methods have generated unprecedented amounts of molecular data that could be used to populate the tree of life. We have shown that phylogenetic placement algorithms perform best among taxonomic classifiers for classifying query barcodes, especially novel taxa. We have leveraged these phylogenetic tools in an iterative grafting pipeline, which places and grafts batches of new taxa onto a reference tree of insects. Using example datasets, we compared the computational time and resulting trees between our new pipeline and standard phylogenetic reconstruction tools. We show that our method, combined with barcoding information enables 1- fast discovery and classification of biodiversity, 2- effective use of large sequence databases, 3- very large tree inferences (optionally time calibrated) and 4- the possibility to “update” large trees rather than recomputing them.

Confluence taxonomy: bridging professional and avocational expertise to tackle dark taxa

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Abstract

The accelerating biodiversity crisis underscores the urgent need for reliable species-level knowledge to inform ecological and conservation research. Yet, taxonomy is constrained by the so-called taxonomic impediment: an imbalance between the vast diversity of life and the limited workforce available to describe it. We address this challenge by examining how avocational expertise, especially from experienced naturalists, can be formally integrated into professional taxonomic workflows. Our aim is to weave fragmented strands of knowledge into a unified, scalable framework that merges available but dispersed sources of morphological knowledge with professional molecular data. We present “confluence taxonomy”, which unites morphological expertise from avocational experts with molecular pipelines, using *Megaselia* (Diptera: Phoridae) as a test system. Rather than treating avocational contributions as peripheral, the framework establishes a feedback loop in which phylogenetic hypotheses are refined and supplemented by morphological observations that can be further molecularly tested. The extensive specimen collection and morphological documentation by experienced avocational experts are combined with a genetic taxonomic pipeline to generate iterative insights into dark taxa. Ultimately, the goal is to determine how innovative, community-integrated methods can accelerate the identification and delineation of species in dark taxa, reduce bottlenecks in taxonomic research, and improve the inclusion of neglected groups in biodiversity monitoring. In direct contrast to traditional models where amateur and professional work remain separate, confluence taxonomy creates a shared stream of knowledge that expands both efficiency and scope. This framework provides a pathway toward more inclusive, effective, and societally connected biodiversity research. More broadly, it highlights how bridging methodological and disciplinary divides can transform taxonomy from a bottleneck into a collaborative stream for biodiversity science in the age of ecological crisis.

Integrative taxonomy an essential step prior to the deployment of biological control agents: the iconic case of the genus *Dicyphus* (Heteroptera: Miridae).

JEAN-CLAUDE STREITO (INRAE CBGP, Jean-claude.streito@inrae.fr)

Armand MATOCQ, Éric PIERRE, Guénaél GENSON, Dominique PLUOT-SIGWALT

Abstract

The genus *Dicyphus* Fieber, 1858 comprises small plant bugs characterised by their zoophytophagous diet and predatory behaviour, traits that make them valuable in biological control programmes. Several species play a key role in conservation biological control (CBC), and one species is even mass-reared and released in North America. Despite their undeniable importance in plant protection, many of the fifteen species occurring in Western Europe remained impossible to identify reliably until recently.

Here, we present the results of our integrative systematic research on Western European *Dicyphus* species: the taxonomic changes we propose, new morphological criteria for identifying both male and female, and a set of DNA sequences that can be used for species identification at any developmental stage.

During our study, we observed numerous misidentifications in both public and private collections. Consequently, all museum and literature records will need to be reassessed. Although the synonymy we established between *Dicyphus tamaninii* Wagner, 1951 and *D. bolivari* Lindberg, 1934 has clarified the identity of the *Dicyphus* species in more than 1,300 publications, the identification of specimens studied in many articles remain uncertain.

Delineating species that appear morphologically similar yet biologically distinct enables more detailed investigations of life-history traits, including host plants, host or prey specificity, and ecological requirements. As this example illustrates, integrative systematic studies are essential for biological control programmes: they allow the delineation of taxa, stabilise species names — an essential prerequisite for legal use — and provide a precise definition of their ecological requirements. This facilitates secure production, optimises costs, ensures efficacy, and prevents unintended effects.

Finally, systematic studies improve our understanding of agrosystem biodiversity, and encourage farmers to adopt biological control measures.

Macroevolution of the New World scarab beetle tribe Phanaeini (Coleoptera: Scarabaeidae: Scarabaeinae)

Conrad GILLETT (Finnish Museum of Natural History (LUOMUS), University of Helsinki, Conrad.gillett@helsinki.fi)

Abstract

The New World scarab beetle tribe Phanaeini contains coprophagous, necrophagous, mycetophagous and suspected myrmecophilous species. We analyse the largest tribal molecular dataset assembled, incorporating, for the first time, the enigmatic monobasic genus *Megatharsis*, the thalassinus group of the subgenus *Coprophanaeus* (*Metallophanaeus*), and the subgenus *Dendropaemon* (*Eurypodea*) (formerly *Tetramereia*), unveiling their macroevolutionary and biogeographical history in light of Cenozoic abiotic changes and inferring shifts in feeding biology through time. We recover the contentious genus *Gromphas* outside an otherwise monophyletic Phanaeini. We infer *Megatharsis* in a clade containing the apparent myrmecophilous genus *Dendropaemon*, within the *Coprophanaeus* clade, and demonstrate that the subgenus *Coprophanaeus* (*Metallophanaeus*) is polyphyletic, whilst species groups within the subgenus *Coprophanaeus* (*Coprophanaeus*) are monophyletic. Our divergence time analyses and ancestral range estimation indicate an eastern South American origin for Phanaeini in the early Eocene, with subsequent colonization of Central America and the Nearctic during the Oligocene, long before a Panamanian land bridge. A shift to necrophagy in *Coprophanaeus* is possibly linked to increasing Neotropical small vertebrate diversity since the Eocene and, astonishingly, myrmecophily evolved from necrophagy 35 Mya. These drastic shifts in lifestyle are not concordant with variations in diversification rates and appear unlinked to Quaternary extinction of large mammals.

From Legacy Morphological Matrices to Semantic Knowledge Graphs: Bridging Phylogenetic Practice and Semantic Data Models in Entomological Research

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Eduardo A. B. ALMEIDA, James BALHOFF, István MIKÓ, Michael ORR, Juho PAUKKUNEN, Katja SELTMANN, Sergei TARASOV, Diego S. PORTO

Abstract

Comparative morphological data constitute a foundational source of knowledge in insect systematics, yet much of this information remains locked in unstructured or semi-structured formats such as text-based character lists and legacy matrices. While these representations are effective for phylogenetic inference, they pose challenges for data integration, reuse, and synthesis across studies and taxa, an issue that becomes increasingly important in the context of high-throughput phenotypic data generation (Phenomics) and the current biodiversity crisis. Here, we present a semantic workflow designed to transform phenotypic character statements and phylogenetic matrices into structured knowledge graphs. The workflow parses characters and states, links them to validated taxa lists and phenotype ontologies, and produces interoperable semantic graphs alongside structured spreadsheet and nested text outputs. This enables phenotypic data intended for phylogenetic analysis to be reused in downstream comparative and integrative workflows. The development of this workflow highlights fundamental conceptual and operational tensions between phylogenetic data models commonly used in morphology and semantic representations. Phylogenetic practice routinely employs absence/presence, inapplicable, and composite character states that do not map straightforwardly onto machine-oriented formalisms. We discuss how practical compromises are often necessary to preserve analytical intent while maintaining logical coherence. By addressing modelling challenges in representing insect phenotypes as knowledge graphs, our workflow aims to bridge traditional morphological systematics and modern semantic technologies without forcing phylogenetic data into ill-fitting formalisms. Rather than replacing existing practices, this approach provides infrastructure for making decades of morphological expertise computationally accessible and reusable, supporting integrative insect studies in an era of accelerating biodiversity loss. Furthermore, our semantic-based approach provides a foundational framework for future expansion allowing morphological phenotypic data to be integrated with other important resources (e.g., environmental, ecological, and genetic data), a fundamental step for developing infrastructure and analytical tools to aid decision makers in conservation efforts.

#10469

INSECTS THROUGH TIME: Paleoentomology

02/07/2026 at 14:00, Villandry

Deep-time perspective on insect pollination

David PERIS (Institut Botànic de Barcelona (CSIC-CMCNB), David.peris@ibb.csic.es)

Abstract

Insect pollination represents one of the most significant mutualistic interactions in the history of terrestrial life, shaping the diversification of both insects and plants. A deep-time perspective reveals that pollination originated long before the rise of angiosperms, with fossil evidence of gymnosperm–insect associations extending back to the Paleozoic. The subsequent emergence and rapid diversification of flowering plants during the Cretaceous catalyzed extensive coevolutionary dynamics, leading to the adaptive radiation of major pollinator insect lineages. Integrating paleobotanical, paleoentomological, and molecular phylogenetic data enables the reconstruction of these evolutionary trajectories across the geological timescale, highlighting the resilience and adaptability of pollination systems through time.

Wasp-flower interactions in the Eocene of Messel: flower visiting, pollinivory, and pollination

Loup BOUDET (Department of Messel Research, Senckenberg Research Institute and Natural History Museum Frankfurt, Location Messel, Germany / Faculty of Biological Sciences, Institute of Ecology, Diversity and Evolution, Goethe University, Frankfurt, Germany, Loup.boudet@senckenberg.de)

Christian GEIER, Friðgeir GRÍMSSON, Michael ENGEL, Johannes BOUCHAL, Silvia ULRICH, Torsten WAPPLER, Sonja WEDMANN

Abstract

For millions of years, the evolution of insects has been closely linked to that of flowering plants. Thanks to their exquisite preservation, fossils from the UNESCO World Heritage Site of Messel, Germany, allow unique insights into the history of flower-insect relationships.

Following a transdisciplinary paleoentomological-palynological approach, 25 specimens of scoliid wasps (Scoliidae) from the Eocene of Messel are documented, 17 of which preserve pollen in situ. Extant Scoliidae are frequently observed on flowers. They are considered as effective pollinators of some plants and potentially pollinivorous. As most of the pollen was found near the mouthparts or inside the digestive tract of the fossil insects, Messel scoliids were probably intensively pollinivores and pollinators in the paratropical ecosystem as well. The diversity of pollen found on individual specimens (Aquifoliaceae, Anacardiaceae, Theaceae, Cornales) suggests a polylectic behaviour for these fossil wasps.

We also introduce other parasitoid hymenopterans as a previously unrecognized component of the flower-insects network. Of the four specimens of crown wasps (Stephanidae) described from Messel, three are preserved with associated pollen. The wide range of pollination strategies observed in extant representatives of the plant families identified from this pollen, together with the low quantity of pollen preserved in situ, suggests that Messel stephanids were opportunistic flower visitors rather than important pollinators.

Therefore, from opportunistic flower visiting in crown wasps (Stephanidae), to intensive polylectic pollinivory and pollination in scoliid wasps (Scoliidae), Messel fossils provide new insights into the broad diversity of wasp-flower interactions during the paratropical Eocene of North-Western Europe.

Acknowledgements: This research is funded in part by the Deutsche Forschungsgemeinschaft (DFG) with a grant to SW, project number 533185608, and in part by the Austrian Science Fund (FWF) via grant DOI: 10.55776/P34303 to FG.

A Preliminary Paleoecological Analysis of Fossil Insects from a Cretaceous Crater Lake at Orapa Diamond Mine in Botswana

Sandiso MNGUNI (North-West University, Msandiso@gmail.com)

Sandiso MNGUNI, Ian James MCKAY, Lelethu Unathi-Nkosi Peter HESHULA, Simon Kamande KURIA, Shaw BADENHORST

Abstract

Taphonomy is a field that explores the intricate processes through which organisms decay and ultimately become fossilized within the geologic record. Since the Devonian period, a diverse array of fossil insects have been uncovered in various ancient environments. In Africa, a particularly noteworthy site is the large Cretaceous volcanic crater lake found inside the Orapa Diamond Mine in Botswana, which was created by an eruption of diamond-rich epiclastic kimberlites. The deposit bears fossil plants and insects that have been studied in the past by many researchers. This work investigated the taphonomy of fossil insects from this deposit through a preliminary analysis of two sediment types, which included 40 brown-red blocks and 20 olive-green blocks. We measured and compared relative abundances of insect taxa, insect body parts, insect size, plant stems, and plant fragments found in brown-red blocks and olive-green blocks. The brown-red blocks contained more complete faunal specimens and had a higher abundance of Diptera, Hymenoptera, and Blattodea, whereas olive green blocks contained more disarticulated wings, elytra, and abdomen and had a higher abundance of Coleoptera and Hemiptera despite having a smaller sample size. In addition, olive-green blocks had more slabs with a high abundance of plant fragments and stems. Both sediment types contained an equal number of small- to medium-sized insects. The results suggest that the two sediment types represent different environments. However, color alone is not a reliable criterion for separating rock facies. More studies are needed to consolidate our findings.

The last of Africa: an historical biogeography of *Gesomyrmex* and *Rhopalomastix* ants revealed by Miocene Ethiopian amber

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Abstract

Ethiopian amber is one of the only two insectiferous amber deposits known in Africa to date, and the primary source of Miocene fossil insects for the continent. Ants are not only abundant but also well diversified in Ethiopian amber, comprising at least 20 genera in six modern subfamilies, as is typical of Neogene ant assemblages. Most of these genera are still present in Africa today, but two records are remarkable: *Gesomyrmex*, a genus otherwise known from fossil occurrences in the Eocene of Europe, and distributed only in southeast Asia today; and *Rhopalomastix*, a genus with few species now restricted to tropical forests of the Indomalayan and Australasian regions.

Presence of these two genera in East Africa was likely favoured by an increase in temperature and rainfall during the Early Miocene, leading to a renewed expansion of warm and humid Afrotropical forests culminating in the Middle Miocene Climatic Optimum (MMCO). The retraction of wet evergreen forests or wet savannas in favour of dry savannas during the Middle Miocene Climate Transition (MCT) probably contributed to their restricted current distribution.

The finding of *Rhopalomastix* supports an Afrotropical origin of this enigmatic genus before a dispersal to the Indomalayan region. The presence of *Gesomyrmex* in the Miocene of Ethiopia reveals a strikingly neglected ancestral dispersal event for the genus; it also challenges its previously estimated crown group divergence ages and south-east Asian ancestral range.

The formicid record in Ethiopian amber is crucial to our understanding of ant evolution, since it represents the last and sometimes only African occurrence of genera formerly with a broader Paleotropical distribution.

Earliest fossil records of pollen-foraging leafcutter bees

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Abstract

Megachilidae bees are important pollinators in both natural ecosystems and crops. Among wild bees they are considered the most successful pollinators. The high efficiency of Megachilidae pollination credits them as critical for ecosystem balance and plant species survival as well as sustaining agricultural productivity. Despite this importance little is known about the origin and evolution of flower visitation as well as paleo-pollination by Megachilidae bees. This is partly due to the meagre fossil record of this group and the lack of methods to study paleo-pollination biology. To resolve part of this evolutionary history we investigated fossil megachilid bees from the Paleogene (56 Mya) maar lake of Menat, France, for adhering pollen.

Each bee specimen had thick pollen loads in their scopa with several different pollen types (five to seven) representing at least 16 different angiosperm taxa. These include Cornaceae, Euphorbiaceae, Fabaceae, Malvaceae, Nyssaceae, Rhamnaceae, Rutaceae, Sapotaceae, Saururaceae, and three Eudicot pollen of uncertain affinity. However, despite the number of different pollen types discovered on each bee specimen, they clearly preferred particular plant taxa. This is reflected in the percentage of said pollen type in the metasomal scopa. Depending on the bee specimen, these plants are Mastixioideae (Cornales), Sapotaceae (Ericales), and an undetermined Eudicot.

Extant relatives of the parent plants producing the discovered pollen are presently confined to tropical and warm temperate climates, particularly in Southeast Asia. Most of the pollen represent plant taxa that have not been reported from Menat prior to this study, and therefore widen our knowledge about Menat's Paleogene vegetation, complementing the current dispersed palynoflora as well as the leaf and fruit/seed record. Our results represent the first and oldest fossil megachilid bees preserved with adhering pollen. This links extant megachilid pollinators and their specialized foraging behaviour to fossil bees dating back 56-million years.

The early evolution of the stonefly lineage (Insecta, Plecoptera) has been revealed by a new Carboniferous stem-group species found in the Piesberg quarry (Germany)

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Abstract

The early evolution of the stonefly lineage (Insecta, Plecoptera) has been revealed by a new Carboniferous stem-group species found in the Piesberg quarry (Germany)

Jakub Prokop, Angelika Leipner, Kateřina Rosová, Pavel Sroka

Stoneflies (Plecoptera) are an ancient lineage of polyneopteran insects, with representatives of the stem-group appearing as early as the Carboniferous Period (Pennsylvanian). However, they are extremely rare in the Carboniferous deposits, which makes knowledge of the early phase of their evolution obscure. Here, we present two new genera and species (*Carbonoperla sowiaki* and *Carbonopteryx heisingi*) belonging to the newly established stem-stonefly family Carbonoperlidae, discovered in the famous Piesberg quarry in Lower Saxony, Germany. This site provides an excellent view of the diversity of insects in the Pennsylvanian period.

In light of this new material, we discuss the distinction between the stonefly stem and crown groups, offering insights into the diversification process of the stonefly crown group, possibly linked to environmental changes during the Late Palaeozoic.

We restrict the occurrence of the genuine stonefly stem group to the Carboniferous period, being limited to the families Gulouidae and Carbonoperlidae. We propose to use the ordinal name Plecoptera for the restricted number of taxa, exhibiting a specialized ra-rp cross-vein, as present in the crown-group.

For the stonefly total group, we designated a new unranked taxon, Plecopterida. The palaeolatitudes of Carboniferous stem-group occurrences were always situated in the narrow equatorial belt, whereas the Permian taxa were uniformly distributed at higher palaeolatitudes, a pattern generally followed by the distribution of stoneflies today. This process began with the progressive aridization of the equatorial belt during the Permian, likely favouring the taxa adapted to higher-latitude environmental conditions.

The participation of JP was supported by the Grant Agency of the Czech Republic (No. 24-11498S).

Bayesian inferences indicate floral turnovers as deep-time drivers of beetle diversification

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Abstract

By far the richest insect order, beetles occupy a broad range of ecological niches in modern ecosystems, and many lineages exhibit tight ecological and evolutionary associations with plants, making Coleoptera an ideal group to investigate how global ecological shifts and floral turnovers have shaped insect diversification over time. The order currently comprises >442,000 described species and 238 families (192 extant and 46 extinct), but the timing and tempo of its diversification has rarely been studied using a fossil-informed diversification framework. Here, we apply Bayesian Birth–Death modelling to a curated dataset of ~32,000 fossil occurrences (representing 187 families and 3,398 genera) to infer the past diversity dynamics of beetles at both the family and genus levels. Our results indicate that Coleoptera exhibit remarkable resilience to major ecosystem perturbations, particularly at the family level, maintaining long-term persistence through multiple global crises. However, we detected significant extinction at the genus level across the Permian–Triassic crisis, revealing selective lineage losses during this environmental and ecological upheavals. In contrast, the Triassic–Jurassic and Cretaceous–Paleogene crises show little evidence of impact on beetles at this taxonomic scale. Furthermore, at the genus-level we observed a major diversification period during the first part of the Early Cretaceous, likely linked with the rise of angiosperms. These originations are followed by extinctions, probably reflecting the disappearance of gymnosperm-associated lineages, highlighting a major turnover in beetle evolutionary history. Our analyses suggest that shifts in plant communities primarily shaped beetle diversification, and the interplay of biotic and abiotic factors, such as temperature fluctuations or continental fragmentation, further drove macroevolutionary patterns in this hyperdiverse order.

Integrating biopesticidal and biostimulant paradigms: a scientific dilemma for the future of plant protection

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Abstract

The interactions of entomopathogenic fungi with plants, as endophytic or rhizosphere-competent microorganisms, extend their current applications beyond conventional pest control. The strain *Beauveria bassiana* EABb 01/33-Su represents a notable example, supported by more than a decade of research demonstrating not only its direct efficacy as an entomopathogenic fungus, but also its plant-mediated indirect lethal and sublethal effects observed following soil, seed, and foliar applications towards chewing and pierce-sucking pests. Our more recent findings provide the first evidence of a functional switch between insect-pathogenic and non-pathogenic states in 01/33-Su strain driven by a *Beauveria bassiana* victorivirus 1 (BbVV-1) acting as an essential virulence determinant. The mycovirus-infected wild-type strain (WMI) demonstrated broad-spectrum virulence across insect orders, whereas the isogenic mycovirus-free strain (MFr) was entirely non-pathogenic, exhibiting a complete suppression of cuticle penetration capability related to the direct effect of the mycovirus on the *pr1* gene transcriptional regulation. Hence, the entomopathogenic isoform of this *B. bassiana* strain integrates biopesticidal and biostimulant functionalities, whereas its non-pathogenic counterpart represents a paradigm shift toward an exclusively plant-beneficial microorganism — a prospective scientific dilemma in the evolution of plant protection strategies.

Susceptibility of adult truffle beetles to the entomopathogenic fungus *Lecanicillium muscarium*, compared to two entomopathogenic nematodes

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Abstract

The truffle beetle, *Leiodes cinnamomeus*, is the most important pest in black truffle (*Tuber melanosporum*) plantations during autumn and winter, especially in Spain. Adults and larvae produce numerous galleries in truffle fruitbodies, causing economic losses of up to 70%. Current control practices are not sufficient to reduce populations to acceptable levels, making new alternatives necessary. Entomopathogenic nematodes (EPNs) are promising biological control agents against *L. cinnamomeus*, while entomopathogenic fungi (EPF) are also commonly used in Integrated Pest Management (IPM) programs to enhance the control of insect pests. The aims of our research were to test the virulence of a cold-adapted commercial strain of the EPF *Lecanicillium muscarium* compared to two EPN species, *Steinernema carpocapsae* and *Steinernema feltiae*, against adults of *L. cinnamomeus* at 15°C and 10°C, and to assess the effect of their combined application.

The experimental unit was a Petri dish (5.5cm diameter) filled with sterile soil and one adult beetle. Two different assays were performed using different EPF treatments: (1) direct soil treatment and (2) immersion of adults in fungal suspension. Two doses of *L. muscarium* were tested, 6×10^6 and 1×10^7 conidia/mL. EPNs were applied directly to the dish at two doses, 10 and 25 infective juveniles/cm². Beetle mortality was recorded 7–12 days post-treatment at 15°C and 20 days post-treatment at 10°C.

Both EPN species showed to be significantly virulent towards *L. cinnamomeus* adults, with *S. carpocapsae* causing the highest mortality rates at both 15 and 10°C. However, the addition of *L. muscarium*, either alone or in combination with EPNs, did not enhance pest suppression compared to EPNs alone. Our results suggest *S. carpocapsae* would be the best option to control adults of *L. cinnamomeus* in field applications. Further research is recommended to explore potential synergistic effects of combining EPNs with other cold-adapted EPFs.

Mosquito Microbiota as a Hidden Driver of Bti Bioinsecticide Efficacy

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Abstract

The Asian tiger mosquito *Aedes albopictus*, is a major vector of human pathogens. To control its populations the bioinsecticide *Bacillus thuringiensis* var. *israelensis* (Bti), has been broadly used against *Ae. albopictus* larvae since early 2000s. It is considered as efficient, with a moderate effect on untargeted species and it does not select for resistances. Its activity relies on Cry and Cyt toxins, which perforate the larval midgut epithelium. Previous studies on different target species and strains of *Bacillus thuringiensis* have suggested that the insect microbiota might contribute to its toxicity while proper demonstrations of this three-way interaction remain relatively elusive.

Here we show that the median lethal dose needs to be increased by ~600% in germ -free mosquito larvae, clearly suggesting an amplification of the toxicity mediated by microbiota. To better characterize this interaction: (i) we further localized the mosquito microbiota among the larval tissues, (ii) we characterized its composition and (iii) we performed transcriptomic analyses on germ free or conventionally reared larvae exposed to low and intermediate doses of Bti. This design allows us to disentangle microbiota-dependent from microbiota-independent effects of Bti. All in all, we showed that the microbiota spread into the larval tissues, with a shift in its composition after exposure to the bioinsecticide. It also correlates with higher metabolic and detoxification responses.

All in all, these results pave the way to a better understanding of a disregarded aspect of indirect toxicity of Bti. It should also help future potentializing improvement of its effect by combining Bti with toxicity enhancing and mosquito specific microorganisms.

A mycovirus uncovers the evolutionary trade-off of *Beauveria bassiana* in its transition from a symbiotic fungus to an entomopathogen

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Abstract

Mycovirus have recently attracted increasing attention due to their potential roles in shaping fungal virulence and ecology and their possible applications in sustainable agriculture, including the improvement of fungal biocontrol agents used against plant pathogens and insect pests. Despite this, their ecological and molecular effects on entomopathogenic fungi (EPF) remain poorly understood. In this study, it is firstly reported a mycovirus as a key element driving the diversification of EPF lifestyles in *Beauveria bassiana* EABb 01/33-Su strain. Bioassays with the melon aphid *Aphis gossypii* revealed two contrasting phenotypes: the mycovirus-infected strain (WMI) retained its insect pathogenicity, while the mycovirus-free strain (MFr) lost its virulence but significantly reduced aphid fecundity through plant-mediated effects. Quantitative PCR analyses showed that MFr exhibited a much higher capacity for endophytic colonization than WMI, reaching 89.6–94.3% higher fungal biomass in sprayed leaves, and remaining detectable in unsprayed tissues where WMI was absent. This enhanced colonization correlated with a stronger activation of plant defense pathways related to ethylene, jasmonic and salicylic acid, particularly after aphid infestation. Transcriptomic analyses confirmed that defense-related genes were consistently more expressed in MFr-colonized plants, indicating a close relationship between fungal abundance and the magnitude of the plant immune response. The surprising capacity of this *B. bassiana* strain to harbour a mycovirus functioning as a full virulence factor has enabled elucidating the evolutionary trade-off undergone by this EPF fungal species in its transition from a symbiotic fungus to an entomopathogen—namely, a partial reduction of its direct benefits to the plant in exchange for protection against insect pests. This unexpected finding would place us in the previously unprecedented position of entering the agricultural market with the two isoforms of the same strain through two distinct applications: crop protection or biostimulation.

Technological analyses and selectivity of innovative chitosan-EO nano-aphicides

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Abstract

Although their global market is still limited, botanical insecticides may be valuable alternatives to synthetic insecticides. Essential oils (EOs) are acknowledged for their bioactivity, however low persistence, volatility, and hydrophobicity are critical shortcomings that can be overcome using innovative formulation strategies, including encapsulation with biopolymers.

Here, a natural biopolymer, chitosan, has been formulated with sweet orange EO using an ionotropic gelation method to obtain a chitosan-EO nano-emulsion with an average dimension 264.9 ± 1.8 nm and a good homogeneity, with PDI of 0.193. Furthermore, technological analyses (viscosity, pendant drop, contact angle) were performed and compared to a commercial biopesticide, to assess the suitability for field application, demonstration optimal characteristics for operative conditions.

Chitosan-EO nano-formulation was effective to control against a key polyphagous aphid widespread worldwide, *Aphis gossypii* Glover, by topical (spray) and residual (leaf-dip) application. In topical trials, the mortality achieved by the highest tested doses ($< 0.1\%$) did not statistically differ from the positive controls (lambda-cyhalothrin and PREV-AM[®] at label dose), while chitosan alone nano-formulation showed statistically lower toxicity.

Selectivity of the nano-insecticides was evaluated toward two biocontrol agents, the coccinellid *Propylea quatuordecimpunctata* L. and the parasitoid *Aphidius colemani* Viereck. Neglectable mortality caused by chitosan-EO formulation was recorded toward both non-target insects *P. quatuordecimpunctata* and *A. colemani*, while positive control caused slightly higher mortality in adult parasitoids.

In the last decades, aphid control has become extremely difficult due to the restricted number of effective control tools, the increased emergence of resistance, withdrawal of several insecticides and environmental safety concerns. In this scenario, novel chitosan-EO formulations can be effective, as well as eco-friendly, pest control tools, mitigating the side effects on non-target organisms, including biocontrol agents.

Bugs, plants and peptides – Unleashing the power of chemical ecology for sustainable crop protection

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Abstract

Farmers face globally a shrinking toolkit for crop protection amid tighter regulations, increased public demand for residue-free food, challenges from resistance, and the negative impacts of climate change. At Syngenta Biologicals we are committed to enhancing agricultural productivity in concert with sustainable practices. We pledge to bring to market cutting-edge biocontrol solutions, and one such pioneering approach in our arsenal is the development of peptide-based insecticides. These novel bioinsecticides are designed to provide growers with a targeted and environmentally benign approach to insect pest management, ensuring no residual presence as they degrade into harmless natural amino acids.

Peptide toxins from natural insect predators, such as spiders and scorpions, represent attractive candidates for this purpose as they have been long known for their specificity, potency and rapid onset of toxic effects when injected into insect herbivores. However, their effectiveness is markedly diminished when administered orally, a route for which they have not naturally adapted through evolution, particularly in combating the highly damaging pests of the Lepidoptera order. We have uncovered that peptides of plant origin from the cyclotide family, kalata B1 and B2, when combined with various animal-derived neurotoxins significantly enhance their potency in controlling highly destructive caterpillars through oral ingestion. We report herein our efficacy findings on this concept and our mechanistic investigations, proposing a mode of action wherein cyclotides disrupt the structural integrity of the lepidopteran midgut barrier. This disruption facilitates the translocation of neurotoxins across the gut epithelium into the hemocoel, where they can manifest their lethal effects on the nervous system of insects.

Bowman-Birk protease inhibitor modulates gut proteome and disrupts mitochondrial metabolism in *Achaea janata* (Castor semilooper) larvae

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Abstract

Achaea janata, which belongs to the lepidopteran order, is responsible for significant economic losses in castor oil production, as it feeds on the foliage & capsule of castor and causes a major yield loss up to 63%. The insect digestive proteases play a crucial role in releasing peptides and amino acids from larval protein diets, thereby supporting the growth and survival of these insects. In parallel, several studies have reported plant-derived protease inhibitors as potent biopesticides, which disrupt midgut protease activity in larvae. However, the precise molecular links between gut proteome modulation and disruption in mitochondrial metabolism remain unclear. In the present study, the effect of Bowman-Birk Inhibitor (BBI) purified from the mature seeds of *Rhynchosia sublobata*, a wild relative of *Cajanus cajan*, on *A. janata*, resulted in significant weight reduction and mortality of larvae. Proteomic (LC-MS/MS) analysis of larval midgut revealed substantial numbers of differentially expressed proteins (DEPs) in BBI-fed larvae compared to control larvae. The localization of BBI in midgut cells was revealed by a confocal study, and the top three DEPs were chosen for further validation. Histology and TEM analysis revealed the downregulation of cytoskeleton proteins, leading to changes in midgut cell morphology and tissue degeneration. Also, the downregulation of mitochondrial proteins was accompanied by alterations in cristae morphology, a decrease in mitochondrial membrane potential, a reduction in the activity of ETC complexes, and a shift in the cellular ATP/ADP ratio. Furthermore, BBI feeding also affected cellular redox homeostasis and intracellular glucose-6-phosphate, and pyruvate levels in midgut tissue. Besides, confocal and flow cytometry studies revealed an increase in ROS levels and apoptotic cells in the midgut tissue of BBI-fed larvae. Together, these results indicated that BBI induced modulation in the gut proteome and disrupted mitochondrial metabolism in *A. janata*, leading to larval death.

Optimization of formulations of insect pathogens for a better biocontrol effectiveness

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Abstract

The reliability is one of the limiting factors in the use of microorganism-based plant protection strategies to control insect pests. Fluctuations in effectiveness are largely caused by environmental factors. Humidity, temperature, sunlight, and rainfall all play a key role. Minimizing potential negative environmental influences is a challenge in the development of formulation strategies for insect pathogens.

Four examples will illustrate how to improve the effectiveness through adapted formulation strategies.

We developed a soil granule for insect-pathogenic fungi to control soil pests such as wireworms and grubs. Liquid-fermented biomass was sprayed onto autoclaved millet using a coating process in a fluidized bed dryer, with the use of protective additives. Under moist conditions, the fungus grows on the millet in the soil, sporulates, and can thus infect the pest insects. This formulation could be applied effectively in potato ridges using conventional application techniques. However, further optimization steps are needed to achieve satisfactory effectiveness in the field.

Insect pathogens applied to plant surfaces are particularly exposed to sunlight and rain. To improve sunlight stability, nine different water-soluble UV protectants were compared in terms of their suitability for use in spray-dried formulation based on spores of the insect-pathogenic fungus *C. fumosorosea*. When the formulated fungal spores were exposed to simulated sunlight, black tea provided the best protective effect.

To improve efficacy and sunlight stability, further results on optimized *Bacillus thuringiensis* formulations will be presented.

To achieve a better rain-fastness the adhesion of entomopathogenic spores to leaf surfaces is to be optimized through the use of anchor peptides. First anchor peptides were identified binding on the surface of leaves and spores and the suitability of such anchor peptides for a better rain fastness will be discussed.

Compatibility and vectoring of *Metarhizium brunneum* by entomopathogenic nematodes for biocontrol of soil stages of noctuid pests: is joint formulation the next step?

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Julien BRILLARD

Abstract

Entomopathogenic fungi (EPF) and entomopathogenic nematodes (EPN) are two of the most important microbial agents for controlling soil-dwelling insect pests. These organisms possess complementary traits—most notably the mobility of EPN—that may enable the transport of fungal propagules, a hypothesis explored in this study. We evaluated the compatibility between the EPF *Metarhizium brunneum* (strain EAMa 01/58-Su) and the EPN *Heterorhabditis bacteriophora* and *Steinernema carpocapsae*, with emphasis on the ability of nematodes to vector fungal conidia.

Co-application produced additive effects against the last larval instar of *Spodoptera littoralis*, which enters the soil to pupate, yielding 90–100% mortality. While *H. bacteriophora* and *S. carpocapsae* did not affect the pupal stage, *M. brunneum* significantly reduced adult emergence. Importantly, conidia transported by nematodes initiated fungal infection in pupae, demonstrating for the first time that EPN can facilitate EPF transmission beyond their own host range.

These results confirm that combining EPF and EPN can enhance pest suppression and reveal a novel mechanism of microbial biocontrol based on nematode-mediated fungal dispersal. This opens promising avenues for the management of geophilic and even geobiont noctuid pests—raising a key question for future development: is joint formulation the next step?

Management of *Chaetanaphothrips orchidii* (Thysanoptera: Thripidae) by applying entomopathogenic fungi to the soil

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Abstract

Chaetanaphothrips orchidii (Moulton) is a tropical thrips that has been causing serious damage to Spanish citrus crops, especially sweet oranges and grapefruits, since 2016. The current management strategy for this pest relies on the application of insecticides to the tree canopy during the summer months. However, this thrips species has been reported to pupate exclusively in the soil near water emitters during this period, which makes this area a prime candidate for the application of microbiological biopesticides, such as entomopathogenic fungi. Our study evaluated the efficacy of five mycoinsecticides against *C. orchidii* prepupae. All five products caused mortality rates above 63% at a concentration of 10^8 colony-forming units (CFU)/ml, and two of the products caused nearly 100% mortality six days after application. A product was selected based on its virulence and formulation for further testing, where different concentrations were applied to sieved and sterilized soil to assess its efficacy against *C. orchidii*, under laboratory conditions. The tested product was estimated to have an efficacy of $75 \pm 6\%$ when applied to the soil at a concentration of 1×10^8 CFU/g. In subsequent field trials, this mycoinsecticide was administered to *C. orchidii*-infested orchards using two application methods which use the pest location near water emitters to their advantage. Our results have important implications for the management of *C. orchidii* by using a targeted application of microbiological biopesticides in the soil.

Evaluating Mineral and Plant-based Dust for Sustainable Control of the Cabbage Stink Bug and Associated Brassica Pest under Laboratory and Field Conditions

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Abstract

The cabbage stink bug (*Eurydema ventralis*; CSB) has become an increasingly important pest of cabbage and other *Brassica* crops. At the same time, there is growing pressure to reduce reliance on synthetic insecticides, creating a need for alternative and more sustainable pest control approaches. This study explores the potential of locally available inert and plant-derived dusts as non-chemical control options for sustainable pest management.

Laboratory experiments examined the effects of five dust materials on mortality and feeding activity of adult and nymphal CSB. The tested materials included diatomaceous earth, zeolite, quartz sand, wood ash from Norway spruce (*Picea abies*), and leaf dust of tree of heaven (*Ailanthus altissima*). Diatomaceous earth showed the highest insecticidal activity, causing 78.3% mortality in adults and 55.2% in nymphs, while reducing the feeding damage index. Zeolite and wood ash exhibited moderate efficacy. In contrast, *A. altissima* leaf dust caused low mortality ($\leq 14.5\%$) but significantly reduced feeding activity, indicating a deterrent or antifeedant effect.

Field trials were conducted over two consecutive growing seasons and revealed a strong dependence of dust efficacy on weather conditions. Treatments performed best during dry periods, while rainfall and elevated air humidity reduced dust persistence and overall effectiveness. In addition to CSB, dust applications were evaluated against other major cabbage pests, including flea beetles (*Phyllotreta* spp.), lepidopteran larvae, and thrips. Under dry conditions, diatomaceous earth and wood ash reduced CSB damage indices and increased average cabbage head weight.

To better explain the observed weather sensitivity, ongoing research focuses on the hygroscopic and hygrophilic behavior of the selected dusts, aiming to clarify how moisture uptake affects dust activity and persistence on plant surfaces. Overall, our results demonstrate that inert dusts, particularly diatomaceous earth, can contribute to cabbage pest management when applied under favorable environmental conditions.

Development of Eco-friendly Pest Management Solutions Using Native Plant Extracts

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Abstract

The global agricultural sector and food security are increasingly threatened by the rapid proliferation of pesticide-resistant insect pests. Although conventional synthetic pesticides can provide rapid and immediate control, their long-term use has contributed to ecological imbalance, residue accumulation, and accelerated resistance development, ultimately destabilizing agricultural environments. To overcome these limitations, this study focuses on the development of an eco-friendly pest-management solution based on bioactive compounds extracted from native plants.

Insecticidal activity screening of plant-derived candidates demonstrated strong efficacy against *Aphis gossypii*, *Bemisia tabaci*, *Tetranychus urticae*, and powdery mildew—pests widely recognized as major drivers of economic crop losses and vectors of plant pathogens. The optimized formulation exhibited a dual mode of action, inducing cuticle disruption and feeding inhibition for insecticidal effects while simultaneously providing antifungal activity. Crop safety was fully maintained without phytotoxic responses.

Test-field evaluations conducted in South Korea, Vietnam, and Indonesia confirmed an 87–100% reduction in pest density within 72 hours after treatment, with stable performance across diverse climatic and cultivation conditions. No phytotoxicity or harmful chemical residues were detected before or after application, and compatibility with beneficial insects was verified, indicating strong suitability for Integrated Pest Management (IPM) programs.

Overall, this research demonstrates the potential of plant-extract-based formulations as practical and scalable alternatives to conventional pesticides. By reducing dependence on synthetic chemicals and mitigating resistance-driven crop damage, eco-friendly biocontrol solutions can play a critical role in improving agricultural resilience and advancing sustainable crop protection in the context of global climate and food-security challenges.

Efficacy of biodegradable polymeric materials activated with essential oil of *Carlina acaulis* against *Sitophilus oryzae*: sustainable methods for the control of storage insects

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Abstract

Botanical insecticides can represent a useful alternative with multiple modes of action, making the development of resistance in targeted pests unlikely. In this framework, essential oils (EOs) and their components are a sustainable option. For example, carlina oxide, a polyacetylene isolated from *Carlina acaulis* L. (Asteraceae) roots, represents a valuable tool for Integrated Pest Management strategies. Herein, the toxic activity of this EO component towards adults of the rice weevil *Sitophilus oryzae* (Coleoptera: Curculionidae) and the development of biodegradable polymer systems with repellent properties was investigated. Specifically, two biodegradable polymeric materials activated with the EO component were prepared: one consisting only of polybutylene succinate-co-adipate (PBSA) with carlina oxide and another PBSA matrix biocomposite system loaded with 20% depleted biomass of *C. acaulis* (i.e. residual roots after distillation of its active component). The toxicity was evaluated in glass Petri dishes using carlina oxide solutions in hexane at different concentrations (1, 5, and 10%) and the mortality was assessed after 5 days. The results showed that mortality of adult when exposed to the three different carlina oxide concentrations was significantly higher than the control. Moreover, the repellent activity was evaluated with two-way static olfactometer by comparing the two polymer systems activated with carlina oxide and the homologous inactivated materials. The results showed significant repellent activity of activated biodegradable polymer systems against *S. oryzae* adults. Considering the promising results obtained, our experiments suggest the potential use of carlina oxide as a sustainable alternative to synthetic insecticides and as packaging component with bioactive repellent properties.

Effect of azadirachtin on the tomato pinworm *Phthorimaea absoluta* and the parasitoid *Dolichogenidea gelechiidivoris*

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Abstract

Azadirachtin is one of the main biorational pesticides and the principal active compound in neem-based formulations used against the tomato leaf miner, *Phthorimaea (Tuta) absoluta* (Lepidoptera: Gelechiidae). *Dolichogenidea gelechiidivoris* (Hymenoptera: Braconidae), a parasitoid species of South American origin, but unintentionally introduced into Spain and Algeria is an important biological control agent against *P. absoluta*. Within the framework of integrated pest management (IPM), the compatibility of neem products with those parasitoids has not been thoroughly investigated. This study provides preliminary insights into the use of the product NeemAzal T/S, with azadirachtin as active ingredient, in combination with *D. gelechiidivoris*. At first instance we focused on its toxicity to 1st instar *P. absoluta* larvae mining inside tomato leaves. Therefore five concentrations of azadirachtin (0.25, 0.1, 0.05, 0.025, 0.01% active ingredient) and a water control were applied using the leaf-dip method with n=25 insects in each treatment. Mortality of larvae was subsequently observed for 24, 48, 72 and 96 hours. Next, olfactometer assays with parasitoids were conducted to assess behavioral responses towards treated and control leaves (n=24). Finally, toxicity of azadirachtin to *D. gelechiidivoris* on treated leaves was evaluated (n=20).

Azadirachtin caused significant mortality in *P. absoluta* larvae, with $LC_{25}=0.006\%$ and $LC_{50}=0.017\%$ after 72 h. The olfactory assays indicated a response of *D. gelechiidivoris* towards tomato leaves, however azadirachtin did not significantly influence this response. Azadirachtin caused mortality at lower doses in the parasitoids than in *P. absoluta* larvae, with $LC_{25}=0.001\%$ and $LC_{50}=0.01\%$ after 72 h. These results provide a foundation for further studies on the impact of neem-based bioinsecticides on the parasitoid *D. gelechiidivoris*.

Insect Multitrophic Interactions for Sustainable Plant Protection

Francesco PENNACCHIO (University of Naples Federico II - Department of Agricultural Sciences, F.pennacchio@unina.it)

Abstract

A growing body of evidence supports the hypothesis that the soil microbiome and its interactions with other microbiomes in the trophic networks are central to the context of “One-Health”. However, our knowledge of how these microbial communities interact and are influenced by upper and lower trophic levels remains fragmented, and a comprehensive framework connecting the soil microbiome to plant and animal health is still incomplete. The analysis of these complex networks of interactions across multiple trophic levels is currently limited, as is our understanding of the contribution of inter-kingdom interactions. I will discuss some of the mechanisms that govern these interactions among holobionts, affecting energy and material flow in insect trophic networks, and outline how we can exploit this knowledge to enhance crop health and for developing sustainable plant protection strategies with low impact on functional biodiversity and ecosystem services. Unravelling the mechanisms underlying resource competition in insect multitrophic interactions allows the identification of key molecules and genes that can be used to develop plant protection tools mimicking natural pest suppression strategies. However, predicting ecosystem response to anthropogenic perturbations remains challenging, and we still lack a robust approach to assess their impact on trophic interactions that underpin ecosystem stability and resilience. A holistic understanding of trophic interactions among holobionts can provide a robust framework for addressing this challenging objective. Multi-scale modelling based on trophic resource dynamics in food webs represents a novel integrative biology approach which can offer the opportunity to advance ecosystem study. By embracing trophic network complexity through advanced molecular and computational technologies, we can improve our ability to understand, predict, and manage the impacts of human activity on natural ecosystems and agroecosystems.

How effective is biological control and can it be scaled? Insights from fields and models

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Abstract

Harnessing agroecological functioning to improve the biological control of insect pests depends on a range of ecological, social, economic and cultural mechanisms that can hinder or support the success of this endeavour. Against the backdrop of the push-pull technology, a mixed cropping strategy aiming to increase biological control in smallholder farms of Sub-Saharan Africa, I show that biological control can be an effective strategy to sustainably control pests, and that a nuanced understanding of its mechanistic underpinnings helps navigate apparently high context-dependency across systems. Such improved predictive ability supports synergistic landscape design towards provision of multiple ecosystem services. However, scaling biological control approaches among practitioners requires more than effective, even synergistic management strategies: the long-term adoption of practices hinges instead on stimulating and sustaining knowledge networks within the wider governance and socio-economic context of farming systems.

Impact of climate change on pollinators and pollination service in agriculture

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Abstract

Within the NCCS programme «Decision Support for Dealing with Climate Change in Switzerland» (NCCS-Impacts) actionable climate services for the environment, economy and society will be developed from 2023 to 2026. The aim of the project «Impacts of climate change on ecosystem services in Switzerland» is to describe the projected changes in ecosystem services and functions caused by climate change for the forest, agriculture and aquatic ecosystems.

As part of this broader initiative the EGU presentation will focus on the impact of climate change on wild-bees and pollination service in Switzerland up to 2074 as one of the most important ecosystem services and additionally related to other ecosystem services such as agricultural production. We will demonstrate how we model a high-resolution index of pollination service using a hierarchical framework at local scale considering species occurrence data from species distribution models, habitat indices related to floral resources and nesting habitat, pollination relevant species traits and pollination dependent crops. For future ESS projections we use the CH2018 climate scenarios that are based on socioeconomic mitigation pathways. Wild-bee monitoring data from the Agricultural species and habitats' monitoring programme in Switzerland is used to validate the pollination service index. Preliminary results show that the impact of climate change on pollination service is strongly influenced by the pollination dependent crop, the region and pollination relevant species traits.

Five years of field releases reveal establishment and competitive constraints of the exotic parasitoid *Ganaspis kimorum* against *Drosophila suzukii* in Trento Province, northeastern Italy

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Asia COLMAGRO, Lorenzo FELLIN, Gianfranco ANFORA

Abstract

The invasive spotted-wing drosophila, *Drosophila suzukii* (Diptera: Drosophilidae), continues to cause severe economic losses in European fruit production systems, where control strategies remain largely dependent on insecticides. The search for sustainable alternatives has led to the introduction of specialized larval parasitoids from the pest's native range. Among these, *Ganaspis kimorum* (Hymenoptera: Figitidae) has been identified as a promising biological control agent; however, its establishment may be influenced by interactions with resident parasitoid communities.

A propagative release program of *G. kimorum* was initiated in 2021 in Trento Province (northeastern Italy). Here, we synthesize five years of field data (2021–2025) from 20 release sites to evaluate establishment success, parasitism rates, host specificity, and competitive interactions with other parasitoids, particularly the dominant exotic species *Leptopilina japonica* (Hymenoptera: Figitidae).

Although *G. kimorum* successfully established at multiple sites, field parasitism levels were substantially lower than those predicted from laboratory assays, averaging approximately 60% below expected values. Sites characterized by high *L. japonica* prevalence exhibited delayed establishment and reduced parasitism by *G. kimorum*, indicating strong competitive interactions during host exploitation. Despite this suppression, *G. kimorum* persisted over multiple seasons and maintained strict host specificity, with no evidence of parasitism on non-target drosophilids. No displacement of *L. japonica* was observed, suggesting asymmetric competition rather than replacement.

These results highlight the critical role of interspecific competition in shaping the outcomes of classical biological control introductions and underscore the need to account for established exotic parasitoids when evaluating the field performance of newly released agents against *D. suzukii*.

Exploring host?plant biological control as an indirect strategy for managing invasive insect pests

Chandra MOFFAT (Agriculture and Agri-Food Canada, Chandra.moffat@agr.gc.ca)

Hester WILLIAMS, Sonja STUTZ, Phil WEYL, Francesca MARINI

Abstract

Biological control programs generally target one or more closely related organisms to directly reduce invasive species abundance. However, opportunities may also exist for indirect biocontrol, in which control targets an organism the pest relies upon for survival, reproduction, or spread. This strategy is valuable when the pest exploits multiple host species and no adequately host specific natural enemy is available.

The agricultural pest spotted lanternfly *Lycorma delicatula* (SLF) provides a compelling case study. Since its detection in the United States in 2014, SLF has caused substantial impacts in horticulture and poses emerging risks to forestry, ornamentals, and natural ecosystems. Despite extensive international exploration, no direct classical (importation) biocontrol agents with adequate host specificity have yet been identified, however research efforts are ongoing.

SLF shows a strong ecological association with several hardwood trees of Asian origin, particularly the invasive tree-of-heaven (*Ailanthus altissima*, ToH), which it preferentially feeds on but does not strictly require for development. ToH is invasive globally, and in many regions where SLF occurs, is expanding or threatens to invade, ToH has itself become widespread, forming dense stands in disturbed habitats and agricultural landscapes, particularly in proximity to wine grape production. This overlap raises the possibility that reducing ToH abundance could indirectly limit SLF establishment, population growth, and spread by removing or diminishing a key resource.

We present research on two candidate biocontrol agents for ToH, one of which is adventive in Europe presently. If these agents prove effective in reducing ToH density and distribution, such a program could function dually: mitigating the significant ecological impacts of ToH while also serving as an indirect biocontrol strategy for SLF.

This case illustrates the potential for managing invasive insects impacting agriculture or other sectors, via direct classical biocontrol of invasive host weeds, offering a broader framework for integrated invasive species management globally.

Remnant vegetation impacts on ground-dwelling predatory arthropods and their mediated ecosystem services in citrus orchards

Shaun MANZINI (Rhodes University, Manzinis080@gmail.com)

Martin HILL, Reyard MUTAMISWA, Sean MOORE

Abstract

Land use change and agricultural intensification have led to a decrease in farmland biodiversity and its ecological functions. Arthropod decline in many terrestrial ecosystems is linked to agricultural intensification. Considering their critical functional role in ecosystem processes and services, they severely threaten human wellbeing and ecosystem function. Information about the impact of agricultural intensification on many crops and our understanding of the response of ground-dwelling predatory arthropods is still limited, thus hindering the development of mitigation measures. Here, the study assessed the community composition of ground-dwelling arthropods, diversity, abundance, and pupal predation of two soil-pupating pests (*Thaumatotibia leucotreta* and *Ceratitis capitata*) in citrus orchards and their adjacent remnant natural vegetation. Species richness, abundance, and pupal predation decreased with increasing distance from the remnant natural vegetation. There was no significant difference in pupal predation between soil-pupating pests. The community composition was more pronounced in the remnant vegetation than in citrus orchards. The increase in pupal predation seems to be related to an increase in invertebrate community diversity, and although the mechanisms related to this are not always clear, our results suggest that arthropod diversity could be a good proxy for these processes.

How the new biopesticide, surfactin, impacts buzzing pollinators ?

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Marion SUSINI, Clément TOURBEZ, Kévin TOUGERON

Abstract

In response to the rizing food demands of a rapidly expanding global population, pesticide use has increased significantly since the 1960s. Although this intensification has substantially enhanced agricultural productivity, it has also generated widespread ecological costs, highlighting the need for alternative pest management strategies that are compatible with environmental sustainability, biodiversity conservation, and human health. Within the framework of ecological intensification, microbial-derived biomolecules have emerged as promising tools for crop protection. Among these, lipopeptides, extracted from the genus *Bacillus*, and particularly surfactins, exhibit insecticidal properties.

From an ecological risk assessment perspective, their deployment raises a fundamental question: to what extent do these compounds act as selective filters targeting pest species, or as broader environmental stressors affecting non-target beneficial insects ? Despite a growing interest, knowledge of the lethal and sublethal effects of surfactins on beneficial insects remains scarce. Toxicological responses in insects are strongly mediated by temperature, as both pollutant toxicity and insect physiological performance depend on thermal conditions. In the context of climate change, rising temperatures are expected to modify dose–response relationships, potentially amplifying or mitigating the effects of biopesticides.

In this context, this study aims to investigate the lethal and sublethal effects of surfactin on *Bombus terrestris*, a key pollinator commonly encountered in agricultural landscapes. *B. terrestris* were exposed to surfactin via topical application and ingestion under two temperature scenarios based on IPCC climate projections. Beyond mortality, we quantified sublethal effects on mating success and behaviour and on flight and foraging behavior of individuals.

We hypothesize that surfactin is not fully pest-specific and may exert negative effects on pollinators, with outcomes depending on both exposure pathway and temperature. By combining ecotoxicology and thermal ecology, this study aims to assess whether surfactin can be integrated into sustainable pest management strategies without undermining essential ecosystem services such as pollination.

Behavioural responses to abiotic stress: from evolutionary feedback to survivor persistence in the Colorado potato beetle

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Philippa MUSIOLIK, Martin KALTENPOTH, Shuqing XU

Abstract

Abiotic stress not only influences behaviour; behavioural responses can also determine how stress is experienced, with consequences for adaptation and persistence. Here, we use the Colorado potato beetle, *Leptinotarsa decemlineata*, to ask how insecticide-related environments shape behaviour, fitness, and population responses across ecological and evolutionary timescales. Drawing on two complementary studies, we show that these links emerge through behavioural feedback during adaptation and through phenotypic filtering after stress.

In one context, we examine how maternal oviposition behaviour generates evolutionary feedback in heterogeneous environments, where females choose between toxic (insecticide-treated) and non-toxic host plants and where offspring exposure depends on whether that choice is preserved or disrupted. Preserving maternal choice was associated with lower mortality, higher later fecundity, and distinct resistance trajectories relative to disrupted choice or constant exposure, showing that behaviour can actively structure selection rather than merely respond to it. In a separate context, we examine survivor persistence after developmental stress, where inbreeding together with sublethal insecticide exposure reduced emergence before adulthood and filtered which phenotypes reached the adult stage. Among surviving adults, responses were trait-dependent: male locomotor activity declined, feeding increased in both sexes, and reproductive performance varied with insecticide stress history and inbreeding status.

Together, these results show that behaviour is central to understanding abiotic stress since environmental effects are shaped not only by direct physiological impacts, but also by how behaviour structures exposure, how stress filters developing individuals, and how survivor phenotypes influence subsequent ecological and evolutionary dynamics. More broadly, responses to anthropogenic environments cannot be understood from mortality or resistance alone; explaining persistence under stress requires linking behaviour, exposure, development, demography, and selection across scales.

Brood presence shifts bumble bee foraging toward metal-free food despite lower sugar

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Timothy SNOWDEN, Théau MASSON, Mark J. F. BROWN, Antoine GEKIERE

Abstract

Metal pollution is increasing worldwide and poses a growing risk to pollinators. Although the toxic effects of metals on bees are well documented, it remains unclear whether bees can behaviorally avoid contaminated food sources, and whether such choices depend on social context. We tested metal avoidance and its plasticity in the buff-tailed bumble bee (*Bombus terrestris*) using copper (Cu; essential but harmful at elevated concentrations) and cadmium (Cd; non-essential).

Workers were offered a two-choice feeding assay between a metal-laced sucrose solution and an uncontaminated alternative, and we quantified preferences by measuring intake of each solution. We first provided two 50% sucrose solutions (treated vs untreated) to assess baseline avoidance. We then imposed an energetic trade-off by reducing the sucrose concentration of the uncontaminated solution to 20% while keeping the contaminated solution at 50%, creating a choice between safer but less rewarding food and sweeter but potentially toxic food. To evaluate social context, workers were tested either with larval siblings (brood present) or without larvae (brood absent).

When both options contained 50% sucrose, workers consistently avoided Cu- and Cd-contaminated solutions, regardless of brood presence, indicating reliable detection and active avoidance of contaminated resources. Under the sugar–toxicity trade-off, decisions became context dependent. In brood-absent groups, workers preferentially consumed the higher-sugar contaminated option, suggesting that immediate energetic gains can outweigh contamination avoidance. In contrast, in brood-present groups, workers favored the uncontaminated but sucrose-poor solution, consistent with risk-averse provisioning behavior to protect larvae.

Overall, these findings show that bumble bee workers can actively avoid metal-contaminated food and flexibly adjust risk-taking according to social context and nutritional constraints. Incorporating colony state into ecotoxicological assays and exposure models may improve predictions of pollinator vulnerability in metal-polluted landscapes, where contaminated nectar or honeydew can impose hidden trade-offs between energy intake and toxicant exposure.

Facultative parthenogenesis can enhance resilience in light polluted tropical forests

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Janine SOH, Ning HO, Zou YAN, Sebastian POHL, Ewan FLINTHAM

Abstract

Artificial light at night (ALAN) is a widespread pollutant that can disrupt animal behaviour and threaten species viability. Rapid land-use change is intensifying ALAN across the tropics, but regional estimates are lacking, and the sensitivity of species to ALAN in these biodiverse and threatened habitats is rarely studied. Here we report an intensification of ALAN and land-use change using satellite data from 2013 and 2021 to estimate proportions of forest disturbed by ALAN across Borneo (0.22% to 0.26%), Peninsular Malaysia (2.71% to 3.39%), and Singapore (78.5% to 91.5%). We further investigated feeding, walking, and mating activities under ALAN (relative to day and night light treatments) of three stick insect species native to these respective regions, showing that the least diurnally active (and most regionally ALAN-exposed, i.e. Singapore) species was proportionally more sensitive to ALAN via reduced activity. We then compared egg laying, incubation time, hatching success, and nymph survival across sexual and parthenogenetic origin for 5833 eggs and 11490 nymphs to show that facultative parthenogenetic viability was greatest in this species. Finally, we used matrix population modelling to suggest that this quantified parthenogenesis can comfortably offset the expected mating disruption revealed by our mapped distributions, although we caution that ALAN disruption to feeding was also evident, and effects on predatory evasion remain unknown. Taken together, our results suggest an unexpected resilience to ALAN for some facultative parthenogens, but emphasise that it can still disrupt a variety of behaviours fundamental to many species' survival.

Near-infrared vision guides parental investment in a burying beetle

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Sheng-Feng SHEN

Abstract

Animals inhabit terrestrial environments where near-infrared (NIR; >700 nm) radiation is abundant, yet current paradigms in sensory biology assume that such long wavelengths are effectively invisible to visual systems and accessible only via thermoreception. Whether animals can see NIR and use it to solve ecologically critical problems, such as assessing risk and allocating parental investment, remains unknown. Here, we present physiological, behavioral, and genomic evidence of functional NIR vision in the burying beetle *Nicrophorus nepalensis*. We show that these insects use NIR cues to evaluate competitive risk and adjust their reproductive investment accordingly. Using an optomotor assay with a rotating black-and-white striped drum under NIR illumination only, we demonstrate that beetles exhibit robust, directional tracking responses, indicating that they can resolve motion contrast from NIR wavelengths alone. This response disappears when the compound eyes are painted opaque, confirming that NIR detection is mediated by the visual system rather than by somatic thermal sensors. Field and laboratory experiments further reveal that forest detritus, enriched in long-wavelength light, functions as a visually defined “safe” microhabitat in which competition for vertebrate carcasses is reduced. Under NIR-rich conditions, beetles exhibit behavioral plasticity by decreasing their investment in the energetically costly behavior of burying carcasses, consistent with a lower perceived risk of exploitation by competitors. In contrast, the absence of NIR cues, mimicking exposed conditions, triggers immediate and intensive burial of carcasses to secure the resource. Genomic analyses identify an expanded opsin repertoire, including a *Drosophila* Rh7-like opsin, as a strong candidate underlying NIR sensitivity. Together, these results overturn the assumption that NIR is inaccessible to animal vision and reveal a specialized adaptation in which *N. nepalensis* “sees” safety in the infrared spectrum to optimize parental investment in a competitive environment.

Species-specific behavioral consistency suggests a phylogenetic component to personality in ants

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Grant N. DOERING, Patrizia D'ETTORRE, Timothy LINKSVAYER

Abstract

Animal personality, defined as consistent individual variation in behavioral expression, has been studied in several vertebrate and invertebrate species, including ants. Understanding the evolutionary basis of animal personality requires investigating how consistent individual behavioral differences are distributed across species and possibly shaped by phylogeny.

In this study, we assessed the temporal repeatability and interspecific variation of three colony-level behaviors—sociability, exploratory activity and response to food—in 15 ant species from two closely related genera, *Temnothorax* and *Leptothorax*, using at least two colonies per species. Each behavioral trait was measured twice, two days apart, to evaluate temporal consistency. Sociability was assessed directly in the nest by quantifying the mean dispersion of ants. Exploratory activity was assessed by quantifying the cumulative proportion of surface explored by the ants in a new arena. The response to food was measured by recording the average number of ant foragers gathering around a food source.

Repeatability analyses, accounting for colony and species size, revealed clear consistency across time for sociability and exploratory activity, but this was less strong for the response to food. However, integrating phylogenetic structure to our models allowed to show that the response to food was significantly correlated with both exploratory activity and sociability across species, indicating that different collective personality traits may be evolutionary integrated.

These findings may reflect underlying phylogenetic patterns, paving the way for future studies examining the phylogenetic basis of interspecific variation in personality.

Combination of senses: odour and colour in *Drosophila suzukii* traps

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Zainat AL MASALMEH, Bruna CZARNOBAI DE JORGE

Abstract

The Spotted Wing *Drosophila*, *Drosophila suzukii*, invaded Europe starting in 2011. Despite ample research efforts this invasive species is still devastating to growers of berry fruits and cherries. Due to its rapid population growth and its susceptibility to climatic conditions in spring, it remains difficult to forecast population dynamics and subsequent potential damage of fruits. Development of specific monitoring tools is therefore decisive as a tool for growers. For their orientation and host choice the flies use a combination of visual and chemical cues. Therefore, the design of traps should stimulate both senses. Based on previous studies we used an attractive yeast, *Hanseniaspora uvarum*, and raspberry concentrate as olfactory lures. To detect colour preferences we measured the reflected wave lengths of fruit colour in sweet cherries at several stages of ripeness. We compared various translucent plastic foils in red hues to those wave lengths as potential attractant for monitoring traps. Both lures and all colours were tested with summer and winter morphotypes of the flies. Non-metric multidimensional scaling analysis (NMDS) was used to visualize similarities and differences between fruits and foils. Behavioural experiments tested for attractiveness of odour or colour and their combination. Results were discussed for possible use in regulatory strategies under field conditions.

Autonomous behavioural monitoring in earthworms: a scalable platform for high-throughput ethological studies

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Zixuan HE, Quentin GIESSMAN

Abstract

Earthworms are vital soil engineers whose burrowing, feeding, and casting behaviors maintain ecosystem health by supporting nutrient cycling and soil structure. Despite their ecological importance, the behavioural mechanisms underpinning these functions—and their sensitivity to environmental stressors such as warming, drought, and agrochemical exposure remain poorly understood. Traditional observation methods are labor-intensive, limited in temporal resolution, and prone to observer bias, constraining progress in quantitative behavioural ecology.

We present a modular, scalable platform for continuous, autonomous monitoring of earthworm behaviour. The system integrates high-resolution imaging, acoustic sensing, and automated machine-learning analysis within a flexible experimental framework that permits precise control of environmental conditions, including moisture and lighting. It captures both aboveground and underground activity, enabling long-duration, fine-resolution behavioural assays across a broad range of experimental contexts.

Pilot studies demonstrate that the platform reliably detects food-preference behaviour under simultaneous choice conditions, expressed as biased surface movement and prolonged residence near preferred resources. These movement patterns indicate non-random foraging and active resource discrimination, illustrating the system's utility for studying foraging decisions, activity timing, and movement ecology in soil-dwelling invertebrates.

By removing the need for human observers, the platform supports high-throughput behavioural studies and captures subtle dynamics often missed by manual methods. Its modular design facilitates adaptation to other invertebrate taxa, providing a flexible methodological framework for advancing experimental ethology under controlled environmental conditions.

#11947

INSECTS AS SOLUTIONS: Ecosystems services - Soil managers and Architects

03/07/2026 at 08:30, Bourgueil

Towards a Large-Scale Understanding of Soil Insect Effects on Ecosystem Functions

Jerome MATHIEU (Sorbonne Université, CNRS, INRAE, Jerome.mathieu@sorbonne-universite.fr)

Abstract

Soil insects play a central role in soil and ecosystem functioning. They influence a wide range of processes and underpin key ecosystem services, including nutrient cycling, water regulation, and primary productivity. However, quantifying their contribution to global biogeochemical cycles and climate change mitigation remains in its infancy. This gap largely stems from our limited understanding of how these effects vary within and among species across large spatial scales.

In this talk, I will present a recent global synthesis of the effects of ants, termites, and earthworms on multiple ecosystem functions, revealing impacts that are not only consistently strong, but also highly dependent on environmental context.

Building on these results, I will introduce PEPR SolsVivants (“Living Soils”), a new French National Research Program designed to quantify how soil biodiversity shapes ecosystem functioning, and present opportunities for active involvement.

Ants in restoration ecology: Why, what's and the way forward

Tania DE ALMEIDA (Université de Lille, Institut Mines-Télécom, Université Artois, Junia, ULR 4515 - LGCGE, Laboratoire de Génie Civil et géo-Environnement, Lille, France, Tania.dealmeida@univ-lille.fr)

Xavier ARNAN, Yvan CAPOWIEZ, Mickaël HEDDE, François MESLÉARD, Thierry DUTOIT, Olivier BLIGHT

Abstract

Global changes call for more nature-based solutions, especially in nature conservation involving ecological restoration. Current methods essentially based on civil engineering are both expensive and costly in non-renewable energy consumption and pollution terms. The non-sustainability of these techniques is leading to the direct use of certain species to restore degraded ecosystems. Ants, because of their central role in ecosystem functioning and their occurrence on almost all terrestrial ecosystems, are promising candidates for environmental monitoring and such ecological restoration projects. In this study, we provide a narrative review of the ecological functions performed by ants, and we take stock of how ants are currently considered in passive and active restoration. We also propose a trait-based approach to facilitate their use in future restoration projects. We list and discuss both life-history traits relevant for environmental monitoring and functional traits known to affect abiotic (physical and chemical soil properties) and biotic (plant and fauna communities) components.

Influence of Thermal Conditions on Early Colony Dynamics in the Black Garden Ant *Lasius niger*

Rafael DA SILVA (Institut d'Ecologie et des Sciences de l'Environnement de Paris (iEES Paris), Sorbonne Université, Université Paris Cité, Université Paris Est Créteil, CNRS, INRAE, IRD, France, Rafael.carvalho_da_silva@sorbonne-universite.fr)

Angélique BULTELE, Thibaud MONNIN

Abstract

Global warming affects living organisms at many levels, from molecular processes to behavior. Social insects are especially vulnerable because their body temperature closely follows environmental conditions. Ant queens are particularly exposed in species founding colonies during the summer. To understand how external temperature shapes nest excavation and early colony development, we designed an experimental setup in which founding queens of the black garden ant *Lasius niger* were placed either alone or in groups of three in two-dimensional nests. These queens were exposed to mild, moderate, or high soil surface temperatures, allowing us to assess how temperature influences both the speed and depth of nest construction. Throughout the experiment, we monitored brood presence over time and recorded the number and size of workers produced at the end of the founding phase. We hypothesized that soil surface temperature would influence nest excavation and early colony development. Specifically, higher temperatures would promote deeper excavation as a mean to provide optimal temperatures to the developing brood (workers that developed under warmer temperature are smaller). We expected this factor to interact with queen number. Excavating deeper is costlier to a solitary queen, which would excavate a relatively shallower (warmer) nest and hence produce smaller workers, which are less competitive and shorter-lived. Our work aims to provide insights into how thermal stress shapes early nest establishment, including the cooperative strategies of queens, brood development, and colony dynamics in ectotherms under climate change scenarios.

Dung Beetle Diversity and Function in Mediterranean Landscapes: Effects of Habitat, Landscape, and Resource Availability.

Mélanie BERTRAND (Centre d'Ecologie Fonctionnelle et Evolutive, Melanie.bertrand@univ-montp3.fr)

Matthias BRAND, Pierre JAY-ROBERT, Quilina LANFRANCHI, Perrine GAUTHIER, Camila LEANDRO

Abstract

In Mediterranean landscapes, the decline of traditional grazing practices since the mid-20th century has led to the regression of high-value open habitats, with cascading effects on biodiversity and key ecological processes such as organic matter decomposition and nutrient cycling. Dung beetles, as major contributors to these recycling functions, offer an ideal model to understand how shifts in land management and resource availability affect the maintenance of ecosystem services in these rapidly changing environments.

This study was conducted over two seasons across 14 sites in a Mediterranean area of southern France, combining deciduous forests and grazed open habitats. It explores how dung beetle community diversity—both taxonomic and functional—and dung degradation efficiency vary with habitat type, landscape structure, and resource availability. Baited pitfall traps using two types of dung—sheep, representing traditional transhumant pastoral systems, and wild boar, a species of growing ecological and societal concern—were deployed to assess the relative attractiveness of each resource under different local conditions.

Results indicate that both dung types were used in both seasons, although not in equal proportions: in spring, herbivorous dung was clearly preferred, whereas in autumn, both resources were important. This pattern may indicate a complementarity of resources, supporting community persistence even when domestic inputs are reduced. Moreover, the historical pastoral practice and current landscape composition, particularly the proportion of open habitats, play major roles in shaping dung beetle diversity and abundance. However, the composition of the community differed, as some species were only found in open habitats and others accommodated well in forests, although the degree of canopy openness and grazing history appear decisive, highlighting that grazed woodlands may provide favorable conditions for some species. Maintaining a mosaic of habitats remains essential to sustain functionally rich communities, offering nuanced insights for adaptive habitat management strategies.

Soil fauna taxonomic and functional responses to vineyard management intensity in Mediterranean context: a multi-taxa approach

Clara ZIMMERMANN (CEFE, Univ Montpellier, CNRS, EPHE, IRD, Univ de Montpellier Paul-Valéry, Montpellier, France, Clara.zimmermann@univ-montp3.fr)

Alan VERGNES, Jérôme CORTET, Ninon DELCOURT

Abstract

French vineyards significantly contribute to global wine production, but conventional intensive practices have degraded soils, particularly their biodiversity. Defining alternative practices to conventional ones are gaining interest, yet identifying management strategies that actually preserve soil biodiversity remains a key challenge for more sustainable vineyards.

We assessed the effects of various management practices on spider, ant, and Collembola communities. These organisms are fundamental to soil ecosystem functioning, and while their ecology is well documented, knowledge of their responses to agricultural practices varies among taxa, being well known for Collembola and spiders but less so for ants. We investigated 37 vineyards in Southern France (Occitanie region), focusing on four types of practices: (i) vegetation cover, (ii) organic matter inputs, (iii) soil tillage intensity, and (iv) pesticide treatment intensity. Spiders and ants were sampled using pitfall traps, and Collembola with soil cores. We hypothesized that intensive tillage would reduce soil fauna through disturbance and loss of vegetation cover, whereas organic amendments would increase resource availability, supporting decomposers like Collembola and their predators, spiders. Ants, occupying both below- and above-ground niches, were expected to be particularly sensitive to pesticide intensity.

Generalized linear models showed that overall soil arthropod communities responded negatively to soil tillage. Ants were negatively affected by pesticide intensity but benefited from organic matter inputs, whereas Collembola showed no significant response. Soil properties effects were taxon-specific. A complementary functional approach is further used to explore the strategies soil fauna react under different management practices and to uncover the ecological mechanisms behind these responses.

Integrating taxonomic and functional approaches highlights the key mechanisms for preserving soil arthropods and their associated functions in vineyard agroecosystems.

Field-based and experimental insights into how disturbance shapes bioturbation in tropical ecosystems

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Abstract

Soil insects play an integral part in many ecosystem functions and services. One of the key processes provided is bioturbation, the turnover of soil material caused by various organisms with termites and to some extent ants being the most important ones. Despite the importance of bioturbators there are not many studies that would aim to assess effect of disturbances on their communities across multiple habitats. The response of bioturbators to the disturbances is crucial in tropics where alterations of natural ecosystems by human activities are particularly rapid, especially in Southeast Asia. Here we investigated aboveground bioturbation in two natural (rainforest, tropical wetland) and two anthropogenic (urban park, agriculture field) habitats in Terengganu, Malaysia. Additionally we performed manipulation experiment in which we observed production of soil structures between disturbed and undisturbed plots in the field. Across the studied habitats, termites were the biggest contributors to the bioturbation with the exception of the wetland. The amount of standing bioturbated soil was comparable between the natural and anthropogenic habitats. However when not considering the termites, bioturbation was higher in anthropogenic habitats. The results from manipulation experiment showed that disturbance had a significant positive effect on amount of bioturbated soil. This effect was most prominent in ants and was consistent through time. Our results emphasise the role of termites in contributing to the soil turnover in different habitats. Contrary to other studies comparing bioturbation between natural and altered habitats our results suggest that mild disturbances increase the soil turnover. At the same time they show that the method of removing soil structures and letting organisms to raise them again commonly used for measuring bioturbation may actually lead to its overestimation.

Global distribution of soil fauna its effect on litter consumption and organic matter incorporation in soil

Jan FROUZ (Biology Centre CAS, Frouz@natur.cuni.cz)

Abstract

Bioturbation by soil fauna is an important process by which soil fauna facilitates soil mixing and incorporation of plant litter in soil. Bioturbation effects microbial activity, soil formation, soil C storage, and many other key processes. Despite this bioturbation is seldom measured and data about rate of bioturbation around the world are rare.

In this contribution and combined data about global distribution and litter consumption of insectes and other important bioturbatin invertebrates and data from global bioterbation experiment, where mesocosms, that were either accessible or inaccessible to soil fauna, were used to quantify the effect of soil fauna on organic matter incorporationin moneral soil. Soil fauna that may contribute to bioturbation was dominated by earthworms, ants and termites, the later on dominated in topics . The overall amount of litter consumed by some fauna across biomes, represents about half of annual litter fall. Soil fauna access in mesocosm significantly increased incorporation of organic matter in mineral layer of mesocosms. Fauna mediated increase in organic matter incorporation in mineral layer is promoted by increasing actual evapotranspiration and decreasing C/N ratio of litter. When one compare estimated amount of litter consumed by soil invertebrate fauna to carbon Incorporated to solve one can see that about half of the litter eaten by soil faina has been incorporated in soil.

Evaluating the impact of climate change on the decline of European bumblebee populations

Bastien DE TANDT (Spatial Epidemiology Lab (SpELL), Université Libre de Bruxelles (ULB), Brussels, Belgium; Laboratory of Zoology, Research Institute for Biosciences, University of Mons, Mons, Belgium, Bastien.de.tandt@ulb.be)

Kyla SERRES, Rosa PIETROIUSTI, Diana ERAZO, François MASSONNET, Denis MICHEZ, Wim THIERY, Guillaume GHISBAIN, Simon DELLICOUR

Abstract

Climate change is a major driver of biodiversity loss, particularly for insects that are experiencing widespread and rapid declines. However, quantifying the specific contribution of climate change among multiple co-occurring pressures remains challenging. Here, we apply a formal climate-attribution framework to estimate how much historical climate change has altered the ecological suitability of European bumblebees between 1901 and 2019. We trained species-specific ecological niche models on contemporary occurrence records and projected them onto two climatic scenarios: (i) a factual reconstruction of historical climatic conditions and (ii) a counterfactual baseline in which long-term climate trends were removed. The comparison between the two projections isolates the portion of ecological suitability change attributable solely to climate change. Across Europe, climate change has reduced ecological suitability for the bumblebee community, with an averaged decline of 5% and local decreases reaching 19%. Losses are spatially clustered in the Atlantic, Continental, Mediterranean and Pannonian European regions. In contrast, Alpine and Boreal regions show no clear net change in mean ecological suitability, with gains in some high-latitude (e.g., parts of Scandinavia) or high-altitude areas (e.g., the Alps) offset by losses in other sub-regions. Species responses were similarly heterogeneous: cold-adapted and montane taxa exhibited the strongest losses, while several lowland generalists showed moderate suitability gains. Overall, our results demonstrate that climate change has already reshaped the ecologically suitable areas to this key pollinator group and impose a pervasive pressure on European ecosystems.

Bias-aware species distribution modelling of data-deficient Southeast Asian fireflies reveals patterns of habitat suitability and exposure to light pollution

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Jackson CLIVE, Eunice J. TAN

Abstract

Fireflies are charismatic insects renowned for their bioluminescent displays, yet in Southeast Asia (SEA) their distributions and conservation status remain poorly resolved due to sparse and geographically biased occurrence records. Here, we present a small-sample species distribution modelling (SDM) framework to map suitable habitats for ten data-deficient SEA firefly species.

We compiled multi-source occurrence records and defined species-specific accessible areas (M) as the intersection of TEOW ecoregions containing focal presences and a geographic buffer around occurrences. Using a varying-extent approach, environmental predictors including climate, land use and vegetation structure, and hydrological proximity were curated to a parsimonious set and cropped to the bounding box of M.

To account for sampling bias, we constructed a kernel density estimate (KDE) bias surface from pooled, all-species occurrences. KDE was computed in a metric projection with padding to reduce edge effects, then reprojected and aligned to the environmental grid. Background points (e.g. 20,000) were sampled from non-NA predictor cells with probability proportional to KDE intensity, while focal presences were filtered and thinned to one occurrence per pixel. Preliminary outputs reveal fragmented and spatially restricted areas of predicted suitability across species, underscoring the vulnerability of SEA fireflies to ongoing land-use change

MaxEnt models were tuned in ENMeval using sample-size-dependent partitioning rules (jackknife, checkerboard, or block), with feature classes and regularisation grids adjusted accordingly. Best models were selected by minimum AICc and projected as cloglog suitability. Building on these distributional outputs, we will quantify encroachment of artificial light at night (ALAN) into predicted suitable habitat by overlaying VIIRS-derived nighttime light rasters across years to estimate temporal changes within high-suitability areas. Finally, we propose integrating SDM-derived predictors with life-history traits and IUCN Red List data to model relative extinction risk for data-deficient SEA fireflies, supporting conservation prioritisation in rapidly urbanising tropical landscapes.

Surviving in a changing world: lessons from habitat suitability modelling of a specialist species *Oedipoda caerulescens* (Orthoptera: Acrididae)

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Betija RUBENE, Ainārs AUNIŅŠ, Andris AVOTIŅŠ

Abstract

According to the reports under Article 17 of the Habitats Directive, the quality of grey dune, dry heathland and xeric sand grassland habitats in Latvia and Lithuania is deteriorating, and the overall conservation status of these habitats is unfavourable. The main threats are habitat conversion, abandonment, and natural succession, resulting in species composition change. The functioning of these habitats can be indicated by the presence and abundance of specialist species. *Oedipoda caerulescens* is a typical species for these EU habitat types and a known indicator of dune and heathland habitat quality. Additionally, it is one of the only two Orthoptera species that are legally protected in Latvia. However, with no monitoring scheme in place, acquiring data for informed decisions on conservation measures for this species and its habitats is challenging.

Using expert filtered presences from citizen science data, we employed maximum entropy analysis to create a high-resolution nation-wide habitat suitability model for *Oedipoda caerulescens*. Using state-of-the-art approaches, we addressed land use and land cover changes since each observation, corrected for the sampling bias in occurrence data, and employed model training and testing withholding both species presence and background data. With a large set of 538 ecogeographical variables describing Latvia, we analysed the species response to environment in multiple spatial scales, from 100 m analysis cells to home range and dispersal scale, offering a unique insight in the ecology of Orthoptera in an underrepresented region. In a time of climate change and biodiversity loss, we argue the need for monitoring and regular suitability modelling as tools for researching potential changes in species distribution and habitat requirements. We highlight the importance of citizen science data for a protected species and discuss how SDMs can help to identify new areas for the conservation of the species and its suitable habitat.

NSDM-based prediction of an invasive species' distribution on a small tropical island using a surrogate region

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Dominique CARVAL, Johanna CLÉMENCET, Paul KRUSHELNYCKY, Laureline LESPINASSE, Leïla BAGNY-BEILHE

Abstract

Predicting the potential distribution of widespread, invasive species at fine spatial scales on small tropical islands is particularly challenging when these islands exhibit strong environmental heterogeneity.

Classical Nested Species Distribution Modeling (NSDM) combines global, coarse-grain models with regional, fine-grain models to address spatial niche truncation. However, when the environmental conditions of a newly invaded area extend beyond the range of values documented in other regions, the selection of global predictors may become biased, leading to the overemphasis of variables that are not ecologically relevant in these new environments. Furthermore, in cases of recent invasion, the regional component of the model may be strongly truncated because occurrence data are limited and spatially restricted.

To address these limitations, we proposed a new approach based on the NSDM framework that we applied to the case of the recent detection of *Linepithema humile* and its early invasion at La Réunion, a small tropical island characterized by steep elevational gradients (0–3,070 m) and extreme rainfall variation (450 to >10,000 mm).

We first applied NSDM approaches based on simple combinations and sequential modelling using bioclimatic variables as global predictors and additional local variables (*e.g.* land use, radiation) as regional predictors. We then used the Hawaiian archipelago as a surrogate region, taking advantage of its environmental similarity to La Réunion and the long-standing establishment of *L. humile*. Using extrapolation metrics to ensure niche conservatism, we aimed to improve the representation of environmental conditions relevant to the species. Finally, to account for the specificity of rainfall variation on La Réunion, we built a global model using only temperature-based predictors and a refined regional model that explicitly included rainfall-derived predictors.

This study highlights how methodological choices in NSDM influence the reliability of biological invasion forecasts, and therefore the effectiveness of invasion risk management.

Sampling bias correction when combining structured and opportunistic data for wild bee species distribution models: A case study from Latvia

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Janis GAILIS, Ainars AUNINS, Andris AVOTINS

Abstract

Data-driven conservation planning lacks information on the distribution and ecological requirements of wild bee species. In most regions, the data on wild bee species observations is scarce and mostly opportunistic. In Latvia, the abundance and spatial distribution of structured monitoring data is too low for integrated distribution modelling. Hence, there is a need to combine observations from datasets with differently structured data within a presence-only species distribution modelling framework, where sampling effort bias plays a crucial role.

In this study, we developed a maximum entropy analysis workflow for modelling the distribution of bee species at a national scale in high resolution. The workflow combines structured (research) and opportunistic (citizen science and expert databases) occurrence data and tests different methods with increasing complexity for sampling bias corrections. Approaches range from traditional spatial thinning, through simple target-group weighing, to more sophisticated assignment of dataset-specific seasonal weights within the target-group. The workflow was tested across a range of wild bee species, comparing model performance metrics and expert-based evaluation of both the projected distribution map and marginal response curves between different bias corrections.

The results show that using different methods for sampling bias correction can yield models that have very different outcomes, including model evaluation metrics, response curves, relative variable importance, and habitat suitability projections. These variations highlight the critical importance of addressing biases in sampling effort for such datasets to ensure the development of more reliable models. This is particularly important if the model is used in conservation planning or ecological inference, as biased estimates could mislead conclusions and lead to ineffective or harmful interventions in conservation planning.

Wireworms and click beetles in Quebec (Canada): what is new?

Julien SAGUEZ (CÉROM, Julien.saguez@cerom.qc.ca)

Regine GRIES, Gherard GRIES, Wim VAN HERK

Abstract

Wireworms, the larval stage of click beetles (Coleoptera: Elateridae), represent a major threat to field crops in Quebec and across Canada. Several species are present, including native species from North America, and invasive species from Europe, each differing in distribution, phenology, and risk levels for crops.

Understanding the biodiversity and the ecology of these pests is essential for accurate diagnosis and targeted management. Several studies have been conducted during the past decades to identify the different species and their distribution. Seed treatments are generally used to manage these soil pests to reduce damage to seedlings and plantlets. However, it has been shown that the use of seed treatments is not justified in more than 90% of the fields in Quebec.

At the same time, in the province of Quebec (Canada), the regulations have evolved to reduce the health and environmental risks associated with pesticide use. Alternative strategies, including biological control agents (entomopathogenic nematodes and fungi) and pheromone traps are studied.

Together, these developments contribute to disrupting wireworms and click beetles, to reduce population pressure and to develop a more resilient and environmentally responsible approach to managing these pests. This poster will present the recent results obtained with these strategies, during recent years, in the province of Quebec.

Advancing from urban ecology to Ecology-based Solutions

Stephen VENN (University of Oulu, Stephen.venn@oulu.fi)

Abstract

The academic discipline of urban ecology initially developed as a body of research on organisms that inhabit urban regions, and the effects that urbanization has on those organisms. The discipline of urban ecology seemed to have great potential for influencing practice, as it combined ecological concepts and research with urban practice. The results, particularly for insects, can be summarised in that species assemblages were altered, a minority of mostly eurytopic species thrived and the most stenotopic and vulnerable species declined or were lost. These results are satisfying for the community of urban ecologists, but without suitable interpretation for policymakers and practitioners, have minimal impact on practice and governance. After its period in the limelight, the stage has since been taken over by such topics as resilience, sustainability transitions and Nature-based Solutions, as means of addressing societal challenges, such as declining biodiversity and safeguarding the provision of essential ecosystem services. As scientists, we need to bring urban ecology into this multidisciplinary space. Nature-based solutions are not going to resolve such crises as climate change and loss of biodiversity unless they are founded on a sound understanding of the ecology of the taxa and ecosystems involved. And we, as ecologists, need to raise the level of our game, from demonstrating urbanization affects on organisms of diverse taxa, to the construction of Ecology-based Solutions to provide ecosystem services and conserve biodiversity and taking ecology into the dialogue on sustainability transitions.

Arthropod biodiversity and ecosystem services in recent urban micro-ecosystems

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Anne-Violette LAVOIR, Elodie VERCKEN

Abstract

Because urban green spaces provide multiple services like temperature regulation or water management, as well as direct benefits for human health, the renaturing of cities has become a major focus of urban environmental policies. In addition, urban green spaces can also play a role in the urban meta-ecosystem as biodiversity refuges, yet these services have been less documented. In recent years, schoolyards have been identified as key reservoirs of space that can be used for greening within dense urban fabrics. A common feature of such spaces is that their area is often limited, and they are disconnected from other green areas, which may limit their potential to act as functional ecosystems within the urban landscape.

The Bug2School project aims at evaluating the actual contribution to biodiversity of these urban micro-ecosystems, by describing the arthropod communities and related ecosystem services in recently greened schoolyards within the city of Nice (France). Arthropods are valuable indicators of both the quantity and quality of ecological processes, particularly in the case of small-sized ecosystems. Over the year 2024, we sampled arthropod diversity using a combination of methods targeting different communities. We analysed the influence of two categories of ecological factors on different diversity metrics (abundance, taxonomic richness, functional richness) : (i) local factors related to the green space itself like area or plant richness ; (ii) landscape-scale factors related to the greenness of the environment around the schoolyard, like the quantity and fragmentation of green cover. In 2026, we measured three arthropod-related ecosystem services (pollination, biological control, organic matter decomposition) in a subset of the same schoolyards using experimental controlled approaches. We analyzed how the realization of these services varies across schoolyards, and how it can be related to the composition of the plant layout and to the diversity of the local arthropod communities.

Impact of urban gradient on bee and hoverfly communities

Thibaud CHALET (Université de Rennes, Thibaud.chalet@univ-rennes.fr)

Dorian MERIGNAC, Solenn FRABOULET, Iris RAULT, Benoît GESLIN, Andreas PRINZING, Joan VAN BAAREN

Abstract

Human activities are leading to a rapid and huge collapse of biodiversity. Through the increase of impervious surface and induced urban heat island, urbanization greatly contribute to this collapse, especially on pollinators which are sensitive at different levels to both habitat loss and thermal stresses. Bees and hoverflies are the two most efficient taxa among pollinators. Using a multi-taxon approach studying multiple anthropogenic stressors, we want to address how bee and hoverfly communities are impacted by the loss of habitat and urban heat island effects? We hypothesized a decrease of abundance and specific richness of wild bees and hoverflies caused by the habitat loss and thermal stresses in cities. Regarding honey bees, thanks to the presence of managed colonies within the city, we only expect a negative effect of the thermal stresses in the most urbanized sites. To answer this question, we followed plants – pollinators interactions on eighteen flower strips sown to control their floral composition and density spread across the entire urban area of Rennes (France). Sites have been chose for their location along two urbanisation gradients, one of impervious surfaces and one on urban heat island. The amount of habitats was estimated within a 250m buffer centered on the flower strip. Urban heat island has been estimated using the climatologic monitoring network RUN deployed in the city of Rennes. Here, we will present the first results of our study which is the first looking toward the pollinating fauna in this city. This work will provide strong bases for futures analyses on the effect habitat loss and thermal stresses on life history traits and how cities filter communities from regional pool to communities within flower strip.

A Summer in the City: *Platanus* lace bug, *Corythucha ciliata*, and Holm oak bark scale, *Nidularia pulvinata* - Two newly reported Hemipteran pests in Central London

Anna PLATONI (Forest Research (UK), Anna.platoni@forestresearch.gov.uk)

Sarah FACEY, Chris MALUMPHY

Abstract

Platanus lace bug, *Corythucha ciliata* (Say) (Hemiptera: Tingidae), was first described in the UK in 2006. Following treatment of this early establishment with pesticide however, no evidence of its continuing presence in the UK has been found in the years since. In the summer of 2024 however, an iNaturalist report was made by a member of the public travelling on a bus in central London, showing a *Corythucha ciliata* adult crawling over a rucksack. Inspectors headed to the site and confirmed the presence of *Corythucha ciliata* breeding in London. During the same field visit inspectors visited a nearby site to follow up a report, this time submitted via Forest Research's tree health reporting platform Tree Alert, of a mystery scale insect affecting Holm Oak trees. This scale insect was later confirmed to be *Nidularia pulvinata* (Planchon) (Hemiptera: Kermesidae), Holm oak bark scale, the first record of this pest in the UK. A summer of city-wide surveillance for these two pests followed revealing further populations of both insects.

This presentation will introduce these pests in their London context, describe the surveillance which took place in the city during the summer of 2024 and update on their current known distribution. The implications of their discovery on London's treescape and the complications and opportunities of surveying for and managing tree pests in an urban environment will also be discussed.

Spatiotemporal dynamics of breeding site composition: what impact on the Asian tiger mosquito biology and behaviour?

Axelle GENTIL (Axelle.gentil@univ-lyon1.fr)

Jonathan GERVAIX, Edwige MARTIN, Laurent VALLON, Aurelie FILDIER, Laure WIEST, Claire VALIENTE MORO, Emmanuelle VULLIET, Patricia LUIS, Amelie CANTAREL, Remy CAZABET

Abstract

The Asian tiger mosquito, *Aedes albopictus*, is considered one of the world's most invasive species and is responsible for the transmission of various viruses to humans, such as dengue and chikungunya viruses. Native to the tropical forests of Southeast Asia, its strong ecological plasticity has allowed it to thrive in contrasted environments, particularly urban areas, where numerous artificial breeding sites (e.g., storm drains, utility boxes) serve as larval habitats. In cities, these breeding sites are exposed to various pollutants resulting from human activities, including micropollutants that alter their physicochemical and microbial characteristics. However, the biotic and abiotic properties of these habitats, as well as their influence on the mosquito's life cycle and oviposition behaviour, remain poorly understood. In this context, we conducted a spatiotemporal analysis of microbial diversity and physicochemical properties across six larval habitats colonized by *Ae. albopictus* over a five-month period, with samples collected twice a month. In parallel, monthly laboratory experiments were performed using water collected from three sites to assess their attractiveness for oviposition and their effects on key mosquito life-history traits (i.e., development time, survival, sex ratio, and fecundity). Our results revealed a strong preference of female mosquitoes for artificial breeding sites over controls. On average, females laid 3.3 times more eggs in the water collected from urban breeding sites. Significant variations in life-history traits were also observed, both among different habitats and within the same habitat over time. Ongoing analyses aim to identify the microbial and physicochemical factors—individually or in interaction—that drive these variations, as well as to characterize the specific environmental determinants that promote the urban success of this mosquito species.

Pretty vacant: disputed value of bee hotels for urban conservation initiatives

Simon HODGE (University College Dublin, Simon.hodge@ucd.ie)

Abstract

Bee hotels are a popular tool for involving schools, businesses, and the wider public in urban pollinator conservation efforts. However, even when following published guidelines on design, materials, and placement, bee hotel occupancy is often disappointingly low, leaving participants discouraged and less likely to continue. To better understand the potential of bee hotels in urban settings, 130 bee hotels were installed at 20 sites in Dublin city and across south-east Ireland. These sites included orchards, parks, universities, and private gardens, with bee hotels ranging from commercially available products to homemade designs using bamboo canes, cardboard tubes, paper straws, and drilled wooden blocks.

Over 1000 individuals and 20 hymenopteran species emerged from the bee hotels, and included solitary bees, kleptoparasites, parasitoids, and cavity-nesting wasps. There was a strong negative relationship between bee hotel occupancy and proximity to Dublin city centre, with the hotels placed out within greater Dublin displaying minimal use regardless of the hotel design and local habitat. Home-made bee hotels comprising of drilled wooden blocks achieved reasonable levels of occupants, whereas hotels based on paper straws were not so well used, and some commercial products were not used at all. There were clear species differences in nest hole use, with small bees (e.g. *Hylaeus*) emerging from small 4-5mm diameter holes and larger bees (e.g. *Megachile*; *Anthidium*) emerging from 8-10mm nest holes.

Based on these findings, it is recommend selecting or constructing bee hotels with a variety of hole sizes to accommodate a variety of species, and that simple homemade designs can be equally as effective as more elaborate commercial models. To improve user expectations, it is important to communicate the possibility of low hotel occupation, particularly in urban areas, but also emphasise that any observations or records from bee hotels can be of high ecological, biogeographical, and educational value.

Pollinator community assembly in urban green spaces is shaped by trait filtering at broader spatial scales

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Ria DUNKLEY, Juan MORALES, Davide DOMINONI, Dominic MCCAFFERTY

Abstract

Urbanisation acts as an environmental filter during pollinator community assembly, shaping trait composition through impacts of anthropogenic conditions. Although trait-environmental relationships have been widely examined, many studies do not provide a holistic view of the community assembly process. Furthermore, environmental heterogeneity within the urban mosaic may shape pollinator communities amongst city green spaces, yet environmental drivers of community assembly at this scale remains poorly understood. Here we used a two-fold approach to investigate bee and hoverfly community assembly at the regional-city interface and among two types of urban green spaces in Glasgow, Scotland. Firstly, to determine environmental drivers of pollinator community assembly within urban green spaces we applied hierarchical modelling of species communities (HMSC) framework, which accounts for both biotic and abiotic processes. Secondly, we assessed whether community weighted means of pollinator traits within Glasgow differed from expectations based on a regional trait pool using null models. We found that pollinator communities in Glasgow were filtered by specific traits in comparison to a regional trait pool. In contrast, HMSC revealed little evidence of trait filtering among urban green spaces. Instead, environmental variables in urban green spaces influenced species occurrence in consistent directions across the community, although the strength of these relationships varied among species. Overall, we provide evidence that trait filtering of pollinator communities occurs at the city scale, while environmental conditions within urban green spaces primarily influence species presence. Although urban green spaces can support pollinator diversity, urban communities are more homogeneous in their traits, with implications for conservation strategies in urban green spaces.

#10635

INSECTS AS SOLUTIONS: Ecosystems services - Pollination

03/07/2026 at 08:30, Loches

Restoring pollinators: research, policy and practice

Jane STOUT (Trinity College Dublin, Stoutj@tcd.ie)

Abstract

Restoration of pollinators has long been recognised as a key part of the European biodiversity strategy and has recently been mandated by the EU Nature Restoration Regulation. This is because of the key role that pollinators play in supporting food production in agricultural systems, and widespread evidence for their decline. Whilst well-meaning “save the bee” campaigns have raised awareness among the general public and in policy, more understanding of the role of different pollinator species for crops and wild plants, and how to reverse drivers of decline to restore healthy pollinator communities, is needed. Research has shown that a wide range of pollinating insects contribute to pollination services, and that species respond to local and landscape restoration features in different ways. In Ireland, a country where agriculture dominates landscapes across the island, one third of bee species are at risk of extinction and even common species of bee and butterfly are showing declines. Agri-environmental schemes of recent years seem to have had little positive impact on restoration of pollinators. In this presentation, I will focus on recent and on-going work in Ireland, both in terms of research, but also in translating that research into implementable policy and best practice on the ground. Reflecting on 10 years of action via the All-Ireland Pollinator Plan, it is clear that restoration of pollinators takes a whole-of-society approach.

Soil – Plants – Pollinators networks of pesticides in agricultural landscapes

Benoît GESLIN (University of Rennes, Ecobio Laboratory, Benoit.geslin@univ-rennes.fr)

Aude ERNOULT, Cecile SULMON, Hugo FABRE, Abigaël HERVIEU, Frederique PALLOIS

Abstract

In agricultural landscapes, wild pollinators are increasingly threatened by pesticide exposure throughout all stages of their life cycle. Growing evidence shows that these toxic substances permeate entire ecosystems, reaching even habitats that supposedly remain pesticide-free. To effectively mitigate this exposure, it is essential to identify the multiple potential sources of contamination. In particular, understanding the relative contribution of field-level versus landscape-level pesticide exposure can help guide management recommendations and protect biodiversity. In this project, we investigated 20 landscape windows of 1 km² chosen to represent a double gradient of compositional and configurational heterogeneity. Within each landscape window, we selected three permanent grasslands (60 in total), which act as non-target habitats and are therefore not expected to receive direct pesticide applications. In these grasslands, we collected soil, flowers, and foraging bumblebees, and analysed their pesticide residues. In total, we measured the presence of more than 30 active ingredients, including herbicides, fungicides, and insecticides. Our objectives were to (a) characterize the pesticide transfer network linking soil, plants, and pollinators; (b) disentangle the respective contributions of local versus landscape-scale contamination sources; and (c) evaluate how landscape heterogeneity influences the accumulation of pesticide residues in soils and in bumblebees. The results of this study will provide important insights for evaluating pesticide-related risks to pollinators in agricultural environments and for understanding how landscape structure can modulate these risks. This will also help to design more effective, landscape-based mitigation strategies to support pollinator conservation.

Plant-Pollinator monitoring for rural ecosystem sustainability: two Italian experiences

Marta GALLONI (Department of Biological, Geological and Environmental Sciences - University of Bologna, Marta.galloni@unibo.it)

Fotunato Fulvio BITONTO, Marta BARBERIS, Laura BORTOLOTTI, Theodora PETANIDOU

Abstract

Pollinator decline is a serious issue that needs to be urgently addressed to safeguard biodiversity, preserve nature's resilience, and ensure food security. In line with EU environmental and agricultural policies, there is currently strong pressure, both from the competent authorities and ordinary citizens, to adopt strategies to protect wild pollinators. Scientific monitoring that supports planning for degraded ecosystem restoration is crucial for assessing the success of restoration efforts, as mandated by the EU Nature Restoration Regulation.

I present two case studies where similar field protocols were applied: the first is the Gello Revival Project (Tuscany), where a priori monitoring aimed at guiding the restoration process promoted by a private owner, while the second is the scientific assessment of the effectiveness of pollinator-friendly actions implemented within the LIFE 4 Pollinators project (LIFE18 GIE/IT/000755) in 9 farms in Emilia-Romagna Region.

In both cases we recorded plant-pollinator interactions, plant and pollinator diversity, and floral resource availability throughout the vegetative season, to obtain a comprehensive picture of the pollination networks in the study sites.

Overall, the pre- and post-intervention assessments in the Emilia-Romagna farms show an increase in the diversity and abundance of the main functional groups of pollinators, i.e. bees. Network analysis revealed higher linkage density and functional complementarity, indicating strengthened ecological interactions and greater network stability, while weighted connectance decreased. Some bee genera increased specialization, while several plant species became more generalized. Overall, post-intervention networks appeared more resistant and resilient, confirming the effectiveness of pollinator-friendly actions.

The monitoring conducted in Gello made it possible to propose a list of species to be planted for restoration purposes, detect species of conservation interest, and identify microsites of high biodiversity value to be preserved within the area. This experience represents a rare example of scientifically-driven restoration planning, to be later evaluated through ex-post monitoring.

Databases on distribution and traits of the European wild bee and hoverfly fauna

Sara REVERTE SAIZ (Laboratory of Zoology, University of Mons, Sara.revertesaiz@umons.ac.be)

Denis MICHEZ, Andrijana ANDRIĆ, Jordan BENREZKALLAH, Marija MILIČIĆ, Elif KARDAS, Ahlam SENTIL, Natasha DE MANINCOR

Abstract

Pollinators face multiple threats, but the spread of anthropogenic chemicals (i.e. pesticides) forms a major potential driver of these threats. The WildPosh project is a multi-actor, transdisciplinary project whose overarching mission and ambition are to significantly improve the evaluation of risk to pesticide exposure of wild pollinators and enhance the sustainable health of pollinators and pollination services in Europe.

In order to define exposure and toxicity scenarios, WildPosh is developing databases on ecological traits and the spatial distribution of pollinators which will be used in the integrated systems-based risk assessment tools created during the project. Specifically, WildPosh aims to: (i) compile a comprehensive trait database which will include traits reflecting sensitivity and exposure risk of European pollinators to pesticides and other stressors; (ii) compile distributional and occurrence information on European pollinators at national and continental levels.

The traits and distributional databases synthesize the information available for the European hoverfly and bee fauna (913 and 2,138 species, respectively). In the traits database, thirty-eight traits are included (classified into 5 sections, i.e., nesting, larva, adult morphology, ecology/behaviour, and distribution), of which 17 traits are mutual for hoverflies and bees, 7 traits are available only for hoverflies, and 14 only for bees. The distribution database comprises more than 4,34 million and 1,04 million records for wild bees and hoverflies, respectively.

Both databases build upon data and insights gathered from previous and ongoing projects, including data from the STEP, SAFEGUARD, ORBIT and TAXO-FLY projects, and the IUCN Red Lists for hoverflies and bees. Also, both databases are converted to data papers that have been submitted for publication. The databases on the manuscripts correspond to the version in the date of submission, but they continue to be worked on parallelly.

Wetland pollination networks: new insights into the role of riparian plants and aquatic insects in agricultural landscapes

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Abstract

Pollination research has traditionally focused on a limited number of insect taxa, potentially underestimating the role of other groups. Winged aquatic insects (such as Ephemeroptera or Plecoptera...) are abundant, diverse, and widespread, suggesting that they may contribute to pollen transfer between plants in riparian areas and adjacent grasslands or cultivated fields. To explore this, we conducted field surveys in French agricultural landscapes incorporating riparian areas and built plants-insects interaction networks.

Our objectives were to (i) evaluate the potential of aquatic insects to pollinate wild and cultivated plants, and (ii) assess the potential contribution of riparian areas as floral and relay resources for crop pollinators.

Although relatively scarce in surveys, we recorded aquatic insects visiting flowers, including rapeseed visitation suggesting potential avenues for further studies. Interaction networks revealed high pollinator richness in riparian areas, which provide significant resources, positively influencing pollinator presence and offering relay resources beyond crop flowering. These results highlight the overlooked potential of aquatic insects in pollination processes and underscore the importance of preserving diverse aquatic and riparian vegetation within agricultural landscapes.

Landscape, management and seasonality drive flora functional structure, and flower-visiting insect diversity in Mediterranean vineyards

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Abstract

Weed flowers constitute important resources for many insects. In that regard, vineyards represent an interesting agroecosystem, due to the wide spacing between rows, which allows the development of spontaneous vegetation. Their floral potential depends on inter-row vegetation and its management, field margins, which are often more diverse and complementary to the field core, and the surrounding landscape. However, existing studies have mainly focused on weed vegetative traits and on wild bees, while floral traits and other groups of flower-visiting insects (beetles, flies) remain largely understudied.

In this context, this study aimed to (i) compare weed and flower-visiting insect communities between field cores and field margins, and (ii) assess their responses over time to landscape context and management practices in vineyards. We surveyed 30 vineyard plots in the Montpellier area, distributed along two orthogonal gradients across three periods in one year: vineyard management intensity and landscape heterogeneity. Plant communities were characterised through vegetation surveys. Flower-visiting insects were sampled with pan traps and identified using quantitative metabarcoding.

Both the quantity and diversity of floral resources were negatively affected by management intensity, with herbicide use being particularly detrimental, whereas mowing practices and the presence of semi-natural habitats had positive effects. Flower-visiting insects responded primarily to landscape configuration. The negative effect of intensive practices on wild bee diversity was amplified in heterogeneous landscapes, whereas low-intensity practices more strongly promoted wild bee diversity in more diverse landscapes. Landscape context alone is insufficient to maintain biodiversity when viticultural practices are intensive, highlighting the need to consider both local management and landscape-scale strategies.

The resource competition between honeybees (*Apis mellifera*) and wild bees (Hymenoptera: Apoidea) in anthropogenic landscapes

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Alžběta VOLDŘICHOVÁ, Jaco VISSER

Abstract

Pollination by wild bees provide essential ecosystem services and support plant reproduction in agricultural and urban landscapes. However, populations of wild bees are declining due to multiple stressors, including competition with managed honeybees.

Our study investigates the impact of honeybee abundance on wild bee community structure and examines competitive mechanisms through plant-pollinator network analysis.

Honeybee abundance did not correlate with registered hive density, suggesting that landscape factors, habitat fragmentation, and floral hotspots shape local foraging patterns. Contrary to predictions of competitive displacement, wild bee species richness increased with honeybee abundance at sampling locations, likely reflecting effectiveness of honeybees in locating high-quality floral resources. However, higher registered hive densities were marginally associated with reduced wild bee species richness, indicating the negative impact of high honeybee densities on a landscape scale.

Network analysis revealed honeybees as hyper-generalists with the highest potential for apparent competition, imposing disproportionate competitive pressure on the wide pollinator community while experiencing minimal competition themselves. Notably, generalist wild bee species experienced greater competitive pressure than specialists, as they share more floral resources with the hyper-generalist honeybee.

Habitat context strongly modulated the intensity of competition: landscapes with greater suitable habitat cover, small woody features, and urban or agricultural land showed reduced honeybee mediated competition, whereas homogeneous grassland dominated areas amplified it. Higher floral diversity alone did not significantly mitigate competitive effects.

These findings suggest that while honeybees and wild bees can coexist at resource-rich patches, high stocking densities of managed hives pose landscape-scale competitive challenges that filter sensitive species. Conservation strategies should prioritize maintaining and expanding structurally complex habitat to buffer wild bee communities from competition with honeybees.

Botanical Nano-Insecticides in Pest Management: Formulation, Bioactivity, and Constraints

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Abstract

In the last decade, the use of botanicals as insecticides has attracted increasing interest from different stakeholders. However, some drawbacks (i.e., phytotoxicity, rapid degradation, flammability, and others) currently limit their practical application under real conditions. In this context, nanotechnologies offer a promising strategy to overcome these limitations by developing botanical nanocarriers (i.e., nanoparticles and nano-emulsions) able to shift laboratory results into real-world conditions while improving physical, chemical, and biological properties.

Here, a series of studies on the formulation of highly stable and effective botanical-based nano-insecticides, evaluating the impact against different crop pests, as well as their selectivity towards non-target organisms (i.e., pollinators, natural antagonists, and plants) are reviewed.

These nano-delivery systems were developed using both bottom-up and top-down approaches in order to identify the best method to obtain stable nano-formulations. Dynamic Light Scattering analyses allowed the characterization of key physical properties (i.e., particle size, polydispersity index, and surface charge), revealing excellent values and long-term stability.

The biological activity against crop pests was assessed through different exposure routes (residual contact, topical application, and ingestion) to simulate real-world scenarios. Results showed strong insecticidal effects, with LD₉₀ values consistently below 2.5% EO as active ingredient. Gene-expression analyses further indicated a multisite mode of action, with several detoxification-related genes significantly upregulated compared to controls, suggesting complex physiological interactions between pests and nano-formulated botanicals.

Selectivity toward non-target organisms was also investigated using multiple exposure routes. While mortality towards non-target insects depended on the exposure route, negative effects on plants were negligible, and analyses of plant defense responses revealed a clear enhancement.

Overall, these results demonstrate the high potential of botanical nanocarriers as sustainable, effective tools for modern pest management.

Oregano essential oil nanoemulsion for the control of the cotton leafworm *Spodoptera littoralis*

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Weidson SUTIL, Antonino MODAFFERI, Antonio GUGLIUZZO, Michele RICUPERO, Orlando CAMPOLO, Lucia ZAPPALÀ, Antonio BIONDI, Eya HMAD

Abstract

Spodoptera littoralis (Lepidoptera: Noctuidae) is a major agricultural pest widely distributed across Africa, Mediterranean Europe, and the Middle East, causing severe damage to numerous crops. Its control largely relies on synthetic insecticides which raise serious concerns due to resistance development, side effects on non-target organisms, and ecosystem disruption. Plant essential oils (EOs) are a promising tool for the sustainable control of agricultural pests, however, their field application is often limited by high volatility, low stability, and rapid degradation. Encapsulation of EOs within nanostructured delivery systems can effectively overcome these drawbacks. In this study, we developed and evaluated the efficacy of oregano EO-based nanoemulsion with a high EO concentration (15%) and low surfactant content for the control of *S. littoralis*, targeting both egg and larval stages. In addition, larval feeding activity and detoxification-related enzymatic responses, including esterase and cytochrome P450 activities, were assessed at two lethal concentrations (LC₅ and LC₃₀). Laboratory bioassays revealed significant ovicidal and larvicidal activity of oregano-EO nanoemulsion. Egg mortality was extremely high, with complete inhibition of hatching at EO concentrations of 3, 4.5, and 6%. Larval susceptibility was confirmed, with LC₅₀ and LC₉₀ values ranging from 4.10% to 8.20%. Moreover, leaves treated with the oregano EO nanoemulsion showed a significant reduction in leaf area consumed by larvae. Transcriptional analyses suggest that EO-based formulations interfere with insect physiological processes by modulating detoxification pathways involved in stress response. Overall, these findings highlight the potential of nano-formulated oregano EO as an effective and environmentally sustainable botanical insecticide for the control of *S. littoralis*, supporting its integration into integrated pest management strategies, which should now be tested under field conditions as well as on non-target organisms and its potential phytotoxicity on different crops to move forward in the development process of a new biopesticide

Encapsulation of mustard essential oil in chitosan: technical aspects and aphicidal activity

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Abstract

Essential oil (EO)-based pesticides are an eco-friendly tool for managing arthropod infestations in agriculture. However, although they often perform well under laboratory conditions, certain properties of EOs can reduce their effectiveness in field conditions. To overcome their high susceptibility to environmental degradation, these biopesticides can be protected through encapsulation in nanoparticles. Cruciferae are particularly valued for their oil composition profiles. Mustard seed EO has a high content of allyl isothiocyanate, a hydrolysis product of sinigrin catalysed by myrosinase, which is known for its notable insecticidal properties.

The aphicidal activity of two nanoformulations containing mustard EO encapsulated in a chitosan shell were evaluated. Chitosan-EO nanoformulations were obtained through two different physical processes: sonication (UP200ST ultrasonic immersion homogenizer) and high-pressure microfluidization (HPM) using an LM20 Microfluidizer™ Processor. Both nanoformulations exhibited a good polydispersity index and a nanoparticle size within the nanometric range, with a particularly reduced particle size in the HPM-treated formulation. The aphicidal activity of the developed formulations was evaluated using two different methods (*i.e.*, residual contact toxicity and topical application), with the cotton aphid *Aphis gossypii* Glover and zucchini plants as model species. Aphicidal activity was compared with that of lambda-cyhalothrin. Short- and long-term effects on fecundity were also recorded at sublethal doses.

Topical application produced aphid mortality comparable to the positive control for both tested formulations. In particular, the microfluidized formulation showed higher aphicidal activity than the sonicated formulation. Regarding residual toxicity, considerable mortality was observed only for the microfluidized formulation. A reduction in fecundity was also observed: high doses induced immediate decrease, while sublethal doses could impact long-term fecundity. No phytotoxic effects were observed on zucchini plants. Chitosan-EO nanoformulations are promising candidate for pest control in field conditions, although formulation techniques should be carefully evaluated.

DsRNA-based biopesticides for sustainable control of the Cabbage Stem Flea Beetle (*Psylliodes chrysocephala*)

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Abstract

Oilseed rape (*Brassica napus*; OSR) is an important break crop and source of vegetable oil, yet cropping area has declined by 11% in Europe over the past decade, in part, due to rising pest pressure from the Cabbage Stem Flea Beetle (*Psylliodes chrysocephala*; CSFB). The 2013 EU ban on neonicotinoid insecticides, coupled with rising pest resistance to pyrethroid alternatives, has made OSR a risky crop choice for farmers. With CSFB pressure predicted to further increase under climate change, there is an urgent need for sustainable alternatives to conventional chemical controls. DsRNA-based biopesticides offer a possible solution, eliciting species-specific pest mortality and protecting farmland biodiversity and pollinators. This technology utilises the endogenous RNA interference pathway for targeted mRNA degradation of essential transcripts, resulting in insect mortality. This project assesses the potential of dsRNA-based biopesticides for CSFB control by testing a range of gene targets. We then outline a whole plant, controlled testing system which allows for the comparison of formulation efficiency and stability in a live plant, treatment spray scenario. Through this it is possible to identify optimal dsRNA concentration and treatment regimes which maximise CSFB mortality. This research contributes to a rising body of knowledge on the potential benefits of sustainable biopesticide use and highlights their potential for effective CSFB control, aiding in reversing the decline in OSR production. Further, we outline a protocol for whole plant, controlled formulation testing, with potential applications to a range of biopesticides used against herbivorous insect pests.

Nanocarrier-Mediated Delivery of dsRNA for RNAi-Based Control of *Brassicogethes aeneus*

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Abstract

RNA interference (RNAi) is widely recognized as a promising tool for species-specific pest control, yet its practical application faces challenges related to dsRNA instability and limited uptake in target organisms. Nanocarrier systems have been developed to improve dsRNA protection and delivery, but their effectiveness varies depending on physicochemical properties and biological context. In this study, we explored different carrier types, including clay-based layered double hydroxides, peptide-based systems, and synthetic cationic polymers, for oral delivery of dsRNA targeting essential genes in the pollen beetle *Brassicogethes aeneus*.

All carriers successfully formed stable complexes and provided protection against enzymatic degradation, but stability alone did not guarantee improved RNAi outcomes. Some carriers resulted in later-onset gene silencing and mortality compared with naked dsRNA, indicating slower release or delayed intracellular processing. Other carriers showed clear transcript suppression but showed little or no effect on survival, suggesting that downregulation alone was insufficient to reduce survival. Furthermore, responses varied between target genes, with one gene showing measurable downregulation and another exhibiting inconsistent patterns, including occasional upregulation. These findings suggest that the relationship between dsRNA stability, release dynamics, and biological efficacy is complex and influenced by multiple factors, such as particle size, gut physiology, and intracellular processing.

Overall, the results highlight that achieving effective RNAi-based pest control requires more than ensuring dsRNA protection. Successful strategies must integrate carrier design with species-specific delivery mechanisms to balance stability, timely release, and efficient cellular uptake. This work emphasizes the need for a deeper understanding of nanocarrier–dsRNA interactions within relevant biological systems to develop practical and reliable RNAi technologies for agricultural pest management.

RNAi-based bait formulation reduces target gene expression and medfly pupal emergence

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Abstract

BACKGROUND: RNA interference (RNAi) has emerged as a promising tool for species-specific pest control, yet its practical implementation in field-oriented delivery systems and its ecological safety remain major barriers for adoption. Here, we present a novel bait-based dsRNA delivery strategy targeting *Ceratitis capitata* and applied as proteinaceous droplets under semi-field conditions. We evaluated the silencing efficiency of two genes (V-ATPase and RPS13) and quantified their impact on fruit infestation, larval development, and adult emergence from sentinel fruit. Additionally, we performed the first biosafety assessment of dsRNA baits on two key non-target species, the parasitoid *Diachasmimorpha longicaudata* and the frugivorous fly *Drosophila suzukii*.

RESULTS: Our results demonstrate robust gene knockdown for both dsRNAs in adult medflies, but only V-ATPase dsRNA translated into a significant reduction in pupal emergence and fruit damage under semi-field exposure. Non-target assays revealed no detrimental effects on survival, fecundity, or gene expression in either *D. longicaudata* or *D. suzukii*. Surprisingly, dsRNA exposure increased parasitism rates in *D. longicaudata*, suggesting unforeseen physiological interactions with potential implications for integrated pest management.

CONCLUSION: Overall, this study provides the first evidence that dsRNA bait-droplet applications can effectively suppress medfly reproductive success in realistic conditions while maintaining high ecological safety for beneficial and non-target insects. These findings advance RNAi-based technologies toward field-ready, environmentally compatible fruit fly control strategies.

Efficacy of Zinc Oxide Nanoparticles and Entomopathogens against the Khapra Beetle (*Trogoderma granarium*)

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Abstract

In both industrialized and developing nations, pest infestation of stored grains and their byproducts is a serious issue. Numerous pests that damage the nutritional composition of the goods being stored have a significant impact on Pakistan's agricultural economy in addition to lowering their worth for human consumption. *Trogoderma granarium*, also known as the Khapra beetle, is one of the most damaging, devastating and destructive pests of stored grain, namely wheat, rice, maize, and others. It damages cereals that have been stored, lowering their nutritious value and having an impact on the national economy. Green manufactured ZnO nanoparticles and two additional protectants were used in the study to lessen the catastrophic losses of grain products caused by this dangerous pest, which is often referred to as a quarantine pest since it moves from one nation to another. Data on mortality was documented at 3, 6, 9, 12, and 15 days. According to the findings, the maximum mortality rate of 83.33% was noted at the highest concentration of ZnO NPs (600 ppm). It has been determined that using ZnO nanoparticles is a good alternative to chemical pesticides for control and an effective IPM strategy.

Example of a science-based implemented pest control programme

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Abstract

Un Hyménoptère africain a été caractérisé comme parasitoïde spécifique de la sésamie du maïs. Pour comprendre la spécificité parasitaire, des lignées plus ou moins virulentes du parasitoïde et des souches plus ou moins résistantes de sésamies ont fait l'objet d'analyses génomiques et protéomique associées à des suivis de comportement et développement. Le risque pour l'environnement est celui pour des espèces non-cibles, définies selon l'écologie de *C. typhae* dans son aire d'origine. Les chenilles non cibles ont été collectées dans l'environnement français pour étudier au laboratoire leur risque d'être parasitées et d'en mourir. Ce risque s'est révélé faible. Il dépend aussi de la probabilité du parasitoïde à s'établir en France, qui devrait être très faible d'après la forte vulnérabilité de *C. typhae* à des températures hivernales. L'efficacité du parasitoïde a été évaluée au laboratoire par des études de fécondité puis sous serre selon différents protocoles. Deux aspects de faisabilité économique ont été établis : une étude de marché, et le coût de la production de parasitoïdes à l'hectare, évalué en massifiant un élevage de laboratoire.

Un fait marquant diffusé aux producteurs de maïs et aux acteurs de la protection des plantes est la réussite des essais sous serre, où le parasitoïde a entraîné jusqu'à 98% de réduction de la population de sésamie. Associé au faible risque environnemental et à la faisabilité économique, ce fait a justifié un nouveau projet en partenariat public-privé, Biocosma, visant à tester l'efficacité de lâchers du parasitoïde au champ.

Ce projet financé par le programme Ecophyto-maturation a pour objectif de passer de la preuve de concept (technologie validée en laboratoire) à la démonstration dans un environnement opérationnel voir à l'atteinte d'un système complet et qualifié. Il permettra une réduction de l'utilisation de pesticides si la solution peut être appliquée par les agricultures.

For a better understanding of Conservation Biological Control methods : assessment of the rate of use, feasibility and cost-effectiveness

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Abstract

Over the past half-century, the need to feed a growing global population has led to the expansion and intensification of agricultural production, transforming many regions into simplified landscapes through the introduction of high-yield crop varieties, intensive mechanisation and the use of various agrochemicals, particularly pesticides. Whilst this transformation has contributed to increased agricultural production in the short term, it has also led to widespread environmental degradation. The loss of biodiversity can disrupt key intermediate services for agriculture, such as crop pollination and biological pest control, which underpin the crop production service. The recent stagnation or even decline in agricultural yields despite general intensification indicates that alternative pathways are needed to maintain stable and sustainable future agricultural production. There is an urgent need to better understand the ecosystem services provided by biodiversity in agroecosystems and their cascading effects on crop production, in order to predict changes in the effectiveness of ecosystem services and to implement sustainable management strategies. POLLINIS, a non-profit organization, is running a project aimed at addressing these issues. At the intersection of environmental, social and economic issues, this project aims to determine: (i) What conservation biological control methods do farmers use as an alternative to pesticides? (ii) What are the environmental, economic and social impacts of these solutions? (iii) How do these solutions affect the diversity, abundance and proportions of the various species of interest? (iv) How do these, in turn, affect the quality and/or quantity of crop production? (v) How are ecosystem services affected?

Extending pesticide risk assessment beyond *Apis mellifera*: a trait-based vulnerability framework for wild pollinators

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Abstract

Pollinators are experiencing a widespread global decline, largely driven by anthropogenic pressures, with pesticide exposure playing a major role through chronic and diffuse environmental contamination. Pesticide risk to pollinators emerges from the interaction between environmental exposure and species-specific characteristics. However, current Environmental Risk Assessment (ERA) primarily relies on the honey bee (*Apis mellifera* L.) as a model species, despite substantial interspecific differences in life history, ecology, and exposure pathways that limit its representativeness for wild pollinators diversity. Given the key role of non-*Apis* pollinators in ecosystem functioning and food production stability, there is an urgent need to expand risk assessment frameworks to better account for their vulnerability.

Here, we develop a trait-based framework to assess pesticide vulnerability across multiple European pollinator species from three taxonomic groups: bees, syrphids, and butterflies. Specifically, we aim to (i) evaluate pesticide vulnerability beyond *A. mellifera* using functional traits, and (ii) produce synthetic vulnerability indicators to support ERA by identifying vulnerable species, taxonomic groups, and exposure matrices.

Functional traits were selected to represent three complementary vulnerability dimensions: external exposure, intrinsic sensitivity, and population resilience. Exposure was characterized across five environmental matrices (nectar, pollen, water, soil, and plant material) by defining functional groups based on ecological and life-history traits reflecting the intensity of pollinator–matrix interactions. Expert judgment was used to assign exposure scores to functional groups and to weight the relative importance of traits within each vulnerability dimensions. Weighted trait values were then integrated into composite vulnerability indicators.

This framework enables the ranking of species, the identification of cross-taxon vulnerability patterns, and the characterization of key exposure pathways across environmental matrices. By linking functional traits to matrix-specific exposure and vulnerability, it supports the prioritization of species and trait combinations for future ecotoxicological testing and provides a flexible tool to inform higher-tier ERA schemes.

Towards knowledge uptake and long-term impact: Science communication strategies of EU-funded research projects on entomology

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Nikolay MEHANDZHIYSKI, Peter BOZAKOV, Teodor METODIEV

Abstract

Insects influence food security, biodiversity, ecosystem health and human well-being. Yet the complexity of entomological research makes it difficult for non-experts to understand and implement the generated knowledge and practices. Effectively translating entomological science for policymakers and practitioners is essential for ensuring that research delivers real societal impact.

This presentation explores how EU-funded entomology research projects have addressed the challenge of making insect science accessible, relevant and useful to diverse audiences through various tools, channels and strategic approaches. Drawing on practical examples, communication strategies and lessons learned from Horizon 2020 and Horizon Europe projects, such as Safeguard, PollinERA, AGRI4POL, VALOR and EUFAWREADY, it highlights what works, what doesn't, and why. Good examples from these projects will demonstrate how co-creation and open-science practices, stakeholder mapping and knowledge-exchange workshops can strengthen both the visibility and usability of scientific outputs. The talk will also focus on the importance of clear messaging, tailored outreach, visual storytelling and early integration of communication and dissemination into project planning, which can transform complex entomological findings into actionable knowledge that supports policymaking, conservation and sustainable land-use practices.

Translating insect science goes beyond mere promotion of results – it is an essential bridge between research and society. It enables informed decisions at local, national, EU and global levels, encourages public engagement and biodiversity-friendly behaviours, and enhances the long-term value, uptake and credibility of entomological research across Europe and beyond. By improving how science is communicated, we also strengthen its understanding, trust and application, benefiting both people and the ecosystems on which humanity depends.

EU LIFE Programme funding direct conservation action to protect Europe's threatened insects

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Gustavo BECERRA-JURADO

Abstract

The European Union protects more than 27,000 natural areas that are of special European importance, covering 18% of the EU's total land area. Known as Natura 2000, this is the largest protected area network in the world, safeguarding Europe's most valuable and threatened species and habitats, as listed in the EU Birds and Habitats Directives. Since 1992 the EU has provided co-funding, through the LIFE Programme, to support direct conservation action aimed at the protection and restoration of Europe's threatened habitats and species; and halting and reversing biodiversity loss.

The global decline of insect diversity and abundance is one of the most urgent ecological challenges and is well documented in the scientific literature (Sánchez-Bayo and Wyckhuys, 2019); with evidence of similar declining trends reported in Europe (Seibold et al. 2019; Powney et al., 2019; and Hallmann et al., 2017). If insect declines are not halted, this will have profound impacts on terrestrial and freshwater ecosystems and human wellbeing. The LIFE Programme has played a part in addressing these declines and has supported over 250 projects across Europe which directly or indirectly benefit threatened invertebrate species listed in the EU Habitats Directive and EU IUCN Red Lists as well as pollinators in general. In some cases, these EU LIFE funded projects have implemented species protection, recovery or re-introduction measures for highly threatened species and/or habitat management and restoration measures. However, of the insect species listed in the EU Habitats Directive, less than half have been targeted for conservation action by LIFE projects to date. The LIFE Programme is seeking to address the general under-representation of target action for insects in LIFE projects as well as the tendency to focus on the same insect species (Neemo, 2020) through communication of its contributions to the conservation of endangered insects and wild pollinators.

Life4OakForests Life16NAT/IT/000245: Conservation management tools for increasing structural and compositional biodiversity in Natura2000 oak forests

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Abstract

Life4OakForests LIFE16NAT/IT/000245: Conservation management tools for increasing structural and compositional biodiversity in Natura2000 oak forests

Serena Petroncini

Ente di gestione per i Parchi e la Biodiversità-Romagna

The oak forests biodiversity is declining because of intensive commercial use. The goal of nature conservation interventions is to promote the regeneration and restoration of the diversity of forest structure, native tree species composition and microhabitats. Mammals, birds, insects, plants, and fungi will increase and preserved.

Objectives: increase the biodiversity of EU priority oak forests (*91AA, *91G0, *91H0, *91I0) & 91M0 in the National Parks' managed protected Natura 2000 sites (Italy-Hungary).

Actions:

(A1) Collection and examination of scientific documents and remaining natural forests. Elaboration of guidelines for ecological forest management based on the image of the natural forest.

(B1) Oak forests purchased for securing the biodiversity of the area.

(C1) Implementation of nature conservation forest management by creating different types of deadwood habitat, reconstructing the diverse, more habitat-rich forests structure, reducing game impact and suppressing invasive species according to the elaborated guidelines. Breeding of *Lucanus cervus* and monitoring of *Cerambyx cerdo* and *Osmoderma eremita*.

(A2, D1) The effect of forest management and interventions are monitored according to the monitoring protocol. The monitoring of the impact of project actions is divided into two main sub-actions: D1.1 – Baseline forest and zoological survey: this concerns the initial assessment of the conditions in the project areas D1.2 – Control monitoring: this is aimed at evaluating over time the effects of the treatments and management actions implemented. Soil invertebrates such as ground beetles (Coleoptera Carabidae) and spiders (Arachnida Araneae) were investigated,

(D2 & D3) Evaluation of the restoration of ecosystem functions and social economic impact.

(E2) Intensive awareness-raising activities for stakeholders and general public.

Project period: 01/07/2017 – 31/12/2026

The project is co-financed by the European Union's LIFE programme.

Conservation-oriented management affects beetle community in forests: results from a multi-year experiment in forest stands in Italy and Germany

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Abstract

The conservation of saproxylic insect species in forest ecosystems is of primary importance due to the key ecological roles they play. Enhancing structural diversity through the diversification of tree microhabitats and deadwood types has been shown to positively influence saproxylic insect diversity. However, implementing effective diversity-enhancing practices in productive forests remains challenging. In this context, the LIFE SPAN project aimed to establish a network of Saproxylic Habitat Sites (SHS) in managed forests in Italy and Germany to demonstrate the effects of different forest management interventions on beetle diversity.

The SHS were designed to enhance habitat heterogeneity and connectivity for saproxylic organisms and included the creation of artificial tree microhabitats (HAB), the implementation of deadwood enrichment strategies through thinning operations (THIN), and the creation of forest gaps (GAP). A total of 25 and 18 SHS were established in Italy and Germany, respectively. Beetle communities were monitored using flight interception traps over three consecutive years in Italy and four consecutive years in Germany, both in SHS and in unmanaged control sites. The effects of SHS on beetle abundance and species richness over time were analysed using linear mixed-effects models.

Preliminary results showed that beetle communities responded differently depending on the type of intervention. In particular, the GAP treatment led to a significant increase in beetle abundance and diversity over time in both Italian and German forests. This result is noteworthy when considering that, in recent decades, the advance of forests on uncultivated land has led to the gradual closure of open areas. In contrast, HAB and THIN interventions did not produce significant effects on beetle abundance or diversity compared to unmanaged sites.

These findings highlight the effectiveness of targeted forest management actions, particularly gap creation, in promoting beetle diversity and enhancing functional connectivity in productive forest landscapes.

LIFE Wild Bees: A Regional Commitment to Pollinator Conservation

Anne-Charlotte MONTEIRO (Parc Naturel Régional Périgord-Limousin, Ac.monteiro@pnrpl.com)

Abstract

The collapse of insect populations is now recognized as one of the most alarming manifestations of the global biodiversity crisis. A growing body of converging scientific studies supports this assessment, including the study by the Krefeld Entomological Society (2017), which reports a 76% decline in flying insect biomass between 1989 and 2016 in protected areas in Germany.

Pollinating insects play a fundamental role in the functioning of terrestrial ecosystems. They are essential for the reproduction of many wild plant species and agricultural crops. It is estimated that 35% of global food production depends directly on animal pollination. In France, the economic value associated with insect pollination services is estimated between €2.3 and €5.3 billion.

In response, the Nouvelle-Aquitaine Region committed in 2017 to a regional pollinator action plan, strengthened in 2021. Within this framework, the five Regional Natural Parks developed the LIFE Wild Bees project, launched in September 2021 and co-funded by the European LIFE programme (60% of a €6.49 million budget), with implementation until 2027.

The project aims to halt the decline of wild bee populations and restore their habitats through four operational pillars: improving knowledge through standardized inventories across 50 reference and 15 restoration sites; restoring a dense network of suitable habitats, including high-value sites and ecological corridors; supporting the “Végétal local” native plant supply chain; and promoting knowledge transfer and dissemination through communication, training, and stakeholder engagement.

BUZZ LIFE: making cities pollinator-friendly in the Mediterranean area

Marta GALLONI (Department of Biological, Geological and Environmental Sciences - University of Bologna, Marta.galloni@unibo.it)

Marta BARBERIS, Laura BORTOLOTTI, Tania DEODATI

Abstract

The rapid decline of wild pollinators, particularly bees, represents a major threat to biodiversity and ecosystem functioning, with factors such as urbanization, pesticide use, climate change, and invasive species acting as key drivers. Mediterranean cities, despite being highly anthropized, can play a crucial role in pollinator conservation by offering refugia, foraging resources, and ecological connectivity. The BUZZ LIFE project 'Integrated actions to safeguard pollinators in urban and peri-urban areas' (LIFE24-NAT-IT-BUZZ LIFE) addresses this challenge through an integrated, transnational approach targeting urban areas in Italy, France, Greece and Cyprus. In particular, the project aims to improve knowledge on the distribution and ecology of wild pollinators, enhance habitat quality and connectivity, strengthen existing policies and raise awareness in civil society to reverse pollinator decline in Mediterranean urban landscapes. The project combines standardized scientific monitoring and citizen science with innovative tools, including IoT-based devices and remote sensing, to collate indispensable flower-insect interaction datasets. Conservation actions include the restoration of degraded habitats, the creation of species-rich meadows, pollinator gardens, refuge oases and linear green infrastructures – these latter designed to increase functional connectivity across fragmented urban matrices. In parallel, BUZZ LIFE promotes pollinator-friendly urban green management through local action plans, with strong emphasis placed on stakeholder engagement, awareness-raising and the establishment of a network of pollinator-friendly cities, fostering replication at national and European levels. By integrating ecological, technological, and governance approaches, BUZZ LIFE seeks to demonstrate how cities can become key actors in pollinator conservation. The project is expected to increase pollinator diversity and abundance in target areas, improve urban ecosystem resilience, and contribute to the achievement of priorities highlighted in the New Deal for Pollinators and the Nature Restoration Law.

Reintroduction of *Parnassius apollo* in Poland and Czech Republic based on researches and project experience (LIFE APOLLO2020)

Aneta SIKORA (Karkonoski National Park, Aneta.sikora@kpnmab.pl)

Tomáš Ernest VONDŘEJC

Abstract

Parnassius apollo is a symbol of insects decline in Europe. Once highly prized by insect collectors, the species has experienced continuous reduction in both the number and size of its populations for the last two centuries. This species is considered extinct in the Czech Republic, although one reintroduced population has been successfully established in the Štramberg quarry. In Poland, a single population in the Pieniny Mountains has been successfully stabilized but historical reintroductions to the Sudetes were unsuccessful.

The general objective of the LIFE Apollo2020 project is to recreate *Parnassius apollo* populations in functional areas including each region's specificity in the Sudetes (Poland) White Carpathians (Czech R.) and Alps (Austria).

In Poland 16 reintroduction sites were selected as a sub-sites and stepping stones and 2 breeding farms were created. In Sudeten region (2019-2025) 28851 specimens of imago and caterpillars were released. The monitoring scheme includes faunistic observation as well as food plant monitoring. Butterfly monitoring shows the possibility of *Parnassius apollo* survival on sub-site and his dispersion range. Our studies also include analyses of host plant reactions to feeding by *P. apollo* caterpillars, showing that these reactions may affect larval development and survival.

The Czech Republic has advanced restoration for *Parnassius apollo*. Priority sites reflecting historic rocky grasslands were selected, followed by habitat management such as removing woody vegetation, restoring stony slopes, and introducing controlled grazing. *Sedum* host plants were cultivated both on-site and ex-situ, ensuring larval food resources. Captive-breeding began with a Slovak pair, producing offspring for future reintroduction. These combined measures have created restored habitats, established host-plant patches, and an emerging breeding stock, forming a strong foundation for the forthcoming reintroduction of Apollo's return.

The project places strong emphasis on education and creating social awareness, fostering social engagement through: Apollo gardens, workshops, citizen-science initiatives, and volunteer programs.

#11195

SYMPOSIUM EU funding programmes: LIFE projects

30/06/2026 at 18:00, Loches

Towards Understanding Ecological Corridors for *Osmoderma barnabita*: Ongoing Mark-Recapture Studies in Urban and Natural Landscapes.

Maksims BALALAIKINS (Daugavpils University, LIFE Osmo Baltic. Baltic Wide Web for *Osmoderma Eremita*: the Creation of an Ecological Network in the Baltic Region, Maksims.balalaikins@biology.lv)

Laura SANDERE, Kristīna AKSJUTA, Uldis VALAINIS, Ieva ĀBELTIŅA

Abstract

The Hermit beetle (*Osmoderma barnabita*) is a priority protected species within the EU and a key indicator of veteran hollow trees. Given increasing habitat fragmentation, its survival depends on dispersal between patches, yet empirical data comparing natural versus anthropogenic environments remain limited.

This study assesses *O. barnabita* populations in natural/semi-natural habitats and urban settings using capture-mark-recapture (CMR), applying differentiated methodological approaches for natural and urban biotopes. Data collection encompassed the evaluation of landscape elements, environmental conditions, sex structure, adult lifespan, and seasonal flight activity periods (start and cessation).

Monitoring (2024–2025) covered Natura 2000 core areas (e.g., Ziemeļgauja, Lubāna) and six urban parks. Natural areas revealed high densities, with 458 individuals marked in Ziemeļgauja. Urban populations appeared stable albeit fragmented. The highest captures occurred in Preiļi Manor Park (114 individuals) with a recorded dominance of females.

Current data indicate that both recapture rates and dispersal distances are higher in natural biotopes compared to urban ones. Notably, the study detected natural movements of approximately 3 km in natural territories. Rapid long-distance flight was evidenced by a recapture 1.5 km away just two hours after release. In contrast, flight distances in anthropogenic environments reached ~1 km, with multiple records exceeding 500 m. These findings challenge assumptions of low mobility, confirming *O. barnabita* covers substantial distances. Finally, the study identified specific factors influencing the results, leading to planned methodological improvements for future research to ensure maximum data reliability.

The research was supported by European Union LIFE+ programme project “LIFE Osmo Baltic. Baltic Wide Web for *Osmoderma Eremita*: the Creation of an Ecological Network in the Baltic Region” LIFE22 NAT/LT/101113698.

#10951

WORKSHOP: Career in Entomology (open discussions)

01/07/2026 at 17:00, Vouvray

Careers in insect science – pathways, case studies and inspiring the next generation

Francisca SCONCE (Royal Entomological Society, Fran@royensoc.co.uk)

Anne WEINHOLD

Abstract

The Royal Entomological Society (RES) has a strategic priority to increase public understanding of insect science, as part of its vision to ‘enrich the world with insect science’.

There are many careers and pathways working with insects; young people, school science educators and those with a keen interest in natural history are however often not aware of these. The landmark ‘Grand Challenges in Entomology’ paper (Luke et al, 2023) lists Societal Engagement and Knowledge Access as key challenges in our discipline, and work at RES is ongoing to provide the next generation with opportunities to choose careers in insect science.

The RES currently offers online resources on careers with insects, and shares UK and ROI courses and jobs on our website. We also take part in careers events including with the British Ecological Society, and organise online events with school science communication networks such as STEM Ambassadors. We organise an annual Student Forum event for students studying insects, and feedback has shown it is beneficial for building a network of early career entomologists and providing a safe space to practice science communication skills.

As part of our 2025-2028 strategy, we are developing new resources to highlight careers with insects to different audiences. From early 2026 we will be sourcing case studies of insect scientists working in a range of entomological disciplines, from diverse backgrounds and with different career pathways. We will develop and test stories about these entomologists, aiming to be engaging and inspiring to a young audience. By late 2026 we plan to create an online resource and printed leaflet to share these case studies at events, such as nature festivals, education conferences and careers events. In 2027 we hope to create short videos with the entomologists for use in online engagement.

Ethics review for insect research in the UK: institutional trends, researcher attitudes, and implications for entomology

Jessica STOKES (Royal Entomological Society, Jessica@royensoc.co.uk)

Bob FISCHER, Meghan BARRETT

Abstract

The Animal Welfare (Scientific Procedures) Act 1986 provides the legal framework for UK research involving ‘protected’ animals, covering all live vertebrates and cephalopods and necessitating ethical review. Insects are currently excluded from this legislation, yet scientific research suggesting a level of sentience for certain insect orders is increasing, with the Royal Entomological Society (RES) advocating a precautionary approach to their welfare. Despite this, it has remained unclear how widely institutional ethics review has already been extended to insect research, or how entomologists themselves experience and evaluate such oversight. We present the first systematic survey of ethics review for insect research in the UK.

First, we contacted ethics boards at 142 UK universities and research institutions. Of the 93 responding institutions that reported conducting insect research, 51.6% require ethics applications for insect work; among 46 universities with identified entomology courses, 43.2% reported such requirements. Notably, more than one third of institutions without current ethics application requirements nonetheless expressed interest in receiving insect welfare resources.

Second, we analysed 129 responses to an online survey of UK-based researchers working with insects. Most respondents (70.9%) were not currently submitting ethics applications; 25.2% reported mandatory and 3.9% voluntary submissions. Perceived impacts on research quality were broadly positive: 44.6% reported ethics applications improve study quality. Early-career entomologists were substantially more likely than senior colleagues to report quality improvements. Qualitative responses highlighted perceived benefits (better study design, reduced waste, increased public trust) alongside concerns (administrative burden, and fears of research constraint).

In parallel, RES and partners have begun developing best-practice guidance and training resources on insect welfare in research and education to support both researchers and ethics panel members. These findings helped to inform ongoing initiatives, discipline-specific guidance, training, and reporting standards which can help embed proportionate ethics review, supporting both insect welfare and entomological science.

Identifying trends in reporting on the ethical treatment of insects in research

Craig PERL (University of Stirling/Indiana University Indianapolis, Craig.perl@stir.ac.uk)

Cat KISSINGER, R Keating GODFREY, Enrique CASTILLO, Bob FISCHER, Meghan BARRETT

Abstract

Transparent reporting on the ethical treatment of research animals (e.g., implementation of the 3Rs, replace, reduce, and refine) is recommended when publishing in peer-reviewed literature. This is meant to foster public trust, safeguard animal welfare, and generate reproducible science. However, entomologists are not expected to engage in such reporting, as their research is not subject to legislated ethical review. Recently, however, entomologists have reported increased concern about the ethical treatment of insects in research, and associated reproducibility and public trust issues. To what degree are these increasing concerns reflected in changes in practices? We surveyed 15 high-impact journals that publish on insects over 20 years to collect data on reporting related to the ethical treatment of insects in research, including animal reduction methods, analgesics/anesthesia statements, and information regarding sacrifice. Out of 1359 sampled papers, no studies reported any methods to reduce animal use. Over 20 years, we found an increase in the proportion of papers reporting insect death and a decrease in the papers reporting significant invasive handling. 84% of papers with significant animal handling or death did not report the use of any anesthetics. We also found an increase in animal-treatment-specific ethics statements (from 0% to 8%), largely driven by the journal *Animal Behaviour*. We end by 1) making recommendations for entomologists looking to improve their reporting practices and 2) providing tools to improve transparent reporting of information related to the ethical treatment of insects in research.

#12520

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

From Conventional to Smart: An Automated Probe Trap System for Stored-Product Insect Monitoring

Paraskevi AGRAFIOTI (Laboratory of Entomology and Agricultural Zoology, Department of Agriculture Crop Production and Rural Environment, University of Thessaly, Agraftot@uth.gr)

Theodora Isavella GOGOU, William Rob MORRISON III, Christos ATHANASSIOU

Abstract

Probe traps are used for monitoring as a decision-support tool for stored product insects, both at an industrial scale and even for producers. In recent years, technological advances have allowed the improvement of these traps into tools for remote, automated, next-generation "SmartProbe Traps." SmartProbe traps are equipped with sensors that enable real-time monitoring of insects, recognition technologies, as well as environmental data collection. This has the potential to bring precision agriculture to the protection of stored commodities. In the present study, the effectiveness of a conventional probe trap and a SmartProbe trap was evaluated against a wide range of stored product insects. Glass containers were filled with soft wheat and 60 individuals were released. The traps were placed inside each container and data were collected daily for five days, through visual inspection of the conventional probe trap and via a smartphone application for the SmartProbe trap. The status of the insects was assessed as alive, affected, or dead. The results showed approximately the same capture rate for both traps. However, in the electronic trap, by the end of the trial most insects were affected or dead, whereas in the conventional trap most of them were still alive. These findings highlight the need for further research, as the integration of smart technologies into probe traps will contribute to the optimization of insect monitoring and management.

Dark spots in the blue: a new workflow to investigate elytral pattern in the long-horn beetle *Rosalia alpina* (Linnaeus, 1758)

Alessandro CAMPANARO (CREA, Council for Agricultural Research and Economics, Italy, Alessandro.campanaro@crea.gov.it)

Alice LENZI, Antonio PROFICO, Silvia GISONDI, Alessandro CINI

Abstract

Insect colouration plays a key role in multiple biological functions, such as predator avoidance or intraspecific communication, and may show substantial variability within and among populations of the same species. Despite extensive research on its physiological, ethological and evolutionary bases, many colour patterns remain poorly understood, even in iconic and well-studied species.

The Alpine longhorn beetle, *Rosalia alpina* (Linnaeus, 1758), is a saproxylic species protected under the EU Habitats Directive and characterised by a distinctive colour pattern consisting of black spots on a light blue background on pronotum and elytra. The species exhibits marked inter-individual and inter-population variability in spot number, size, shape and position, yet this variability has received limited attention and mainly within monitoring frameworks based on photographic data.

Here, we present a new set of R functions designed to automatically identify and quantify elytral spot characteristics from digital images. It converts images of elytra into a black and white grid representing the spot pattern, using landmark-based geometric morphometric approaches that remove variation related to position, rotation and scale. The grid is subsequently deformed according to the closed outline of each elytron, which allows direct comparison among individuals.

As a proof of concept, we applied the method to a dataset of 73 specimens (28 females and 45 males), including both wild-caught and museum samples, to test method robustness and to assess the influence of sex and body size on colour pattern variation. The proposed framework proved to be reliable, user-friendly and easily customisable, enabling the processing of large datasets.

Our approach provides a tool for quantitatively analysing animal colour patterns, with potential applications extending beyond *R. alpina*, and it is particularly suited for integration into image-based monitoring programmes, citizen science initiatives and automated identification pipelines, contributing to a deeper understanding of the mechanisms driving colour variation and its evolutionary significance.

#12511

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Development of DNA Barcodes for biodiversity and biosecurity: filling a gap for the Romanian fauna

Maria-Magdalena DASCĂLU (FUSU) ("Al. I. Cuza" University of Iași, Institute of Interdisciplinary Research, CERNESIM, Iași, Romania, Dascalumm@yahoo.com)

Emanuel BALTAG, Florina-Georgiana CABA, Lucian FUSU, Lucian HĂNCEANU, Marius MIHĂȘAN, Mircea-Dan MITROIU, Ionuț PAVEL, Ovidiu Alin POPOVICI, Cosmin Teodor MIHAI, Adriana MELEN, Irina NUCĂ

Abstract

International trade, climatic and environmental changes accelerate the spread of foreign species and pathogens beyond their native ranges. In front of this input of alien species many phytosanitary services or biolaboratories have increased the use of DNA sequences (barcodes) for diagnostic and discrimination. To avoid false alarms, it is necessary to discriminate between truly high risk or regulated species and those with no impact or autochthonous species. This discrimination success relies on a comprehensive database of sequences for comparison. Our aim is to develop DNA barcode libraries for two groups of invertebrates, with an economic, respectively human health significance. The longhorn beetles are the main group of coleopterans found in wood packing materials used for the global safe transportation of goods. Generally, they are transported as larvae developing inside wood and their identification is difficult for reasons of lack of morphological characters and taxonomic keys. On the other hand, the ticks are the most important vectors of pathogens after mosquitos, being responsible for many diseases in humans and domestic animals. Rapid identification of ticks and their pathogens is paramount for disease control and prevention. This is possible only after filling all the gaps in species coverage and developing methods for the simultaneous identification of ticks and the pathogens they harbor. Financial support provided by Romanian Agency UEFISCDI through the grant 2D-3B (PN-IV-P7-7.1-PED-2024-1951).

Non-lethal identification of a species considered difficult to identify in the field: the case of *Dasypoda morawitzi* (Hymenoptera: Melittidae)

Daphné DEMAZIER (Institut de Recherche sur la Biologie de l'Insecte, Daphne.demazier@univ-tours.fr)

Sébastien MOREAU

Abstract

Currently, most wild bees that are considered difficult to identify in the field are identified post-mortem in the laboratory, using taxonomic identification keys and/or barcoding. However, these methods may have a significant impact on insect populations that are already vulnerable due to the many consequences of human activities on the climate, the quality of the environment, and the functioning of ecosystems.

Faced with the collapse of biodiversity, we must therefore conceive and develop an entomology of scarcity, in which methods and ethics could better take into account the potential rarity and fragility of the wild insects studied.

By combining several complementary approaches, which we will detail and which rely on modern but accessible instrumentation, we were able to identify in the field a cryptic species, *Dasypoda morawitzi* (Radchenko 2016), considered indistinguishable without microscopic examination from the closely related species *Dasypoda hirtipes*. This study, designed as a proof of concept, took place near the Puys du Chinonais, a sensitive natural area that is home to remarkable entomofauna. It could contribute to the development and widespread use of non-lethal study protocols for identification, population monitoring, and behavioral observations, benefiting small populations of threatened insects and more common insects alike.

This work is part of the EXAPICO project, which aims to study the relationships between native wild bees, exotic wild bees, and exotic plants in France's Centre-Val de Loire region, using innovative and exclusively non-lethal methods.

Evaluation of Pheromone Trap Performance and Pest Management Effectiveness in Local Food Storage Facilities in Bangladesh

MD. MAHBUB HASAN (Rajshahi University, Mmhbgsd@yahoo.com)

Mst. Mansura JAHAN, Christos G. ATHANASSIOU

Abstract

The study assessed the frequency and abundance of stored-product insect pests in food facilities within Baneshwar, Rajshahi City Corporation, from September 2024 to March 2025, using dome and box pheromone traps. The dominant species were *Tenebroides mauritanicus* (cadelle), *Rhyzopertha dominica* (lesser grain borer), *Sitophilus oryzae* (rice weevil), and *Tribolium confusum* (confused flour beetle). Significant differences were observed between treated and untreated facilities in pest frequency and abundance. *T. confusum* was most prevalent in control sites (mean ≈ 22), slightly declining under treatment (≈ 18), suggesting moderate control efficacy. Conversely, *S. oryzae* increased sharply under treatment (mean ≈ 53 vs. 4 in control), indicating treatment ineffectiveness or a species-specific adaptive response. Populations of *Trogoderma granarium* and *Alphitobius diaperinus* showed little variation, while *Cryptolestes pusillus*, *R. dominica*, and *C. pumilio* remained consistently low. Notably, *T. mauritanicus* nearly doubled under treatment, implying ecological release or resilience.

Comparative analyses revealed that pest management efficacy differed markedly across facilities. Combined chemical and sanitation measures achieved significant, long-term pest reductions, whereas chemical-only treatments led to temporary suppression followed by resurgence. Dome traps consistently captured more insects than box traps ($p < 0.05$), confirming their superior detection efficiency, although box traps were more effective for low-abundance species such as *R. dominica* and *C. pumilio*. Temporal patterns showed peak pest activity from October to December 2024, corresponding to post-monsoon and early winter, followed by declines from January to March 2025 due to treatment and seasonal effects. Overall, pest densities were highest in unsanitary facilities. The findings highlight that pest control effectiveness is species-dependent and emphasize the need for integrated, species-specific management strategies. Pheromone-based monitoring, especially with dome traps, proved valuable for early detection and improved stored-product protection.

#11208

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

A Red-Light Time-Lapse Camera Trap (miniMon-Red) for Continuous Field Monitoring of Earthworm Behavior

Zixuan HE (Center for Quantitative Genetics and Genomics, Aarhus University, Zixuan.he@qgg.au.dk)

Helena RUSSELLO, Dev MEHROTRA, Marta VITTRUP, Quentin GEISSMANN

Abstract

Understanding the surface behaviors of earthworms is fundamental to revealing their ecological functions, yet direct field observation remains challenging due to their predominantly nocturnal and disturbance-sensitive activity. In this study, we developed a red-light-illuminated miniature time-lapse camera-trap (miniMon-Red) to continuously observe earthworm behaviors at the soil surface without altering their natural activity patterns in the field. Red illumination (650 nm) was selected because the earthworm exhibits low sensitivity to longer wavelengths, enabling non-invasive imaging during the nighttime when their surface exploration is most frequent. Using time-lapse recordings collected over multiple nights, we identified several key surface behaviors, including partial emergence associated with surface foraging and exploratory probing, short-range surface locomotion, and occasional full-body emergence. In order to improve the visibility of subtle movements under low-light conditions, we applied a motion-enhancement imaging algorithm enabling accurate annotation of behavior sequences. The results indicate that miniMon-Red provides a reliable, non-invasive approach for quantifying surface behaviors of earthworms in natural field settings. An important advantage of this methodology is its ability to scale simultaneously across time and space, enabling the investigation of the variation of earthworm behavior over nights, seasons and micro-habits. The methodology offers new opportunities for linking earthworm activity with soil processes, improving behavior classification and developing automated sensing frameworks for ecological research.

CRISPR-Cas aided detection of pest- and beneficial insects in agricultural landscapes using eDNA approaches

Christopher HEINE (Trier University Biogeography, Heinec@uni-trier.de)

Christian MAUS, Christian Ulrich BADEN, Michael Erik GREVÉ, Henrik KREHENWINKEL

Abstract

Environmental DNA (eDNA) metabarcoding paired with high-throughput sequencing has changed biodiversity assessment in agricultural landscapes by enabling the detection of cryptic, rare, and functionally important taxa, as well as providing insights into community composition and population genomics. Despite these advances, widespread adoption beyond research applications remains limited due to lengthy processing times and extensive laboratory workflows. This limits the use of these key technologies by farmers, advisors and other stakeholders who would benefit from field-deployable diagnostics. CRISPR-Cas based detection assays (CRISPR-Cas-Dx) are a promising alternative for single species detection allowing fast and field-deployable applications. These detection assays rely on the programmable specificity of CRISPR-Cas enzymes, which form complexes with guide-RNAs (gRNAs) designed to recognise specific DNA or RNA sequences. Once this complex is activated through the presence of target DNA or RNA, collateral nuclease activity enables highly sensitive signal generation using fluorescence or lateral flow strips. While the use of CRISPR-Cas-Dx in medical applications has been widely established, only few applications have been developed in ecological and agricultural contexts. Here, we present an eDNA-based CRISPR-Cas-Dx assay using the Class 2, Type V enzyme LbCas12a and target-specific gRNA for the detection of rapeseed pest species. The usage of additional gRNA can lead to the detection of pest-associated pathogens and beneficial insects with the same assay framework. To increase sensitivity, samples are amplified with isothermal recombinase polymerase amplification (RPA). Detection is achieved via a FAM-labelled reporter exploiting the trans-cleavage activity, enabling reliable rapid identification of target DNA. We demonstrate, that by combining CRISPR-Cas detection assays with isothermal amplification and fluorescence reporter molecules or lateral flow strips we can successfully detect different pest insects, associated microbial pathogens and beneficial insects in the field. In doing so, we bridge the gap between molecular biodiversity monitoring and real-time, on-site results accessible for farmers and advisors.

Three-Year Evaluation of Mass Trapping and Attract and Kill Systems for Olive Fruit Fly Management in Pilot Olive Orchards in Crete, Greece

IOANNIS KOUEFAKIS (ELGO-DIMITRA, INSTITUTE OF OLIVE TREE SUBTROPICAL PLANTS AND VITICULTURE, Koufakis@elgo.gr)

ARGYRO KALAITZAKI, ELENI MALANDRAKI, EMMANOUELA KAPOGIA

Abstract

The management of *Bactrocera oleae* (Rossi) (Diptera: Tephritidae), the most damaging pest of olives worldwide, has traditionally relied on chemical insecticide treatments applied either as bait or cover sprays. Increasing concerns over environmental impacts, non-target effects on beneficial organisms, pesticide resistance, and the European Union's Green Deal, which aims to drastically reduce pesticide use, have accelerated the search for more sustainable control approaches. Mass trapping and attract and kill systems offer promising alternative control strategies for addressing these challenges under organic farming practices and IPM programs. Pilot field trials were conducted over three years (2023–2025) in olive orchards in Chania, Greece, to evaluate two mass-trapping systems (AttravolTM-Anel, AttravolTM-Attravol TrapTM) and three attract-and-kill systems (Eco-trap[®], Flypack[®]Dacus, Karate Trap[®]) in comparison with ground insecticide bait sprays, for the control of the olive fly. Despite interannual variation in pest pressure, both mass-trapping systems consistently resulted in significantly lower olive fly populations and fruit infestation levels compared with the three attract-and-kill systems as well as the control plots treated with bait sprays. Under low or moderate pest pressure, both mass-trapping systems alone maintained damage below the economic threshold. When pest pressure was high, mass trapping combined with one or two bait sprays resulted in effective control and outperformed the three attract-and-kill systems as well as conventional bait sprays which required multiple applications. Overall, these findings demonstrate that both mass trapping systems using an innovated food-based attractant constitute an effective and environmentally friendly alternative strategy for *B. oleae* management in olive orchards.

#11220

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Comparison of several biological matrices for studying wild bee diversity using metabarcoding

Anaïs MARQUISSEAU (Dynafor, INRAE, 31326, Castanet Tolosan, France, Anais.marquisseau@inrae.fr)

Christophe KLOPP, Kamila CANALE-TABET, Emmanuelle LABARTHE, Elisa SIMON, Rémi RUDELLE, Jérôme WILLM, Adrien CASTINEL, Mélodie OLLIVIER, Magalie PICHON

Abstract

DNA metabarcoding is a molecular method that can be used to effectively study and monitor pollinator communities on a large scale. However, conventional molecular approaches, which involve partial or total destruction of specimens, have several limitations: loss of rare individuals, inability to re-extract DNA in case of sequencing failure, or the need for additional morphological examination when molecular identification fails (incomplete databases, poorly discriminating markers, or contamination). To circumvent these problems, we compared the resolution of metabarcoding from bee tissues with that of an approach using trapping and storage liquids.

Seventeen plots in the Zone Atelier Pyrénées Garonne (ZA PYGAR, Haute-Garonne) were equipped with colored bowls filled with water and detergent for three days. The captured bees were stored in ethanol at -20°C, as were the trapping liquids. After morphological identification by an expert, a leg from each specimen was taken for tissue metabarcoding, while DNA was also extracted from the storage liquids. COI and 16S markers were used for amplification and sequencing.

For the 16S marker, the results show that 27% of species could not be identified molecularly due to incomplete databases at the time of analysis. Furthermore, 67% of species identified morphologically were detected by conventional metabarcoding, compared to only half with liquids (trapping or storage). However, the latter reveal a greater diversity of insects, suggesting preferential amplification of groups other than wild bees by the marker used.

Influence of transport on *Eldana saccharina* (Lepidoptera: Pyralidae) fitness for sterile insect technique applications

Shilombe Tess MATHONSI (University of KwaZulu-Natal, 225195356@stu.ukzn.ac.za)

Zabentungwa HLONGWANE, Caswell MUNYAI, Lawrence MALINGA

Abstract

The sterile insect technique (SIT) is a biological control strategy that promotes sustainable pest management; however, its success depends on the fitness of the insect during release. This study investigated the influence of transportation on the fitness of laboratory-reared, irradiated and unirradiated *Eldana saccharina* Walker (Lepidoptera: Pyralidae) moths intended for SIT field release. Male moths were irradiated at 200 Gy and mated with unirradiated females to produce a sterile F1 generation. Fitness parameters, including longevity, fecundity, mating frequency and flight ability, were assessed in the F1 generation under transported (chilled at 10°C) and non-transported (25°C) conditions. The findings showed a significant reduction caused by transportation on fecundity, mating frequency and longevity. However, no statistical difference was recorded on mean flight ability between the transported and non-transported on both irradiated and unirradiated moths, suggesting that the transportation procedures did not compromise moth's ability to fly. Overall, the results show that the existing transport procedures for *Eldana saccharina* are suitable for SIT programs, however, the observed reduction in longevity and mating frequency may affect mating competitiveness under field conditions. In addition, transportation methods proved to be highly efficient in supporting SIT operations, but the minor effects on longevity and mating frequency highlight the need for continued refinement. These findings help enhance SIT operations within eco-friendly and sustainable pest management systems, supporting efforts to minimize dependence on chemical control methods.

INVGuild: enhancing invertebrate biodiversity assessment through functional classification

Matteo MONTAGNA (University of Naples Federico II, Matteo.montagna@unina.it)

Matte BRUNETTI, Paola COSTAGLIOLA, Marilù CARDINALE, Giulia MAGOGA

Abstract

Ecosystem resilience and functionality emerge from interactions among biotic and abiotic components; therefore, biodiversity monitoring is essential for assessing ecosystem status. Taxonomic inventories provide useful snapshots of community composition, but they do not directly reflect ongoing ecological processes. While the functional classification of organisms provides deeper insights into ecosystem functioning, energy flow and trophic structure than taxonomy alone, detailed ecological information is lacking for most species. In this context, trophic guilds (groups of species sharing similar feeding strategies) offer a practical proxy for ecological roles and have been successfully applied across several taxa (e.g., fungi, nematodes). However, for species-rich groups such as invertebrates, the routine integration of functional information into large-scale DNA-based surveys remains limited. To address this gap, INVGuild was developed. INVGuild is an open-access, literature-derived and expandable reference database that links continental invertebrate taxonomic identities to trophic guild assignments. The database currently contains approximately 1,000 taxa (ranging from species to class level) assigned to seven trophic guilds (bacterivores, carnivores, detritivores, fungivores, herbivores, microbivores and omnivores). The applicability of INVGuild was evaluated through reanalysis of environmental DNA metabarcoding data from the largest study on European soil biodiversity. These analyses demonstrate that INVGuild can be readily integrated into DNA-metabarcoding data-analysis pipelines and that functional (guild-based) metrics uncover patterns that remain undetectable using taxonomic diversity alone. In particular, functional diversity indices and trophic-guild ratios derived from INVGuild revealed trends consistent with ecological theory and provided explicit insight into trophic network features and variations in energy flow across environments. By linking DNA-based biodiversity surveys to standardized functional assignments, INVGuild helps overcome the limitations of taxon-only approaches and facilitates rapid, evidence-based assessment of ecosystem functioning. The resource is intended to support conservation planning, sustainable land management and further research on ecological dynamics.

Biodiversity in vineyards: the importance of trapping techniques for its assessment

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Yohann GRAUX, Martin AUMONT, Pauline GUINET, Théodore RAMANANKATSOINA, Damien MUNIER, Elfie PERDEREAU, Marlène GOUBAULT, Ingrid ARNAULT

Abstract

Vineyards are perennial agroecosystems whose biodiversity in arthropods remains poorly documented. To study these communities, inventories rely on trapping methods; the most used being the pitfall trap. However, the chosen sampling method directly influences the results. This, in turn, affects our understanding of functional biodiversity and associated ecosystem services.

As part of the BioVAL project, Carabidae and Araneae communities were sampled over two years (2016-2017) on 16 vineyard plots in the Loire Valley region. Two devices were used: pitfall traps, targeting epigeal macrofauna, and window flight traps, mainly intercepting arthropods from the shrub layer and active and passive fliers. First, we aimed at increasing our knowledge of the biodiversity of ground beetles and spiders in this still poorly studied environment. Second, we aimed at understanding how the two capture methods influence our assessment of functional biodiversity: is one of method sufficient, or is a combination of both necessary to accurately characterize the taxonomic and functional biodiversity of this habitat?

To achieve this, we identified and compared the number and ecological traits of the ground beetles and spiders captured in the two types of traps. A total of 103 species of ground beetles and 20 families of spiders were recorded. Pitfall traps captured more individuals and provided a fairly accurate picture of the dominant species living on the ground, while window flight traps intercepted a greater functional diversity. Statistical analyses showed that functional assemblages differed according to the type of trap used. Certain ecological traits, such as ballooning or large size, were associated with a single method. The complementarity of the two methods is confirmed by the high functional β -diversity between them.

The combination of the two methods therefore proves highly complementary for inventorying and characterizing functional traits related to biocontrol. However, this benefit must be adapted to the objectives.

Advancing pollinator monitoring: Two years of automated data collection using Insect Detect systems in Transylvanian semi-natural grasslands (Cluj, Romania).

Natalia TIMUȘ (Babeș-Bolyai University, Nataliatimuss@gmail.com)

Iulia MUNTEAN, Zoltán LÁSZLÓ, Cristina CRAIOVEANU, Maximilian SITTINGER, Jonna HEUSCHELE

Abstract

Given the global decline in insect pollinator populations, the development of scalable and efficient monitoring frameworks has become a critical priority. A promising solution lies in the integration of Artificial Intelligence (AI) to facilitate the automated observation of plant-pollinator interactions. Within the framework of the Standardized European Monitoring of Plant-Pollinator Interactions (SEPPi) project, this study provides a comparative analysis of traditional transect counts and automated monitoring in the semi-natural grasslands of the Eastern Hills of Cluj, part of the Natura 2000 network in Romania. Over a two-year period (2024–2025), 12 sites representing various land-use types, including hay meadows, abandoned grasslands, and sheep-grazed pastures, were assessed. Automated monitoring was conducted by deploying Insect Detect camera traps to capture high-resolution images of pollinators interacting with floral resources in situ, while traditional monitoring involved systematic visual observations along established transects. Preliminary findings indicate that automated method captures pollinator abundance patterns comparable to traditional transects, particularly regarding the effects of land management. High abundance was observed in hay meadows, while lower levels were recorded in grazed areas. While both methodologies proved proficient in monitoring Hymenoptera, transects were more effective for detecting Lepidoptera and provided higher spatial resolution. Conversely, Insect Detect systems significantly outperformed transects in monitoring Diptera and offered a better temporal resolution. Bipartite interaction networks revealed that automated methods provide a more detailed view of community dynamics and a broader range of plant-pollinator interactions within specific taxonomic groups. Our results suggest that the Insect Detect system serves as a reliable tool for the rapid and standardized monitoring of pollinators. We conclude that integrating both methodologies may provide a more comprehensive assessment of ecosystem health and pollinator communities across diverse European biogeographical contexts, balancing scalability with taxonomic depth.

Effect of Radio-Frequency Electromagnetic Fields on Insect Presence, Population Fluctuation, and Biodiversity: Preliminary Insights from the ETAIN Project

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Zoi THANOU, Evangelia ARAPOSTATHI, Myrto STAMOULI, Christina PANOPOULOU, Maria BOUGA, Marco ZAHNER, Jürg FRÖHLICH, Fabian SCHNEIDER, Anastasia KALAPOUTI, Fani HATJINA, Leonidas CHARISTOS, Felipe RIBAS OLIVEIRA, Pieterjan DE BOOSE, Anke HUSS, Andri VARNAVA, Menelaos STAVRINIDES, Arno THIELENS

Abstract

The widespread deployment of wireless telecommunication networks results in the emission of radio-frequency electromagnetic fields (RF-EMFs) into the environment, creating a novel source of exposure for insects and other organisms. Within the framework of the ETAIN project (Horizon Europe Grant Agreement No. 101057216), we investigate how exposure to RF-EMFs may influence insect presence, population dynamics, and biodiversity under realistic field conditions.

A dedicated experimental field was established in Nea Moudania, Chalkidiki, Greece, where an RF-EMF antenna system was installed to create well-characterized exposure zones at frequencies of 3.4 GHz and 26 GHz, alongside unexposed control sectors. Insect populations were monitored using Malaise traps (conventional and remote electronic), with samplings conducted biweekly throughout the 2025 season. Collected specimens were identified to order and species level using morphological keys, and biodiversity metrics such as the Simpson index and evenness were calculated.

Results from the first field season indicate discernible patterns in insect abundance and community composition across exposure gradients. Observed differences suggest potential influences of RF-EMF exposure on certain insect groups, though further analyses are ongoing to confirm trends and assess ecological significance.

This study represents one of the first large-scale, controlled field investigations into the ecological effects of RF-EMFs on insect biodiversity, contributing essential data to an emerging research area of environmental importance.

Incidence and severity of mealybugs (*Pseudococcus* spp.) and soft scale insects (*Ceroplastes* spp.) in soursop (*Annona muricata*) agroecosystems of the Ecuadorian Amazon

Segundo VALLE RAMÍREZ (Universidad Estatal Amazónica, Svalle@uea.edu.ec)

Jaime Alexander GONZABAY MARTÍNEZ, Johanna Estefanía RIVERA PARRA, Karina CARRERA SÁNCHEZ

Abstract

Soursop (*Annona muricata* L.) cultivation has been expanding in the Ecuadorian Amazon; however, its production is increasingly constrained by sap-sucking insect pests. This study aimed to evaluate the incidence and severity of mealybugs (*Pseudococcus* spp.) and soft scale insects (*Ceroplastes* spp.) in soursop agroecosystems in Pastaza Province, Ecuador. A one-hectare plantation was selected, where 36 trees were systematically monitored every 15 days. The presence of mealybugs and soft scales was recorded on leaves, branches, and fruits. Mealybug incidence ranged from 45% to 75%, showing a relatively homogeneous distribution across all evaluated plant organs. Infestation severity remained consistently high, reaching approximately 75%, indicating persistent and intensive damage. In contrast, soft scale incidence was lower, with a maximum of 43% on leaves and branches and no infestation observed on fruits. However, infestation severity increased progressively, reaching up to 50%, mainly affecting foliar and woody tissues. Both pest groups caused physiological damage through sap feeding, honeydew excretion, and subsequent development of sooty mold, negatively affecting plant health and fruit quality. The results highlight mealybugs and soft scale insects as major phytosanitary constraints in soursop production in the Ecuadorian Amazon, emphasizing the need for timely monitoring and integrated pest management strategies to reduce severe yield losses.

#11551

Poster Session 1 - Ice breaker party
29/06/2026 at 16:00, Exhibition area

IDMABIO: A Platform for the Molecular Characterization of Biological Agents and Pests

Ionela-Madalina VICIRIUC (INRAE, UMR 1355 Institut Sophia Agrobiotech (ISA), Sophia Antipolis, France, Ionela.madalina-viciriuc@inrae.fr)

Sylvie WAROT, Nicolas RIS, Thibaut MALAUSA, Sophia MARGUERIT, Streito JEAN-CLAUDE

Abstract

The biodiversity of most agrosystems remains poorly understood due to taxonomic issues (cryptic species, species complexes, biotypes, etc), rapid changes in communities (invasive exotic species, re-emerging native species, etc) and limited diagnostic capabilities in terms of throughput, time and/or price.

This context led to the formalisation in 2024 of the IDMABIO platform (<https://idmabio.com/>), a service open to the various players in biocontrol, whether public research laboratories, agronomic players (Agricultural Technical Institutes, Chambers of Agriculture, FREDON, etc.) or private biocontrol manufacturers.

The services offered include DNA barcoding i.e. the use of a short DNA sequence considered necessary and sufficient to affiliate individuals at the species level. Since the launch of IDMABIO, this approach has been successfully applied to a wide range of taxa, crop pests (Coleoptera, Hemiptera, Lepidoptera, Neuroptera, Thysanoptera etc) or biological control agents (predatory bugs as well as egg, larval or pupal parasitoids).

The data generated by the platform, incorporating routine identifications and in-depth analyses, which also feeds into research. The results of this expertise are regularly published in scientific articles and contribute to a better understanding of biodiversity within agrosystems.

#10875

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

A validated European database of wild bees and hoverflies to support large-scale entomological research

Jordan BENREZKALLAH (Laboratory of Zoology, laboratory of Interaction Ecology and Global Change, University of Mons, Jordan.benrezkallah@umons.ac.be)

Natasha DE MANINCOR, Ahlam SENTIL, Denis MICHEZ, Kévin TOUGERON

Abstract

Wild bees (Hymenoptera: Anthophila) and hoverflies (Diptera: Syrphidae) are among the most important groups of pollinating insects, yet both are experiencing marked declines across Europe. Understanding these trends requires large, reliable and standardized datasets, which remain rare due to dispersed sources and heterogeneous data quality.

We compiled and harmonized occurrence records from taxonomists, national experts, museum collections, published literature, verified citizen-science platforms, public repositories, and previous European projects. All records were cleaned, structured using the Darwin Core standard and validated by experts in each taxonomic group.

The resulting resource consists of two comprehensive databases containing over 4.34 million bee records and 1.04 million hoverfly records. Together, they cover 97% of the European bee fauna (2,083 of 2,138 species) and 97% of the European hoverfly fauna (886 of 913 species). These datasets offer an unprecedented overview of the spatial and temporal distribution of European pollinators.

This consolidated database enables robust analyses of species trends, biogeographic patterns, habitat associations, and conservation status. It has already served as a core resource for assessments of the IUCN European Red list of Bees and Hoverflies and provides an essential foundation for future research and monitoring initiatives targeting wild pollinator diversity across Europe.

High Resolution Habitat Suitability Modelling of Grassland Butterfly Index Species for Spatial Planning of the Management of Natural Capital: A Case Study from Latvia

Jekaterina BUTKEVICA (Department of Ecology, Faculty of Medicine and Life Sciences, University of Latvia, Jb22035@edu.lu.lv)

Ruta STARKA, Vita SAKELE, Ainars AUNINS, Andris AVOTINS

Abstract

Butterflies are a critical component of natural ecosystems, providing pollination services and playing a significant role in terrestrial trophic networks. Their responsiveness to habitat changes makes them a key indicator of environmental health. Across the EU, the Grassland Butterfly Index — a metric derived from the abundance of 17 European butterfly species — has declined by 50% since 1991. This trend underscores the importance of the EU Nature Restoration Regulation, which requires Member States to halt the decline of pollinators and ensure population recovery. The Grassland Butterfly Index is one of the main metrics used to measure this.

While the Grassland Butterfly Index reveals national-scale trends, the underlying monitoring schemes frequently suffer from limited spatial coverage and census frequency. Additionally, the scarcity of ecological studies on butterfly species in Latvia constrains the development of targeted, evidence-based conservation strategies.

We present results from national-scale habitat suitability models developed for 11 Grassland Butterfly Index species occurring in Latvia. By employing high-resolution spatial modelling to evaluate species-specific responses to environmental predictors, our approach enables a spatially explicit application of the index concept. Our framework identifies priority areas for management, providing a practical tool to support the objectives of the EU Habitats Directive. Furthermore, this approach establishes a robust scientific basis for evidence-informed land-use planning, which is essential for achieving the mandatory targets of the EU Nature Restoration Regulation and preventing further habitat degradation.

Effects of forest disturbances on ground dwelling arthropods and saproxilic beetle communities

Matilde CASE (University of Padova, Matilde.case@phd.unipd.it)

Davide NARDI, Andrea BATTISTI

Abstract

In recent years, extreme climatic events, such as windstorms, have increased in frequency due to climate change. These forest disturbances often cause widespread tree death by boosting wood-boring insect populations. The European spruce bark beetle, *Ips typographus* (L.), is one of the most destructive forest pests in Europe, affecting Norway spruce, *Picea abies*. Outbreaks of *I. typographus* can generate from high availability of weakened trees. In October 2018, the windstorm Vaia devastated parts of the southeastern Alps, causing its populations to spike. The combination of the windstorm and the bark beetle outbreak rapidly changed the forest landscape throughout the Eastern Italian Alps. Despite extensive research, the effect of different types of forest natural disturbances and their interaction on the arthropod fauna is still poorly understood. As bark beetles create new habitats within forests by opening the canopy due to needle loss, the proximity to already existing windthrown areas may exert a combined effect on diversity patterns at different spatial scales. To test the compound effect of multiple forest disturbances on arthropod communities, we carried out an experiment involving 13 forest areas. For each area, we sampled two bark beetle-killed patch sites, one surrounded by forest, and one by windthrown areas. For each site, we used pitfall traps to collect ground-dwelling invertebrates and cross-vane traps for saproxilic beetles from the end of May to the beginning of July 2025. Here, we present the results concerning the responses of carabid, cerambycid, scolytid beetles and spiders communities. Carabids, being mostly generalists, showed no major differences in overall abundance or richness, although certain species responded differently to the two conditions. Cerambycids varied more in composition, with dead wood-associated groups and flower-visiting species more frequent close to open, disturbed areas. The results will provide indications about actions to take for biodiversity preservation in disturbed areas.

Ecology and Taxonomy of Limoniinae (Diptera) crane fly of Italy

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Sigitas PODENAS

Abstract

The family Limoniidae, comprising more than 10,000 species worldwide, is among the most diverse groups within the lower Diptera. Although the family is traditionally divided into four subfamilies, its internal classification remains unsatisfactory.

Limoniidae have been relatively well studied in the Western Palearctic; however, at the regional scale, knowledge of the group remains limited. Furthermore, information on their ecology and biology is generally scarce. This research has three main objectives: (1) to address existing gaps in the faunistic knowledge of Italian Limoniidae; (2) to improve the taxonomy of selected groups within the family; and (3) to estimate the ecological preferences of selected species through spatial distribution modelling.

To achieve these goals, the study involves both the examination of natural history collections across Europe and Italy, as well as active field sampling, particularly in the southern provinces of Italy. Specimens will be collected using an entomological net, Malaise traps, and light traps.

Collected specimens will be identified and georeferenced, while museum material will be re-examined for accurate identification and georeferenced using the point-radius method when sufficient label information is available. The resulting dataset of georeferenced records will serve as the basis for distribution maps and spatial distribution models. Spatial distribution modelling is a correlative approach that estimates species' potential distributions by relating occurrence data to biotic and abiotic variables. These models will provide insights into the ecology of Limoniidae species, highlight areas of potentially suitable habitat, and identify the environmental variables driving their distribution patterns.

Here, I present my preliminary results.

Mosquitoes (Diptera: Culicidae) and biting midges (Diptera: Ceratopogonidae: Culicoides) in the diverse mangrove forests surrounding Cayenne in French Guiana

Médie COLLET (Institut Pasteur de la Guyane, Mcollet@pasteur-cayenne.fr)

Abstract

The 700 km² of mangroves in French Guiana (FG) are recognized as favourable areas for the resting, nesting and breeding of numerous species of aquatic and terrestrial arthropods, including populations of mosquitoes & Culicoides biting midges not yet documented.

Our study aimed to improve our understanding of the health risks posed by mosquitoes and Culicoides communities found in 7 different types and ages of mangroves surrounding the Cayenne agglomeration in FG. The study assessed their potential involvement as vectors, and identified the hosts on which the engorged females fed. Various correlation analyses were used to explore the influence of environmental parameters in order to gain a better understanding of the health risks and their association with the spatio-temporal dynamics of these mangroves.

A total of 13,968 mosquitoes belonging to 14 genera and 45 species were collected, including *Culex* spp., *Coquillettidia venezuelensis*, *Aedes taeniorhynchus*, *Culex portesi*, and *Deinocerites magnus* (crabhole mosquitoes), which were present in high densities. Of the specimens collected, 11 were *Aedes aegypti* (vector of several arboviruses), while 340 were *Culex portesi*, which is a vector of Tonate fever in French Guiana. In addition, a total of 206 758 Culicoides, belonging to 15 species, were collected, including a dominant number of *C. guyanensis*, *C. fusipalpis*, *C. flavivenula* and *C. leopoldoi*. A single specimen of *C. paraensis*, a vector of Oropouche fever in Guyana, is suspected to have been collected. Preliminary DNA barcodes, dissected genitalia and interspecific morphological features will be presented and discussed. According to scientific literature, some of the species collected could enable the circulation and emergence of several arboviral pathogens, demonstrating the importance of adequate sentinel virological surveillance activities. Detection of arboviruses in mosquitoes and parasites in culicoides is currently underway to assess the health risk to people and animals who live near or visit these mangrove forests.

Directional Reassembly Pathways of European Carabidae Communities Inferred from Biased Occurrence Records and Environmental Time Series

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Abstract

Opportunistic occurrence data dominate large scale biodiversity analyses but are strongly biased in space and time, obscuring directional community change. This study develops a generative community state space framework for European Carabidae that separates ecological signals from observation intensity. GBIF occurrences are used only as a static training sample to learn species environment associations, while temporal trajectories are generated from globally consistent environmental time series for 2001 to 2024 aggregated in five year windows. Communities are represented as low dimensional latent compositions and summarized by state space volume, defined as the log determinant of the weighted covariance of latent states, and by dispersion, defined as the weighted mean distance to the window centroid. Observation driven distortion is evaluated by comparing effort weighted versus uniform summaries and by effort capped standardization that limits leverage from record rich cells. Across Europe, record totals increase by about four fold from the earliest to the latest window, yet the inferred trajectory remains directionally consistent after standardization. Under effort capped standardization, state space volume increases by 2.08 log units from 2001 to 2005 to 2021 to 2024, corresponding to an approximately eight fold expansion in determinant scale, while mean distance increases from 0.010 to 0.015, a roughly 51 percent rise. Archetype dominance rises modestly in later windows, while continuous dispersion expands, indicating differentiation in latent composition with partial convergence toward a limited set of attractors. The framework yields standardized European maps and diagnostics of directional homogenization and differentiation pathways from biased occurrence data coupled to environmental time series.

An exotic ornamental shrub promotes the proliferation of the invasive fruit fly *Drosophila suzukii* at the end of winter season over a wide geographic gradient

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Estelle FOREY, Mégha BOULEMBERT, Nel BRESCIANI, Emilie GALLET-MORON, Astrid BAVAY, Anne BONIS, Hervé COLINET, Lionel DELBAC, Anne DENISSE, Romain GEORGES, Manon HESS, Jordy LARGES, Stéphanie LLOPIS, Lionel VALLADARES, Olivier CHABRERIE

Abstract

The spotted-wing drosophila *Drosophila suzukii* (Matsumura) is an invasive fly spreading in Europe since 2008 and causing large damage to cultivated fruits (cherries, strawberries, raspberries, etc.). *D. suzukii* also exploits fruits of wild and ornamental plants, especially during the cold seasons when crop fruits are scarce. This study aimed to understand the relative effects of climatic, landscape, and local factors on fruits infestation rates of *Elaeagnus ×submacrophylla*, an ornamental shrub largely planted in gardens and bearing fruits in winter and early spring. The study was conducted between March and May 2025 on 110 shrubs across a wide geographic and climatic gradient from the Mediterranean area to temperate ones in the North of France. Fruits collected from the shrubs were placed under laboratory conditions for 2 months and emerging *Drosophila* adults were identified and counted. The results showed that *Elaeagnus ×submacrophylla* is a major alternative reservoir for *D. suzukii*, the latter representing more than 90% of *Drosophila* individuals emerged. A peak of fruit infestation by *D. suzukii* was observed in the end of April, but infestations started in March. Also, increased infestation was associated with the presence of shrubs and ivy, as well as water areas (rivers, riparian forests). These first results provide a better understanding of the role of commercial plants from gardens and urban green spaces in the spread of invasive insects, helping to guide management strategies of their populations.

Clues to a species complex: biological, morphological, genetic, and distributional patterns in *Neoleucopis* spp. linked to *Marchalina hellenica* across Greece and Italy

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M. Lukas SEEHAUSEN, Marc KENIS, Greg LEFOE, Umar K. LUBANGA, Stephen D. GAIMARI, Nathan P. HAVILL, Antonio P. GARONNA, Dimitrios N. AVTZIS

Abstract

Marchalina hellenica (Gennadius) (Hemiptera: Marchalinidae) is a sap-sucking insect endemic to Greece and Türkiye, where it infests various pine species. Within its natural range, *M. hellenica* is an economically important species, significantly contributing to the pine honey production industry. Nevertheless, beyond its natural distribution, this scale insect has been documented as adversely affecting pine populations in Italy, Croatia, and Australia. Within its native range, *M. hellenica* is subject to significant predation pressure from *Neoleucopis kartliana* Tanasijtshuk (Diptera: Chamaemyiidae), which was used on the island of Ischia (Italy) as a biological control agent against *M. hellenica* in the early 2000s. In the current study, 22 Greek and 6 Italian (Ischia) populations of *Neoleucopis* spp. were sampled to investigate their taxonomic identity and distribution patterns. Morphological examinations were combined with DNA barcoding targeting the mitochondrial cytochrome oxidase I gene (mtCOI). Three genetically distinct mtDNA lineages were revealed within *Neoleucopis* populations of Greece: *N. kartliana*, *Neoleucopis* mtDNA lineage A, and *Neoleucopis* mtDNA lineage B. Divergence among these three *Neoleucopis* lineages ranged from 5.6% (*N. kartliana* and *Neoleucopis* mtDNA lineage A) to 10.7% (*Neoleucopis* mtDNA lineage A and *Neoleucopis* mtDNA lineage B), with morphological differentiations in the male genitalia distinguishing all three lineages. In addition, *N. kartliana* and *Neoleucopis* mtDNA lineage B exhibit distinct biological traits, each completing two alternating generations per year, supporting the possibility of two additional species coexisting alongside *N. kartliana*. Lineage occurrence demonstrated a regional partitioning within Greece: southern areas were dominated by *Neoleucopis* mtDNA lineage A, while both *N. kartliana* and *Neoleucopis* mtDNA lineage B were confined to northern sites. Individuals from Ischia, however, belonged uniformly to *N. kartliana*. This study contributes to the foundation required for applied ecological management, providing insights into the diversity of *Neoleucopis* species relevant to the control of *M. hellenica* in the invaded regions.

#11718

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Can ambrosia beetle community in chestnut-growing areas be affected by environmental drivers?

Chiara FERRACINI (University of Turin, Department of Agricultural, Forest, and Food Sciences (DISAFA), Italy, Chiara.ferracini@unito.it)

Eleonora Vittoria FONTANA

Abstract

The study investigates the ecological drivers influencing ambrosia beetle communities (Coleoptera: Curculionidae: Scolytinae and Platypodinae) at a local scale in the Piedmont region (NW Italy). During a biennial monitoring program (2024–2025), 48 ethanol-baited traps were deployed across managed chestnut orchards and mixed forest stands. Of the 118,286 specimens collected, *Xyleborinus saxesenii* (Ratzeburg) was the dominant species (95%). The survey identified three non-native species: *Anisandrus maiche* Stark, *Xylosandrus crassiusculus* (Motschulsky), and *Xylosandrus germanus* (Blandford). Our findings indicate that community structure is dictated by geographic and ecological variables. Specifically, a higher alpha diversity and a greater presence of invasive species was linked to higher humid conditions and "bridge host" availability. In contrast, a more resilient native community was favoured by xerothermic conditions and ecological stability. While chestnut-dominant environments provide vital ecological refuges, their susceptibility to biological invasions remains high, highlighting the need for a long-term monitoring to assess population trends in the context of climate change.

#12027

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

New data on the distribution and genetic diversity of *Osmoderma barnabita* (Coleoptera: Scarabaeidae) in Romania

Lucian HĂNCEANU ("Alexandru Ioan Cuza" University of Iași, Institute of Interdisciplinary Research - RECENT AIR Center, Iași, Romania; "Alexandru Ioan Cuza" University of Iași, Faculty of Biology, Research Group in Invertebrate Diversity and Phylogenetics, Iași, Roma, Hanceanu.lucian@yahoo.com)

Maria-Magdalena DASCĂLU, Lucian FUSU

Abstract

The hermit beetle is the largest cockchafer beetle in the Cetoniinae subfamily. All European *Osmoderma* species are listed in Annexes II and IV of EU Habitats Directive as priority species for conservation, and in Annex II of Bern Convention. In Romania, the single species of *Osmoderma* is *O. barnabita*, included in the Red Book of Invertebrates of Romania as vulnerable. *Osmoderma barnabita* is considered a species-richness indicator of invertebrate fauna and is known as an umbrella species. The biology, ecology, distribution and genetic diversity of this beetle is not well known in Romania due to the low interest in biodiversity research. Knowing the chorology and genetic diversity of the species, improved measures could be proposed for its habitat's conservation, measures that will hopefully ensure a favourable conservation status. We present the most comprehensive map of the species distribution in Romania including data from 1858 to 2024. The more than 130 reports were divided into historical periods to show trends over the last 170 years. We also included data on the molecular diversity of the species in eastern Romania, within and outside the Carpathians, and found a comparatively low diversity over a large geographic area. The authors acknowledge the support provided by the project SIDNER, PR/NE/2024/P1/RSO1.1/1/2.

#12225

Poster Session 1 - Ice breaker party
29/06/2026 at 16:00, Exhibition area

Effect of different land-use types on the diversity and composition of ants in the foothills of the Soutpansberg Mountains

Zabentungwa HLONGWANE (University of KwaZulu-Natal (Westville campus), Nolwazihlongwane20@gmail.com)

Caswell MUNYAI, Sihle BIDLA

Abstract

Land-use change is among the key drivers of global biodiversity loss, particularly in ecologically sensitive regions such as montane ecosystems. These ecosystems often support unique assemblages of species that are highly specialized and sensitive to habitat disturbance. Understanding how land-use transformation affects biodiversity is critical for assessing the resilience of ecological communities and maintaining essential ecosystem functions. This study investigated the effects of three land-use types (cropland, human settlements, and wildlife grazing) and seasonal variation on ant species diversity and composition in the foothills of the western Soutpansberg Mountains, Limpopo province. Ants were sampled using standardized pitfall traps during both wet and dry seasons, yielding 15,621 individuals representing 68 species across five subfamilies. Results showed that cropland supported the highest ant diversity, while wildlife grazing had the lowest diversity. The wet season had greater species diversity than the dry season, indicating a strong seasonal influence on ant activity and diversity. Ant assemblages in the studied habitats were dominated by opportunistic and disturbance-tolerant taxa, while specialist species were less represented. While total species richness showed no significant differences across the different land-use types, noticeable differences were observed in species abundance and the distribution of functional groups. This suggests that land-use change and seasonal variation alter ant assemblages by shifting dominance patterns and community composition rather than simply reducing ant species richness, potentially altering key ecosystem processes and functions.

Taxonomy of the Family Fanniidae (Diptera: Muscoidea) from Korea

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Abstract

The species of family Fanniidae from Korea are reviewed taxonomically. So far, eight species under the genus *Fannia* Robineau-Desvoidy, 1830 from this family have been recorded in the Korean fauna. In the taxonomic survey of the family Fanniidae from Korea, one species new to science, *Fannia* sp. nov., and fifteen newly recorded species from Korea including a newly recorded genus *Piezura* Rondani, 1866 were discovered. Species-level diagnostic characteristics of Korean species are provided here with illustrations and a key. As the result of this review, a total of 24 species with two genera are listed to the inventory of Korean fauna.

The phylogenetic relationships within the family Fanniidae and the species groups within the genus *Fannia* were examined using both morphological and molecular analyses. Morphological analysis, based on external characters and genitalia of male specimens from Korea, supported the monophyly of Fanniidae and confirmed *Fannia* as a distinct monophyletic group separate from *Piezura*. The species of *Fannia* also showed strong alignment with previously proposed species groups. Molecular analysis, based on the Cytochrome c oxidase subunit I (COI) gene, revealed some differences from the morphological analysis, but still supported the monophyly of Fanniidae and placed all *Fannia* species within the same species groups as suggested by the morphological classification.

DNA-based characterization of benthic fauna in Kibune and Kumogahata, the tributary streams of Kamo River system, Kyoto, central Japan

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KEI WAKIMURA, YASUHIRO TAKEMON, KAZUMI TANIDA

Abstract

Kumogahata and Kibune streams are the tributaries of Kamo River system in northern Kyoto City, central Honshu Island of Japan. Recently we have found a habitat differentiation of the two distinct genetic lineages of spiny crawler mayfly *Drunella trispina* (Uéno, 1928) (Ephemerellidae, Ephemeroptera); one occurring in both tributaries and the other only in Kibune Stream, and thus we have hypothesized about parapatric speciation based on habitat preferences (Hamamura et al. 2025; Aquatic Insects **46**, 2505721). We are conducting genetic surveys in these streams to clarify the relationship between habitat characteristics and taxon diversity.

The benthic faunas of these streams are examined by high-throughput parallel sequencing of *cox1* amplicon (*cox1*: a mitochondrial gene coding for cytochrome *c* oxidase subunit 1) and morphological identification. Sampling was performed using a hand net with 200 mesh (aperture width: 0.12 mm) by kicking riverbed in February 2025. The survey site at Kibune Stream situated at an elevation of 382 m in the beginning of third order stream, while the survey site at Kumogahata Stream was located at an elevation of 233 m in fourth order stream. The two survey sites are separated by a ridge at an elevation of more than 600 m and are approximately 4.4 km apart.

Specimens passed through a sieve with an aperture of 2 mm were subjected to DNA metabarcoding analysis. Those trapped on the sieve (>2 mm) were stored in 99% ethanol at 4°C for morphological identification. Metabarcoding results of Ephemeroptera, Plecoptera, and Trichoptera have suggested habitat partitioning in several taxa.

Spatiotemporal dynamics of mosquito communities revealed by long-term monitoring in Slovenia

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Vladimir IVOVIĆ, Kevin REČNIK, Gašper GRUBELNIK, Miša KORVA, Nataša KNAP GAŠPER, Katarina RESMAN RUS, Katja POTOČNIK, Patricija POZVEK, Tomi TRILAR, Tatjana AVŠIČ ŽUPANC, Katja ADAM

Abstract

Mosquitoes (Diptera: Culicidae) are ecologically important components of freshwater-associated ecosystems and represent a key insect group for long-term biodiversity monitoring. Despite their relevance, systematic and spatially comprehensive data on mosquito community dynamics have historically been scarce in Slovenia.

We present results from a long-term, standardized mosquito monitoring programme conducted between 2019–2022 and continued in 2024–2025, covering the entire territory of Slovenia. During the initial nationwide phase, adult mosquitoes and larvae were sampled at 226 locations using a combination of standardized trapping and larval collection methods. Following this baseline survey, monitoring was continued at a reduced number of strategically selected core sites to maintain temporal continuity. Specimens were identified using morphological criteria, with selected taxa confirmed by molecular methods.

The results reveal pronounced seasonal and inter-annual dynamics in abundance and species composition, as well as marked spatial heterogeneity among sampling sites and landscape types. A small number of widespread native species dominated most locations, while temporal patterns and community composition varied across regions and years. These findings highlight the importance of multi-year monitoring for distinguishing consistent spatiotemporal dynamics from short-term fluctuations.

Our study demonstrates the value of combining an initial nationwide survey with continued monitoring at core sites as a robust and realistic framework for insect monitoring programmes. The presented dataset provides a solid baseline for assessing mosquito biodiversity and long-term spatiotemporal dynamics and contributes to broader insect biodiversity monitoring efforts in temperate Europe.

Metabarcoding of pollen carried by insect pollinators along altitudinal gradients in a protected area of Northern Italy.

Serena MAGAGNOLI (Department of Agricultural and Food Sciences (DISTAL-UNIBO), Serena.magagnoli4@unibo.it)

Daniele SOMMAGGIO, Laura ZAVATTA, Claudio RATTI, Riccardo BARONCELLI, Salvatore IACONO, Enrico VETTORAZZO, Giovanni BURGIO

Abstract

Insect pollinators are undergoing a rapid decline caused by multifaceted factors. Among these, ongoing global climatic change play a major role, particularly in natural habitats located in alpine and subalpine regions, where its impact is especially severe. Plant-pollinator networks are typically based on visual assessment of pollinators on plants. However, in recent years, molecular approaches have been highlighted as a potential alternative method for constructing pollen-carriage.

In this study, we evaluated plant-pollinator interactions using metabarcoding analysis of pollen collected from the bodies of insect pollinators sampled along an altitudinal gradient in the Dolomiti Bellunesi National Park (Northeastern Italy).

Insect pollinators were collected from flowers along transects located at three different altitudes (800, 1600 and 2200) surveyed monthly. Pollen samples, obtained by washing the insects, were then subjected to DNA extraction, amplification, and sequencing. Representative sequences of each amplicon sequence variant (ASV) were assigned taxonomically using a reference database, permitting identification to the highest level of taxonomic resolution supported by the data.

In total, we analyzed 87 insect specimens belonging to three orders: Hymenoptera, Diptera and Coleoptera. Pollen composition was highly variable among individuals, with 77 plant genera from 28 families identified. However, some botanical families (e.g., Solanaceae) and genera (e.g., *Ranunculus*) were consistently well represented across samples. Interestingly, we also detected pollen from anemophilous plants (e.g., Poaceae) on both Hymenoptera and Diptera taxa.

Plant-pollinator networks showed a shift in community composition, with Hymenoptera being more represented at lower elevations, while Diptera was the most represented taxon at higher altitudes.

These results highlight the potential of this method for examining plant-pollinator interactions and, at the same time, for gaining a deeper understanding of relationships that are typically difficult to assess visually.

Epicauta chinensis Laporte (Coleoptera:Meloidae), a new alien species in south of Romania

Traian MANOLE (Research-Development Institute for Plant Protection, Traian.manole@gmail.com)

Abstract

Epicauta chinensis Laporte, one of the blister beetle species had found in July c.y. feeding in a little alfalfa crop cultivated mixed with grapes, blackberry and raspberry. Later some other adults had been found in an experimental crop of soybean in experimental field of Research-Development Institute for Plant Protection, Bucharest. In Europe, the Meloidae family (blister beetles) includes several genera and numerous species. In Romania two blister beetle species are present, *Epicauta rufidorsum* Goeze and *Epicauta erythrocephala* Pall. The researches and the study of the new species are carried out beginning with the first collection of the adult from both crop invaded and in the laboratory were identified the species and the activity in the field of the adult (level of plant consumption, which part of plants are preferred). Further studies are necessary to establish the level of damages, the crops attacked, the distribution of the species in Romania after the risk impact analysis

Insect biodiversity in vineyard under organic and integrated management: a multi-year analysis and the role of the Typhlocybae microbiome

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Gonella ELENA, Alberto ALMA

Abstract

Understanding insect biodiversity in vineyard agroecosystems is essential to maintain ecological stability and ensure resilient and sustainable agricultural production. In northern Italy, mandatory applications of insecticides against *Scaphoideus titanus*, vector of Flavescence dorée phytoplasma, exert considerable pressure not only on target species, but also on non-target groups such as Typhlocybae leafhoppers. These insects, although being able of impacting grapevine production locally, are not involved in FD transmission. Establishing complex multi-species communities, they represent an interesting model for assessing the impact of pesticides on species distribution. Additionally, the bacterial microbiome associated with different Typhlocybae species was investigated, in view of its role, recognized as fundamental to understanding host physiology and ecological adaptations. Data on insect occurrence were collected by using yellow sticky traps from ten vineyards located in the Piedmont region in Italy, equally distributed between organic and integrated management. Monitoring was conducted from April to October for two consecutive years. Insect counts from traps specifically focused on Typhlocybae; however, other insects were also monitored, including other sap-feeding Auchenorrhyncha and natural enemies such as chrysops, ladybugs, hoverflies and mimarids. Differences were highlighted in the Typhlocybae species distribution between organic vineyards and those under IPM, especially in the case of *Arboridia kakogawana*, an exotic insect that, showed a greater abundance under integrated management. The stability of the agroecosystem and the impact of environmental factors on species abundance were assessed. The microbiome of collected Typhlocybae was investigated, and differences were found among species in the presence of bacteria. This provided new insights on how insects respond to the pressure exerted by insecticides in vineyard agroecosystems, contributing to a broader understanding of insect dynamics in cultivated areas characterized by high chemical inputs.

Native parasitoids regulating the alien invasive leafminer *Aspilanta oinophylla* in vineyards of southern Switzerland

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Antonio VIOLANTE

Abstract

Aspilanta oinophylla is a leaf-mining moth native to North America that has recently established in Europe, first detected in Italy in 2007 and in the Swiss canton of Ticino in 2019. In Ticino, the species completes two generations per year, with larval feeding producing characteristic circular mines and perforated foliar lobules. Although no yield losses have yet been recorded in Ticino, severe infestations in Italian vineyards can substantially reduce the photosynthetically active leaf area, leading to declines in grape quality and wine characteristics. As observed with the earlier alien leafminer *Phyllocnistis vitigenella*, native generalist parasitoids may contribute substantially to natural control, and similar recruitment is expected for *A. oinophylla*.

Over three years, we investigated interactions between *A. oinophylla* and native parasitoids across twelve vineyards representing Ticino's environmental and management gradients. We combined phenology monitoring via pheromone trapping, field damage assessments, and laboratory rearing of mined leaves to quantify parasitoid emergence and identify species composition. Several parasitoid species, both previously known and newly recorded taxa, were found to attack *A. oinophylla*. Their abundance and diversity vary markedly along a south–north gradient, likely reflecting the pest's invasion pathway.

By linking parasitism, pest pressure, and damage severity with environmental, landscape, and management variables, we identify key drivers shaping these interactions. Our findings support the development of habitat-management strategies that enhance the diversity and effectiveness of native parasitoids, reinforcing natural regulation processes and contributing to low-risk, sustainable viticulture before significant yield losses occur.

Albanian Chrysomelidae (Coleoptera): new faunistic records, DNA barcode library and redescription of *Luperus flaviceps*

Matteo MONTAGNA (University of Naples Federico II, Matteo.montagna@unina.it)

Paola COSTAGLIOLA, Alevtina ANDREEVA, Marilù CARDINALE, Matteo BRUNETTI, Giulia MAGOGA

Abstract

Some Balkan countries, including Albania, are among the least-studied regions in Europe with respect to Chrysomelidae, particularly over the last decades. This study aims to contribute new data to the knowledge of the Albanian Chrysomelidae fauna. Specifically, it aims to: (i) provide new information on the distribution of Chrysomelidae species within the country; (ii) develop a reference library of DNA barcode sequences for the molecular identification of Albanian Chrysomelidae; and (iii) redescribe *Luperus flaviceps* Apfelbeck, 1912, a rare Chrysomelidae species found in Albania whose original description is brief and lacks some key diagnostic characters. Chrysomelidae were collected from multiple localities in central and southern Albania. As a result, 12 Chrysomelidae species are reported for the first time from Albania, together with three additional taxa that likely represent species new to science. Furthermore, updated distributional data for 81 species within the country are provided. A total of 71 DNA barcode sequences representing 57 species were generated; they constitute the only publicly available barcode sequences for Albanian Chrysomelidae, and eight represent new taxa records for public reference databases. The redescription of *L. flaviceps* is provided, including high-quality photographs of both males and females, as well as a detailed description and illustration of the aedeagus morphology, which was previously unknown. The results here presented emphasize the need for further investigations of Albanian Chrysomelidae to improve understanding of their diversity within the country.

TAXONOMIC DIVERSITY AND FUNCTIONAL TRAITS OF WINGED INSECTS ALONG AN ALTITUDINAL GRADIENT OF THE FOGGY FOREST IN CHICAQUE NATURAL PARK (CUNDINAMARCA, COLOMBIA)

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Marlene Lucia AGUILAR BENAVIDES

Abstract

In Colombia, the foggy forest provides many ecosystem services with high impact ecological and economic, among them, the water recharge of 30% of the river basins, provides organic matter and capture the carbon, moreover, its great cultural contribution is demonstrated by high levels of endemism and speciation. However, for the country and the world, these ecosystems have been destroyed and transformed by changes in land use, threatening its prevalence and biodiversity. One of the groups that are most affected are insects, which fulfill key functions like as: pollination, biological control, nutrient recycling, among others. For that reason, this project evaluated the taxonomic and functional composition of winged insects in an altitude gradient (2000-2700m) in the Chicaque Natural Park (Cundinamarca Colombia), theses project was evaluated in two seasons of the year.

The collection methodologies used were the Malaise trap and Pantraps (yellow, blue, red, white and green) located in three altitudinal zones: Low (2060 m), medium (2250 m) and high (2660 m). with a sampling effort of 48h in each season. Were recollected 1662 individuals belong to Diptera (55%), Hemiptera (21%), Hymenoptera (8) and Coleoptera (7%), among others (9%). The Malaise trap captured 41% of individuals, while Pantraps recorded 59%. The yellow Pantrap being the one that collects the most individuals. The main feeding habits were identified as: phytophagous, hematophagous, saprophagous, coprophagous and predatory. Mainly associated with oral apparatuses of the following types: sucking-licking, sucking-lapping, piercing-sucking, chewing and chewing-licking. Preliminary results indicate that saprophagous, nectarivores and phytophagic are the most frequent organisms, exhibiting mouthparts such as sucking-lapping and linking-sucking, this highlighting their different ecological roles and importance. This work is funded by the VICEIN IMP-CIAS-4076 UMNG project.

#12544

Poster Session 1 - Ice breaker party
29/06/2026 at 16:00, Exhibition area

Scale-dependent landscape effects on whitefly natural enemies in southeastern U.S. agroecosystems

Sarah REZENDE (University of Georgia, Sarah.rezende@uga.edu)

Jason SCHMIDT

Abstract

Identifying the spatial scale at which composition influences natural enemies is critical for improving biological control of agricultural pests. In the southeastern United States, whiteflies (*Bemisia tabaci*) are a major pest in diversified vegetable and cotton production systems, yet the landscape determinants of their natural enemy communities remain poorly resolved. We are evaluating how landscape context shapes the abundance and diversity of natural enemies using a large regional dataset from 24 counties and 125 sampling sites collected with yellow stick cards. Abundance of parasitoid wasps and predatory flies (Dolichopodidae) is being quantified through direct counts, and diversity is being characterized using DNA metabarcoding of bulk samples extracted from the same stick cards. We focus on selected sampling dates corresponding to major crop turnover events to test whether landscape effects on natural enemies intensify during periods of agricultural change when resource availability and whitefly movement are likely to shift. Landscape composition is being quantified at multiple spatial extents surrounding each site to estimate the spatial scale at which landscape variables best explain variation in natural enemy abundance and diversity. By integrating morphological and molecular approaches, this study will advance understanding of landscape-scale regulation of whitefly natural enemies. Identifying the spatial scale of the strongest landscape influence will improve predictions of potential biological control in dynamic agricultural landscapes.

Acquiring New Ecological Niche Knowledge from High-resolution Habitat Suitability Models: A Case Study of *Laphria gibbosa* and *Laphria flava* in Latvia

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Dagmāra ČAKSTIŅA, Betija RUBENE, Ainārs AUNIŅŠ, Andris AVOTIŅŠ

Abstract

Knowledge of the ecology and biology of protected species is often incomplete or contradictory, partly because of their limited economic importance, which results in insufficient research funding. However, this information is crucial for targeted nature conservation. This research uses habitat suitability models to derive new ecological insights and to provide high-resolution species distribution maps for conservation planning.

The study focuses on two red-listed robber fly species occurring in Europe: *Laphria gibbosa* and *Laphria flava*. Although both species are generally considered to be associated with pine forests, some sources suggest that *L. flava* may also occur in mixed forests. In contrast, others indicate a stricter association with pine-dominated habitats. This raises the question of the species' actual ecological niche.

Maximum entropy analysis was used with identical sets of initial ecogeographical variables and a thorough variable selection and hyperparameter tuning procedure. Species presence data from a citizen science portal and an official nature data repository were used to develop the base models of both species in Latvia. Once species-specific distribution models were created, modelling was repeated with only variables present in the final model of at least one of the species. Species-specific distribution models can be used for conservation planning, while models with subselected variables were used for comparison of ecological niches.

Both species were positively associated with oligotrophic forests on undrained mineral soils, which are characteristic growing conditions of pine forests. Although the association with drained eutrophic forest was negative, this does not exclude the possibility of associating them with *Laphria*. The main differences between the species are related to tree edges, to which *L. gibbosa* was more strongly associated, as well as mesotrophic forests, which are more suitable for *L. flava*. These results support the conclusion that mixed forests are more suitable for *L. flava* than for *L. gibbosa*.

Population dynamics and habitat-associated occurrence of *Erasmoneura vulnerata* (Hemiptera: Cicadellidae) in vineyard agroecosystems

Ankica SARAJLIĆ (University, Sankica@fazos.hr)

Mato DRENJANČEVIĆ, Ivana MAJIĆ, Mirela VARGA, Helena EREŠ, Tatjana CVRKOVIĆ

Abstract

In recent decades, a continuous spread of newly emerging pest species has been documented across Europe, largely associated with environmental changes and contemporary agricultural practices. Approximately two decades ago, *Erasmoneura vulnerata* (Fitch, 1851) was first recorded in Europe and has since expanded to several countries. Adults and nymphs feed on grapevine leaf mesophyll, causing chlorotic damage and reduced photosynthetic activity, which at high densities may impair grapevine performance and grape quality.

The objective of this study was to assess the occurrence, spatial distribution and relative abundance of *E. vulnerata* in vineyards of eastern Croatia, and to evaluate differences in population density in relation to vineyard management practices and grapevine cultivars.

Field surveys were conducted in vineyards in the Ilok area (eastern Croatia) from June to September during 2023 and 2024. Monitoring was primarily designed to survey *Scaphoideus titanus* Ball, 1932, the principal vector of Grapevine Flavescence dorée phytoplasma, using yellow sticky traps. Five traps were deployed per vineyard, and six vineyards were included: four conventionally managed vineyards (Rhine Riesling, Graševina, Cabernet Franc), one unmanaged vineyard (Graševina (2003) and Frankovka (2004)), and one vineyard with American *Vitis* sp. rootstocks.

During sample processing, *E. vulnerata* was incidentally detected and subsequently identified. The results revealed pronounced interannual variation in population abundance, with a marked population increase recorded in 2024. Cultivar-related differences were observed, with Graševina and Rhine Riesling showing the lowest attractiveness, whereas Frankovka exhibited the highest infestation levels. Significantly higher population densities were recorded in the unmanaged vineyard compared to conventionally managed sites.

These results demonstrate the successful adaptation of *E. vulnerata* to the agroecological conditions of eastern Croatia, highlighting the importance of continued surveillance, long-term population monitoring, and further assessment of its potential economic impact and phytosanitary significance, particularly in relation to vineyard management practices and grapevine cultivar susceptibility within vineyard ecosystems.

Structure of leaf miner communities along an elevational gradient in eastern tropical Andes

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Leticia AVILES, Jill JANKOWSKI, Carlos LOPEZ-VAAMONDE, Diane SRIVASTAVA, Adriana SALVO

Abstract

Elevational gradients offer a unique opportunity for investigating patterns in species diversity, composition and distribution. Climatic variation across mountainous environments is expected to directly impact organisms by influencing their development, morphology and phenology; while also having an indirect effect through shifts in the strength of biotic interactions, such as herbivory and predation. This study uses mountains as natural laboratories to investigate how the community structure of leaf-mining insects, and their interactions with plants and parasitoid wasps, varies along a ~2,300 m elevational gradient in the tropical Andes of Ecuador. Leaf miners, endophytic insects that feed and live between the upper and lower leaf epidermis, serve as ideal models for testing the relative effects of abiotic and biotic factors on diversity patterns and trophic structure along environmental gradients. Their low mobility, specialized diets and high susceptibility to parasitoids, facilitate the quantitative estimates of leaf miner diversity and abundance and their associations with plants and parasitoids. An integrative approach, considering bottom-up effects (e.g., plant traits), top-down regulation (e.g., parasitism) and climatic variation, would provide a more comprehensive understanding of the mechanisms shaping these communities.

Arable land abandonment enhances ground beetles diversity and natural pest control

Silva VILUMETS (Chair of Plant Health, Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Silva.vilumets@emu.ee)

Riina KAASIK, Eve VEROMANN

Abstract

Ground beetles (Coleoptera: *Carabidae*) are widely used as bioindicators of land-use change due to their sensitivity to habitat structure, soil conditions, and management intensity. Nevertheless, responses of ground beetle communities to changes in arable land use are highly context dependent. Consequently, shifts in species composition can reflect underlying changes in ecological processes. In Europe, agricultural expansion continues in fertile soil areas, but farmland abandonment is becoming more widespread in regions with environmental or socioeconomic limits. Agricultural abandonment refers to a land-use change in which farming activities are discontinued and no active management is maintained. However, fundamental uncertainties remain about how biodiversity will respond to the end of agriculture, as the results may vary depending on regional conditions, soil qualities, and other abiotic and biotic factors.

The Horizon 2020 project FrameWork (2020-2025) case study investigated how land abandonment affects ground beetles abundance, species richness, and natural pest control rate in Estonian arable fields, with six clusters of abandoned, managed, and control areas. Abandoned fields had to be unmanaged for at least 5 years before the experiment began, whereas control fields were chosen so they were not surrounded by any natural or seminatural habitats. Pitfall traps were used to assess ground beetles abundance and species richness, and natural pest control was determined using sentinel prey.

Our case study revealed that natural pest control was considerably stronger in abandoned fields than in managed and control fields. The most common species included the polyphagous *Harpalus rufipes* (De Geer). Similarly, ground beetle's species richness varied among field types. Overall, our findings indicate that abandoned fields, through their higher pest control potential could represent essential habitat patches supporting key ecosystem services in agricultural landscapes.

Unveiling the hidden genetic diversity and broad distribution of paedogenetic gall midges of the genus *Heteropeza* (Diptera: Cecidomyiidae) in Japan

Fumito YANO (Kagoshima University, Yanof.2310@gmail.com)

Akihiro FURUKAWA, Mai SASAKI, Kazutaka OSAKI, Takuo SAWAHATA, Yoshifumi SO, Ayman ELSAYED, Makoto TOKUDA

Abstract

Insects represent one of the most species-rich and ecologically successful taxa in terrestrial ecosystems, yet a significant amount of undiscovered diversity remains. Within Cecidomyiidae (Diptera), recent integrative studies combining extensive sampling and DNA barcoding have revealed remarkable diversity, underscoring the need for further investigation.

Several mycophagous species of gall midges exhibit paedogenesis, a highly specialized reproductive strategy. In paedogenesis, ovaries develop within a “mother larva” or “mother hemipupa,” and offspring larvae are produced via ovoviviparous parthenogenesis. This unique strategy is known only in 11 species across eight genera of Cecidomyiidae and one Coleoptera species, and is evolutionarily intriguing and essential for understanding the diversity of Cecidomyiidae. These gall midges can switch their reproductive mode from paedogenesis to holometabolism under certain conditions.

In Japan, two paedogenetic gall midge species, *Heteropeza pygmaea* and *Mycophila speyeri*, were previously reported only in mushroom cultivation facilities, but our recent research confirmed the occurrence of paedogenetic species in natural environments. To clarify the distribution and genetic diversity of these gall midges, we conducted extensive sampling of decayed wood and branches across Japan and performed molecular analyses on collected larvae. Our study revealed that multiple lineages of the genus *Heteropeza* occur across a broad geographic range, from northern to southern Japan, and exhibit substantial genetic diversity. Morphological comparisons of female adults obtained by rearing further indicated variation in the number of tarsomeres, potentially linked to phylogenetic differences.

These findings suggest that numerous unrecorded paedogenetic gall midges likely inhabit natural environments globally, highlighting a considerable amount of hidden diversity. Future studies with larger sample sizes and integrative approaches will be essential to uncover additional lineages and clarify morphological variation among paedogenetic species, providing new insights into the evolutionary significance of this unique reproductive mode.

#11367

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Methodology and conservation methods of endangered butterfly species in Central Europe

Katerina VERISOVA (LIFEApollo2020, Katkaverisova@seznam.cz)

Oto PETRIK

Abstract

Methodology and conservation methods of endangered butterfly species in Central Europe

Butterfly species population are in steep decline in the last decades. In fragmented landscape of Central Europe, some species are now restricted to only a few sites with suitable habitats, often too distant to communicate and exchange genetic information. More than inbreeding, the destruction or/and degradation of their natural habitat poses as an immediate threat. In the Czech Nature Protectors Organization (CSOP), an intense work is being done both in the field – restoring and managing the remaining sites for endangered butterfly species – and behind the desk – proposing sustainable solutions to preserve habitats and stop the decline in butterfly populations.

In some species, their populations are already so small that they would likely go extinct before restoration works on the site would have been done. For this purpose, a breeding farm has been founded in the Czech Republic, breeding butterflies in thousands of specimens for each selected species, to strengthen their native populations and/or create metapopulations in suitable sites geographically close to the original one. The focus of our breeding farm now is on breeding of the Hermit (*Chazara briseis*), the Scarce Fritillary (*Euphydryas maturna*), the Spotted Fritillary (*Melitaea didyma*) and the Apollo (*Parnassius apollo*). Through years of intense work and cooperation with top-tier experts in the field, we try to set new methods of reproductive breeding of butterflies and discovering their needs for thriving in natural habitats.

Can knowing the future influence our decisions? The effect of the olfactory environment on patch exploitation strategies in the parasitoid *Venturia canescens*

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Séverine DEVERS, Emmanuel DESOUHANT, Isabelle AMAT, Miguel PIÑEIRUA

Abstract

The Marginal Value Theorem (MVT) was developed to predict the optimal time a forager should spend exploiting a patch of resources according to its quality and the travel time to other patches. This has been tested in numerous species, notably parasitoid wasps, and it is generally observed that females stay longer on patches rich in hosts. Furthermore, it is now well established that parasitoid wasps can use olfactory cues from the hosts themselves or from plants attacked by their hosts (i.e. herbivore-induced plant volatiles) to locate and assess the quality of host patches from a distance.

Here, we investigated the extent to which olfactory cues from distant host patches can influence the foraging strategies of females when exploiting a patch. We expected that females exposed to the odour of a high-quality patch would leave the current patch earlier than those exposed to the odour of a low-quality patch. Furthermore, we expected female responses to vary according to the quality of the current patch and the difference in quality compared to the distant patch. Females are likely to leave a patch even more quickly if the distant patch is of a much higher quality.

We tested these predictions using females of the parasitoid wasp *Venturia canescens*, which are known to respond to MVT predictions and to assess the quality of distant patches based on host odours. We therefore placed females individually in a patch containing either 0, 4, 8 or 16 hosts while exposing them to the odours of a distant patch containing either 0, 4, 8 or 16 hosts (full cross-design). We recorded the females' host exploitation behaviour and their patch residence time in each treatment. We discuss the extent to which information from the current host patch and from a potential future one influence female foraging strategies.

When pesticides mimic octopamine: consequences for aggression in a beneficial parasitoid species

Angèle NOURTIER (IRBI, UMR 7261 CNRS - Université de Tours, Angelenourtier15@gmail.com)

Charlotte LECUREUIL, Marlène GOUBAULT

Abstract

Accumulating evidence shows that insect behaviour is highly sensitive to environmental pollution. Insects display a high degree of behavioural plasticity, which is shaped by ecological and social contexts. However, this plasticity relies heavily on hormonal and neuroendocrine systems and disruption of these systems can lead to profound behavioural dysregulation. Among the neuroendocrine pathways that modulate behaviour, biogenic amines play a central role. In particular, octopamine (OA) contributes to the regulation of numerous behavioural processes, including aggressive behaviour, although its involvement can vary considerably between insect species.

Among the pollutants likely to disrupt these regulatory pathways, pesticides are of particular concern due to their widespread use and the unavoidable exposure of non-target insects at sublethal doses. The Formamidines, a family of pesticides, act specifically on the octopaminergic system, by being octopamine agonists, directly interacting with OA receptors. Several studies have shown that they induce behavioural changes at sublethal doses. Beneficial insects, including pollinators and natural enemies of pests, predators and parasitoids, are frequently exposed to these compound residues in both natural and agricultural habitats, making them especially relevant models for assessing the behavioural consequences of Formamidines.

In this context, we selected a model species in which aggressive behaviours are well described and essential during reproduction for securing access to hosts on which they lay their eggs and protecting them from competitors: the solitary parasitoid wasp, *Eupelmus vuilleti*, which attacks the food stock pest, *Callosobruchus maculatus*. We propose to investigate the effects of topical application of two widely used formamidines, Amitraz and Chlordimeform, on these aggressive interactions occurring during contest for oviposition sites. We also examine physiological responses such as gonadotropic effects, given that egg load directly influences aggressiveness in this species. This integrative approach aims to clarify how OA-disrupting pesticides affect both behavioural regulation and reproductive physiology in non-target beneficial insects.

Elucidating the Role of Floral and Herbivore-Induced Volatiles in *Maruca vitrata* Oviposition Behavior and Natural Enemy Attraction: Implications for Semiochemical-Based Pest Management in Cowpea (Vign

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Lord OSEI BONSU, Paul ADDAI, Sampson Jonah DZOTEFÉ

Abstract

Cowpea (*Vigna unguiculata*), a vital food legume in Africa, faces significant yield losses due to infestations by *Maruca vitrata*, whose larvae cause extensive damage to flowers, leaves, and pods. This study explores the role of cowpea floral volatiles in attracting ovipositing *M. vitrata* females and evaluates the potential of herbivore-induced plant volatiles (HIPVs) to deter pest activity while attracting natural enemies, specifically *Apanteles taragamae* and *Phanerotoma syleptae*. Oviposition assays confirmed a strong preference of *M. vitrata* for flowering cowpea plants. Through gas chromatography-electroantennographic detection (GC-EAG) and gas chromatography-mass spectrometry (GC-MS), five key floral volatiles, including benzaldehyde and (E)-cinnamaldehyde, were identified as influential in oviposition behavior. A synthetic blend incorporating 3-vinylbenzaldehyde successfully induced egg-laying on non-flowering plants, mimicking the response observed in flowering plants. Furthermore, *M. vitrata* moths exhibited a preference for intact plants over those previously infested. Analysis of HIPVs revealed that *M. vitrata* damaged cowpea plants emitted (E)-DMNT, indole, n-hexyl acetate, 1-octen-3-ol, and linalool, all of which demonstrated electrophysiological activity. A synthetic blend of 1-octen-3-ol and linalool significantly reduced oviposition rates. Y-tube olfactometer assays indicated that both *A. taragamae* and *Ph. syleptae* were attracted to synthetic (E)-DMNT, with *A. taragamae* also exhibiting a dose-dependent response to linalool and (E)-nerolidol. These findings establish a foundation for the development of semiochemical-based pest management strategies targeting *M. vitrata*, with promising applications for smallholder cowpea farming systems in West Africa.

Keywords: *Vigna unguiculata*, *Maruca vitrata*, Herbivore-induced plant volatiles, Natural enemies, Crop protection

Region-specific sexual communication patterns in the globally invasive pest *Spodoptera frugiperda*

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Abstract

In moths, sexual communication is primarily mediated through chemical signaling by sex pheromones. Geographic variation in female sex pheromone signals and male responses have been found in multiple moth species. As such geographic variation affects the reliability of detection and early monitoring of pest species, it is important to assess the level and extent of this variation in different regions. In the globally invasive fall armyworm, *Spodoptera frugiperda*, we previously found geographic variation in the relative ratio of the two major components: (Z)-9-tetradecenyl acetate (Z9-14:OAc) and (Z)-7-dodecenyl acetate (Z7-12:OAc) and male responsiveness to variable sex pheromone blends in different African populations. The recent establishment of *Spodoptera frugiperda* in Southern Europe now highlights the need for region-specific knowledge on female pheromone composition and male responses for effective monitoring and early detection in Europe. Within the EU-HORIZON project “EUFAWREADY” (Enhancing Europe's readiness for managing fall armyworm), we established a laboratory culture of *S. frugiperda* at the University of Amsterdam to determine region-specific sex pheromone ratios. In addition, we aim to identify and characterize possibly novel antennally-active sex pheromone compounds, using gas chromatography coupled with electroantennographic detection (GC-EAD), followed by GC-MS. In this presentation, we will give an overview of the regional variation in sex pheromone profiles and male responses to different pheromone lures that we found so far, focusing on Kenya, Nigeria and Benin. These experiments form the basis to assess regional variation in chemical communication and the effectiveness of pheromone-based monitoring systems in Europe.

#10188

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Pheromone mediated trapping and Management of the Oil palm beetle *Rhynchophorus phoenicis*

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Isona GOLD, Victor ADAIGBE, Daniel ESIEGBUYA, Billy GHANSAH

Abstract

Field trials were conducted at Okomu oil palm field to detect and trap *Rhynchophorus phoenicis* through use of 3-litre bucket traps containing 9mg/day *Rhynchophorus phoenicis* pheromone, impregnated with 20ml insecticide (Cypermethrin) and a control bucket (300ml water). The bucket traps were attached directly to palm fronds. A plantation wide strategy was used at 2 traps per 25 hectares for a total of 8,500 hectares. Bucket traps (2) were attached directly on palm fronds. Observations were made once a week for 12 weeks after pheromone application. In the pre-pheromone assessment survey, fields H, I and G were observed to have been most attacked by *Rhynchophorus phoenicis*. Observations were made once a week for 6 weeks after pheromone application. During the pheromone treatment period under review, adult *Rhynchophorus phoenicis* trapped were a total of 915. Week 7 had the highest number (164) of trapped insects, while week 12 had the lowest trapped insects (17). The control trap without pheromone caught nothing. The P-value of the analysis of variance (0.0000378) indicates that there is a significant difference ($P < 0.05$) among the fields in the number of adult *R. phoenicis* collected due to the pheromone treatment. It was observed that fields G and H had the highest distribution of *R. phoenicis*. This implies that more attention should be paid to these fields. This study confirms the effectiveness of the pheromone for sustainable control of the adult *Rhynchophorus phoenicis* with minimal insecticidal use, and benefit to human and environmental safety.

#10867

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Two olfactory receptors exhibit overlapping tuning breadth in *Spodoptera littoralis*

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Emy CAVICCHI, Marie Christine FRANÇOIS, Sridevi BHAMIDIPATI, Nicolas MONTAGNÉ, Emmanuelle JACQUIN-JOLY, Arthur DE FOUCHIER, Camille MESLIN

Abstract

Olfaction plays a crucial role at the interface between an insect and its environment. Odorant receptors (ORs) are expressed at the membrane of olfactory neurons where they detect odorant cues. To be able to perceive all the odors that are relevant to their ecological niches, each insect species evolved its own repertoire of ORs through gene duplication events and functional divergence. In the polyphagous moth *Spodoptera littoralis*, two odorant receptors (OR24 and OR36) exhibit broad and overlapping tuning breadth despite their highly divergent sequences at the amino acid level. To investigate the molecular basis of this functional convergence, we combined in silico and in vitro approaches. Molecular docking analyses identified two key amino acids within each receptor that could be involved in odorant binding. The positions of these residues are homologous in the 3D structure of both receptors. Site-directed mutagenesis confirmed that substituting these positions affected odor detection, confirming their crucial role in ligand recognition. Our findings show that, despite evolutionary divergence, OR24 and OR36 share key positions in the ligand-binding pocket, highlighting the importance of positional hotspots for the receptors function and providing new insights into the molecular basis of odorant receptor function.

Chemical ecology of host alternation in aphids: insights into plant cues associated with nutritional polyphenism

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Rituparna GHOSH, Maxime BARBERON, Aurélie ETIER, Jean-Christophe SIMON

Abstract

Aphids display striking phenotypic plasticity that enables them to persist across fluctuating seasons, crowding, and dietary conditions. Among the best examples of this plasticity is polyphenism, where alternative morphs are produced in response to external cues. The bird cherry–oat aphid, *Rhopalosiphum padi*, exhibits nutritional polyphenism linked to its seasonal host alternation between the primary woody host *Prunus padus* in winter and numerous secondary hosts among Poaceae in summer. This alternation is mediated by specialized migrant morphs, yet the cues governing their induction remain poorly resolved. Previous work in our laboratory demonstrated that leaf age of the primary host is a critical factor: larvae feeding on young *P. padus* leaves develop into wingless morphs that remain on the tree, whereas larvae feeding on mature leaves produce winged emigrants that disperse to secondary hosts.

To investigate the cues from the primary host that trigger migrant development, we focus on gustatory and volatile cues that may regulate this developmental decision. Phloem analyses revealed that as *P. padus* leaves mature, phloem sugar concentrations increase while amino acids decline. In contrast, secondary hosts in the Poaceae typically contain higher amino acid levels than mature *P. padus* leaves. Using a combination of stylectomy, metabolomics and behavioral assays, we are currently testing the hypothesis that the combination of reduced amino acids and elevated sugars in mature leaves acts as a gustatory signal promoting the development of migrant morphs.

In parallel, we are characterizing volatile organic compounds emitted by primary and secondary hosts to identify chemical cues that may function as repellents from *P. padus* or attractants toward Poaceae. Together, these analyses aim to clarify how changing nutritional and volatile landscapes guide morph induction and host alternation in *R. padi*, providing insights into the chemical basis of aphid polyphenism and seasonal migration.

Assessing the impact of bacterial strain variation in human attractiveness to mosquitoes

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Yulisa MORENO-PATÍÑO

Abstract

Mosquitoes depend strongly on volatile organic compounds (VOCs) emitted in body odours to locate suitable blood-hosts. These VOCs allow them to discriminate between host species and even between individuals at a distance. Most VOCs in human body odours are produced by microorganisms present on the skin. Previous work has identified correlations between mosquito attraction and skin bacterial communities. Several bacterial species have been implicated as enhancers or suppressors of mosquito attraction. However, behavioural validation studies typically test only a single representative strain per bacterial species, assuming species-level uniformity.

Strain-level variation is not a trivial detail: a single bacterial identifier can represent multiple, physiologically distinct strains. Different strains of the same species typically have 80%–90% of their genes in common. These genomic differences between strains are known to include important biological functions and recent studies have shown that bacterial strains belonging to the same species can emit different volatile compounds when grown under identical conditions. This is known to have consequences for the degree of attractiveness or repellence towards insects.

In this project, we systematically assess mosquito attraction across a diverse panel of human-associated bacterial strains to disentangle species- and strain-level contributions to host attractiveness. Using isolates obtained from the DSMZ biobank, we assembled a panel maximising intraspecific diversity across eight skin-associated bacterial species previously linked to mosquito behaviour. Bacteria are cultured under standardised conditions and presented to mosquitoes in a custom two-choice video-tracking arena, enabling quantification of behavioural attraction metrics. In parallel, headspace VOCs from selected strains are collected for chemical profiling (GC–MS). Together, the outcomes will provide systematic evidence of how much intraspecific bacterial variation contributes to host odours, attractiveness and will clarify whether studies focusing only on species-level comparisons risk overlooking critical strain-level effects.

The Scent of Growing Up: Dynamic Larval Profiles in a Beetle With Parental Care

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Abstract

Chemical communication plays a central role in social interactions among insects, but most research has focused on adults. This gap is particularly relevant in species that exhibit parental care. Chemical signals emitted by larvae can influence parental behavior. Previous studies in other insect species have suggested that maternal feeding responses can be modulated by larval odor, but the chemical identity of these signals remains largely unknown. In this study, we investigated the chemical profiles of larvae of *Nicrophorus*, a genus of burying beetles known for their complex biparental care. Larvae from different species and developmental stages vary in their dependence on parental provisioning. We collected first, second, and third instar larvae (L1, L2 and L3) and performed their surface hexane extractions to obtain cuticular compounds. Using gas chromatography mass spectrometry (GC-MS), we detected a diverse range of on their surface cuticular hydrocarbons and lipids. Notably, we observed differences between all species, indicating changes in chemical profiles. These findings provide fundamental evidence that *Nicrophorus* larvae produce chemical mixtures that change throughout development, supporting the hypothesis that such signals may mediate interactions between larvae and parents. Our study contributes to a broader understanding of the role of larval chemical communication in the evolution from subsocial to social insects and points out the importance of examining multiple life stages to fully grasp the dynamics of parent offspring interactions. Our results underscore that larval chemical profiles are dynamic across development. This points out the importance of examining multiple life stages to fully grasp the dynamics of parent offspring interactions. In general, our study contributes to a broader understanding of the role of larval chemical communication in the evolution from subsocial to social insects.

Chemical mating disruption to control *Cacopsylla pyri* L. (Hemiptera: Psyllidae): study of the pheromone activity of four cuticular hydrocarbons

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Abstract

The pear psylla, *Cacopsylla pyri* L. (Hemiptera: Psyllidae), is known in Europe for its extended infestation, which may cause heavy economic losses to most pear-growing regions, such as Spain and Italy. Plant damage is caused by the feeding activity of nymphs and adults, which leads to necrosis of leaf and fruit tissues, and by the abundant honeydew excretion produced by the nymphs, which promotes the development of sooty mold, ultimately reducing fruit quality and market value. The emergence of resistance to the chemicals used to control this species, combined with the withdrawal of key insecticides from the European market, highlights the urgent need for alternative control methods. Among the more sustainable and innovative approaches currently under evaluation, mating disruption based on pheromone-mediated sexual confusion has emerged as a promising strategy for pest control. In *C. pyri*, mate selection relies partly on female-produced volatile cues that enable males to locate and recognize their potential partners. Chemical communication plays a central role in the courtship system of many insects: while moth species use long-range, highly volatile sex pheromones, psyllids mainly rely on low-volatility cuticular hydrocarbons that operate at short ranges. Over the past two decades, efforts to characterize pear psylla semiochemicals have primarily focused on methyl-branched compounds that function as contact pheromones. This study investigated the behavioral and electrophysiological responses of summer and overwintering males of *C. pyri* to four synthetic hydrocarbons previously identified in female cuticular extracts (11,15-dimethylheptacosane, 13-methylheptacosane, 3-methylheptacosane, and 2-methylheptacosane). Using Y-tube olfactometry and electroantennography, we evaluated the attraction across multiple concentrations of compounds, assessing the potential sensory saturation to perform semi-field bioassays in the Potter tower with the selected doses and outline the preliminary steps to develop a mating disruption technique for this species.

Indirect pesticide exposure through woolly apple aphid honeydew on the parasitoid *Aphelinus mali*

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Sonia PANIZZA, Martina FALAGIARDA, Andrea LENTOLA, Andrea RIVELLI, Urban SPITALER

Abstract

The woolly apple aphid (*Eriosoma lanigerum*) is a widespread pest in apple orchards, causing substantial economic damage. Its primary natural enemy is *Aphelinus mali*, a parasitoid wasp that plays a key role in regulating aphid populations in apple orchards. Like other natural enemies, *A. mali* feeds on aphid produced honeydew, which may serve as an indirect route of pesticide exposure and can threaten beneficial insects not only through direct contact but also via contaminated food sources.

We aimed to determine whether pesticide residues are transported from the plants to aphid honeydew following pesticide treatments and assess their potential effects on the survival of *A. mali*.

Four pesticides with distinct active ingredients and properties were applied to potted apple trees: acetamiprid, azadirachtin, flonicamid, and tau-fluvalinate. Honeydew and entire aphids were subsequently collected and analyzed via tandem Mass Spectrometry (LC-MS/MS) to detect the presence of the active substances and their degradation products. In laboratory assays, *A. mali* adults were fed with sugar solutions containing concentrations of the pesticides corresponding to those found in the honeydew, in order to evaluate potential effects on their survival.

Chemical analyses detected flonicamid residues in aphids and in their honeydew. Additionally, laboratory trials showed that *A. mali* survival was significantly reduced when exposed to pesticide contaminated solutions, with a significant decline in survival.

This result confirms that pesticide residues can be present in aphid honeydew and that even indirect exposure through feeding may significantly impact the survival of key natural enemies like *A. mali*. These findings highlight the importance of evaluating the impact of pesticide exposure through honeydew contamination on parasitoids and underscore the need for detailed information on pesticide effects and persistence to preserve beneficial insect populations within integrated pest management systems.

Toward a better understanding of the role of olfaction in the foraging ecology of carabids

Pierre GENDRON (UMR IGEPP - team EGI, Pierre.gendron@agrocampus-ouest.fr)

Camille FABER, Sylvia ANTON, Olivier FALOYA, Yann TRICAULT, Bruno JALOUX, Anne-Marie CORTESERO, Benjamin CARBONNE

Abstract

Carabid beetles are widely recognized as effective biocontrol agents of crop pests and weed seeds. Yet, their trophic ecology remains insufficiently understood, particularly regarding interspecific variation in diet range and prey preferences along the carnivory–granivory gradient. The mechanisms enabling carabids to respond to changes in prey availability - potentially driving switches between agronomically relevant prey and alternative resources - also remain unclear. We hypothesize that carabid trophic behaviour also relies on the perception of resource-derived odours as a key mechanism governing prey choice, prey location, and switches in resource use. This study therefore examines the perception and attractiveness of resource-derived odours to carabid beetles.

We first assessed the olfactory sensitivity of ten carabid species using electroantennography (EAG). Species were selected to span a presumed gradient from granivory to carnivory. Antennal responses were recorded for seven potential prey resources, including four weed seed species (*Viola arvensis*, *Taraxacum officinale*, *Chenopodium album*, *Capsella bursa-pastoris*), one collembolan species (*Folsomia candida*), one aphid species (*Sitobion avenae*), as well as several synthetic VOCs (the aphid alarm pheromone: (E)- β -farnesene, a collembola aggregation pheromone: (Z)-11-hexadecenoic acid, and a HIPV: Dimethyl Disulfide). Subsequently, behavioural assays using olfactometry were conducted on a subset of species to assess whether odours triggering antennal responses in EAG also led to attraction or avoidance behaviours.

Overall, our findings support the hypothesis that olfaction contributes to food-resource perception in carabids and may constitute a key mechanism underlying variation in their foraging strategies. However, further work is required to determine whether behavioural responses are driven by specific compounds or by volatile blends, and to clarify how odour perception influences movement trajectories and prey selection in these predators.

Application of Mating Disruption for *Rusicada privata*, a Major Pest of *Hibiscus syriacus* in Urban Forests

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Eunji YU

Abstract

Rusicada privata (Lepidoptera: Erebidae) are one of the major lepidopteran pests of *Hybiscus syriacus* (Malvaceae; Malvales), a common ornamental tree planted in urban landscapes in Korea. To facilitate control using mating disruption (MD) method, forecasting seasonal occurrence of *R. privata* was considered essential. Therefore, the occurrence of this species was monitored in Suwon for one year using its sex pheromone, 7-mehtyl-heptadecane. The moth exhibited two flight peaks; the first from early May to late May and the second from late August to late October. Field experiments evaluating of MD against *R. privata* were conducted over a three-year period in Suwon and for one year in Sejong. The applied amount of MD was 35g/0.4 ha per application. The MD application was conducted three times in the first year (late April, early July, and mid-September); twice in the second and third years (late April and late July) in Suwon; and once in late July in Sejong. Male catch inhibition by MD ranged from 82.1 to 100% in Suwon and 100% in Sejong, and control efficacy, calculated based on leave damage, ranged from 61.8 to 74.7% in Suwon. These results suggest that the use of MD can effectively protect *H. syriacus* in urban forests by suppressing populations of *R. privata*. In addition, the adoption of this technique is expected to enhance public safety by reducing reliance on conventional chemical insecticides.

A repellent plant to regulate sap-feeders: Testing the continuum trait-function-service from the lab to the field

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Abstract

In the context of agroecological transition, enhancing plant functional diversity is a key strategy to provide multiple ecosystem services, including soil fertility, pollination, biodiversity conservation, and pest regulation. Biocontrol plants—species intentionally introduced in an agrosystem to regulate pest populations—can act through direct or indirect (i.e. through an intermediate organisms) mechanisms. Among them repellent plants help deterring pest and are one of the element of a potential push-pull systems. Among them, *Tagetes* spp. have been identified as promising candidate to deter sap-feeding insects. Yet, their efficacy must be validated across scales, from laboratory assays to field applications, following the trait–function–service continuum.

We conducted a series of experiments to assess the biocontrol potential of *Tagetes* spp. Laboratory trials confirmed that three species limited whiteflies settlement and oviposition on tomato plants through both physical barriers and repellent olfactory cues (traits driving function). In greenhouse experiments, intercropping tomatoes with *Tagetes minuta* reduced whitefly populations over time, demonstrating a clear ecosystem service. Finally, field trials in pepper crops under tunnel conditions revealed that *Tagetes erecta* significantly decreased pest abundance and taxonomic richness when intercropped.

Together, these findings highlight the capacity of marigolds to function as effective biocontrol plants, reducing airborne pest pressure in vegetable systems. This work underscores the importance of integrating plant trait-based approaches into agroecological strategies for sustainable pest management.

Signalling or surviving? Insect cuticular hydrocarbons and same-sex sexual behaviour under heat stress

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Johannes STÖKL, Nathan BAILEY, Sandra STEIGER, Natalie PILAKOUTA

Abstract

Chemical communication is increasingly disrupted by climate change-associated stressors, with cascading consequences from individuals to ecosystems. Insects are particularly vulnerable because they rely heavily on olfactory signals which are sensitive to environmental variation. Among these signals, cuticular hydrocarbons (CHCs) are of special interest due to their multifunctional nature: they convey information about sex, species identity, and breeding status while providing protection against thermal stress. Empirical evidence suggests a trade-off between the signalling and waterproofing functions of CHCs, indicating that heat-induced changes in CHC profiles may alter behavioural and reproductive outcomes. We investigated this trade-off in the subsocial burying beetle *Nicrophorus vespilloides*, whose reproduction depends on effective parental care enabled by reliable chemical communication. We experimentally tested the effects of heat stress on the frequency of same-sex sexual behaviour by examining male-male interactions and associated cuticular hydrocarbon profiles. Male beetles were individually exposed to either benign temperatures (20°C) or a simulated 3-day heatwave (26°C). They were then paired and their mounting frequency recorded using focal sampling, after which cuticular compounds were analysed using gas chromatography-mass spectrometry. Based on the hypothesis that same-sex sexual behaviour arises from recognition errors, we predict a shift in cuticular hydrocarbon composition under heat stress, leading to an increase in male-male mounting. If sex recognition errors increase under thermal stress, the presumed fitness costs to males exhibiting same-sex sexual behaviour are also expected to rise. Overall, this study aims to advance knowledge of mating interactions in insects and highlight how thermal stress may interfere with chemical communication.

Skin microbes, volatiles, and vector behaviour: A strain-level perspective

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Niels O. VERHULST, Dani LUCAS-BARBOSA, Mitchel E. BOURNE

Abstract

Mosquitoes depend strongly on volatile organic compounds (VOCs) emitted in body odours to locate suitable blood-hosts. These VOCs allow them to discriminate between host species and even between individuals at a distance. Most VOCs in human body odours are produced by microorganisms present on the skin. Previous work has identified correlations between mosquito attraction and skin bacterial communities. Several bacterial species have been implicated as enhancers or suppressors of mosquito attraction. However, behavioural validation studies typically test only a single representative strain per bacterial species, assuming species-level uniformity. Different strains of the same bacterial species typically share 80%–90% of their genes. Still, genomic differences between strains are known to include important biological functions, and recent studies have shown that strains belonging to the same species can emit different VOCs when grown under identical conditions. This is known to have consequences for the degree of attractiveness or repellence towards insects.

In this project, we systematically assess mosquito attraction across a diverse panel of human-associated bacterial strains to disentangle species- and strain-level contributions to host attractiveness. Using isolates obtained from the DSMZ biobank, we assemble a panel maximising intraspecific diversity across eight skin-associated bacterial species previously linked to mosquito behaviour. Bacteria are cultured under standardised conditions and presented to mosquitoes in a custom two-choice video-tracking arena, enabling quantification of behavioural attraction metrics. In parallel, headspace VOCs from all strains are collected for chemical profiling (GC–MS). Together, the outcomes will provide systematic evidence of how much intraspecific bacterial variation contributes to host odours, attractiveness and will clarify whether studies focusing only on species-level comparisons risk overlooking critical strain-level effects.

Preliminary behavioural and chemical results will be presented, providing first insights into variation in mosquito attraction and VOC profiles among human-associated bacterial strains.

Chemical Characterisation of Fly Species Used by Wild Chimpanzees during Wound Care

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Harshith GURUSWAMY

Abstract

While medicative behaviours are widespread across the animal kingdom, no animal has been documented using another animal in wound care. However, recently, Central chimpanzees (*Pan troglodytes troglodytes*) have been observed deliberately catching flying insects and placing them onto their own or conspecifics' open wounds. This novel behaviour raises questions about the chemical ecology of synanthropic flying insects and their potential role as reservoirs of bioactive compounds. It also questions whether the chimpanzees benefit from the insects properties. Since direct experimental testing of wound-healing effects in chimpanzees is not ethically feasible, we combined bioassay-based assessments of antimicrobial activity with chemical analyses to identify insect-derived compounds potentially underlying this wound care behaviour. Initial antibacterial assays revealed growth-inhibiting effects of insect extracts. To identify candidate compounds, we conducted gas chromatography–mass spectrometry (GC/MS) and liquid chromatography–mass spectrometry (LC/MS) analyses of both the insect's cuticular surfaces and whole-body extracts.

Cuticular hydrocarbon profiles showed species-specific chemical signatures, validated by morphological identification, enabling chemotaxonomic species identification. Notably, we detected compounds present exclusively in specific sympatric flying insect species observed to be used in wound application and absent from closely co-occurring species not involved in the behaviour. In parallel, fragmenting the plethora of compounds into groups based on their chemical properties helped to further narrow down candidate antibacterial substances.

In conclusion, this work bridges primatological and entomological research questions, providing a mechanistic framework for evaluating insect-based wound care behaviour in non-human primates. More broadly, it also highlights insects as a source of potential antimicrobial compounds.

Field and transcriptomic evaluation of herbivore-induced plant volatiles for sustainable citrus aphid management

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Abstract

Activation of plant defenses through exposure to defense-eliciting herbivore-induced plant volatiles (HIPVs) represents a promising sustainable strategy for pest management in citrus production systems. During three years, we evaluated the efficacy of the green leaf volatile (Z)-3-hexenyl propionate (Z-3-HP), in reducing populations of the citrus aphid *Aphis spiraecola* across three commercial citrus orchards in eastern Spain. In each orchard, a randomized block design with four replicates per treatment was applied, where exposure to (Z)-3-HP (through polyethylene dispensers) was compared with a control treatment without exposure. Biweekly monitoring consistently showed ~50% reductions in *A. spiraecola* densities in plots exposed to (Z)-3-HP compared to unexposed controls. A higher presence of natural enemies, including chrysopids, coccinellids, and coenobitids, was recorded in the (Z)-3-HP exposure treatment. Transcriptomic analyses of aphids feeding on exposed versus unexposed plants revealed extensive reprogramming of gene expression. Detoxification- and stress-related pathways (e.g., glutathione metabolism, amino acid metabolism, ribosome biogenesis) were activated, indicating increased physiological costs. In contrast, key metabolic and signaling routes (starch and sucrose metabolism, arginine metabolism, glutamate metabolism, immune signaling) were suppressed. These transcriptomic shifts indicate that defense-eliciting volatiles increase stress costs while impairing key metabolic and immune functions in *A. spiraecola*, ultimately reducing fitness. Overall, our results demonstrate that harnessing induced defenses can contribute to sustainable citrus protection by reducing dependence on synthetic insecticides, enhancing the activity of natural enemies, and improving pest management balance. While (Z)-3-HP served as an anoded compound in this study, the broader concept of defense induction represents a promising frontier for the development of innovative integrated pest management strategies.

Repellent potential of clove and lemongrass essential oils against *Halyomorpha halys* (Hemiptera: Pentatomidae)

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Darija LEMIC, Martina PAJAC BEUS, Helena VIRIC GASPARIC, Marko VINCEKOVIĆ, Višnja STEPANIC, Dalibor HRŠAK

Abstract

The brown marmorated stink bug (*Halyomorpha halys* Stål, 1855) is a highly invasive and polyphagous pest for which environmentally acceptable management options remain limited, motivating interest in plant-derived volatiles as behavior-modifying tools. We assessed olfactory-mediated orientation of adult *H. halys* to clove and lemongrass essential oils using a Y-tube olfactometer, in which individuals choose between two airflow-separated odor sources under controlled conditions (25 ± 1 °C, $65 \pm 5\%$ RH, 16:8 L:D; 5-min observation). Essential oils were microencapsulated in an alginate-based biopolymer matrix to ensure standardized volatile release. In total, 240 adults were tested (30 females and 30 males per treatment across three independent replicates) in dual-choice assays comparing oil treatments (single oils or their blend) against an identical blank matrix control or, alternatively, against another oil. In treatment–control comparisons, adults consistently preferred the control arm (clove: 6/60 vs 42/60; lemongrass: 2/60 vs 39/60; blend: 4/60 vs 38/60), indicating pronounced avoidance/repellent responses to microencapsulated oils under these conditions, with a moderate proportion of non-responders. Direct oil–oil comparisons were equivocal overall (lemongrass 20 vs clove 19 among responding individuals), with only weak sex-dependent tendencies, supporting the interpretation that the dominant behavioral effect was repellency relative to the control rather than differential attraction between oils. Additionally, the results were analyzed in terms of the chemical composition of essential oils using LOTUS data.

This work was supported by the Croatian Science Foundation (project LAIDYGRID, IP-2025-02-7105) and partially funded by the University of Zagreb Faculty of Agriculture through the institutional project DEMO IPM.

Essential Oils and Beneficial Predators: Evaluating Their Compatibility in IPM Strategies

Rosenthal Pereira Lima MARINA (INRAE - Sophia Antipolis, Marina.rosenthal-pereira-lima@inrae.fr)

Abstract

Botanical pesticides, particularly essential oils (EOs), are increasingly investigated as sustainable alternatives to synthetic insecticides within Integrated Pest Management (IPM). Their natural origin, rapid degradation and broad bioactivity make them promising candidates for reducing reliance on synthetic chemicals. However, despite their perceived safety, the potential side effects of EOs on beneficial arthropods remain insufficiently understood.

This study evaluates the lethal and sublethal effects of anise (*Pimpinella anisum*) and fennel (*Foeniculum vulgare*) essential oils, together with pure anethole, their major compound, on two key natural enemies of aphids: the predator *Chrysoperla affinis* and the parasitoid *Aphelinus abdominalis*. For both species, concentration–response assays were designed to determine LC₅₀ values, while sublethal endpoints include predation capacity in *C. affinis*, and parasitism rate and offspring sex ratio in *A. abdominalis*.

By integrating multiple endpoints across two functionally distinct natural enemies, this work aims to provide a comprehensive assessment of the selectivity of anise and fennel essential oils, within the context of IPM. The results will contribute to evaluating the compatibility of these botanical pesticides with biological control agents and to guiding their safe use in sustainable pest management programs.

Reconstructing the morphological and chemical evolution of the prothoracic repellent glands in stick and leaf insects (Phasmatodea)

Thomas SCHMITT (University of Würzburg, Thomas.schmitt@uni-wuerzburg.de)

Marco NIEKAMPF, Sven BRADLER

Abstract

Phasmatodea are well known for their astonishing ability to disguise themselves as twigs, leaves, or bark, and are therefore commonly known as stick and leaf insects. In addition to this beneficial defensive strategy, many phasmatodean species use prothoracic repellent glands to spray defensive chemicals when disturbed by predators or parasites. We investigate the anatomy and the chemical substances for a global and representative sampling of stick and leaf insects by use of μ CT scans and gas chromatography/mass spectrometry (GC/MS). The glands are located pairwise inside the thorax. In some species developed as small sac-like structures at the tip of the prothorax, in other species as massive tubes proceeding through the whole thorax. Thus, the size and structure can notably differ and several taxa independently evolved huge glands in the new world and old world Phasmatodea. Regardless of the gland size, numerous stick and leaf insects use the same chemical compound as main ingredient of their repellent secretion, a bicyclic monoterpene, which is highly irritating for mucus membranes and the eyes, likewise functions as a repellent against parasites. We could identify the ground pattern molecule of the defensive secretion of the Phasmatodea, which seems to be unchanged in several taxa since 150 million years. This molecule is often modified and an isomer is used in the Euphasmatodea. However, there are many species that evolved completely new substances in their repellent gland secretion, especially in the Necrosiinae and the Malagasy clade.

#11058

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Chemical cues driving early-season colonization of oilseed rape fields by the cabbage stem flea beetle

Nicolas SLOMIANY (IGEPP - Université de Rennes, INRAE, Institut Agro Rennes Angers, Nicoslomiany@gmail.com)

Margot TIXERONT, Anne-Marie CORTESERO, Philippe LUCAS

Abstract

Volatile organic compounds (VOCs) are central mediators of behavioral decisions in phytophagous insects, shaping host location, resource selection, and interactions with conspecifics. Most studies examine either plant-derived cues or pheromonal signals separately, although both categories of VOCs can interact and jointly influence host-finding strategies.

This study examines how these combined chemicals signals structure early-season field colonization in the cabbage stem flea beetle *Psylliodes chrysocephala*, a major pest of winter oilseed rape in Europe. The main question is to determine which plant and insect-derived VOCs attract this insect and whether their interaction modulates this attraction.

Preliminary results reveal a marked differential attractiveness among Brassicaceae species and have enabled the identification of key plant volatiles, including green leaf volatiles, isothiocyanates from glucosinolate breakdown, and several terpenoids. In parallel, morphological and behavioral evidence suggests that male antennal glands may produce pheromonal cues capable of reinforcing or modulating attraction to plant odors.

By combining analytical chemistry, electrophysiology, and behavioral assays, we have identified VOCs eliciting sex-specific responses and behavioral choices in *P. chrysocephala*. These findings clarify how plant cues and pheromones interact during host location and provide the first indications of intraspecific chemical communication in this species. They will guide the development of selective lures to improve monitoring and develop attract-and-kill or push-pull strategies as ecological alternatives to conventional insecticides.

Wing-beat frequency of Asian hornets determined by their unique 24 GHz micro-Doppler radar signature

Herbert AUMANN (University of Maine, Herbert.aumann@maine.edu)

Maxime GOURLAY, Pons LORENZO

Abstract

A technique is described for detecting invasive Asian Hornets (*Vespa velutina*) flying in front of a honeybee hive by analyzing the spacing of micro-Doppler harmonics of the wing-beat frequency observed by a 24 GHz continuous-wave radar.

The motion of insect wings, as determined by high-speed video recordings, consist of an asymmetrical, but nearly sinusoidal, up and down stroke at the wing-beat frequency, which creates aerodynamic forces containing mostly odd harmonics. There is also an abrupt reversal of the wing's angle of attack at the end of the upstroke and at the end of the downstroke, which adds even harmonics to the wing beat spectrum. The wing's motion is mechanically coupled to the insect's body, which has its own vibrational frequency response. Thus, the resulting vibrational spectrum will contain both even and odd harmonics, spaced apart by the wing-beat frequency.

The maximum radar cross-section (RCS) of an Asian hornet at 24 GHz was determined by electromagnetic modeling to be about -39 dBsm. The wings alone contributed less than 1 dB to the RCS. Thus, the micro-Doppler radar response will be primarily due to the mechanical vibration of the insect's body rather than the insect's wings.

We observed Asian hornets in front of a honeybee hive near Gelos, France, using a 24 GHz automotive collision-avoidance Doppler radar. Video recordings confirmed the presence of hornets. Base-band radar data were processed offline by overlapping 0.1-second Short-Time-Fourier-Transforms followed by Cepstrum analysis to extract the spacing of harmonic frequencies in the Doppler spectrum. For $N = 162$ distinct hornet observations, the dominant wing-beat frequency was found to be 114 ± 6 beats / second. By comparison, the reported wing-beat frequency of honeybees is 230 ± 2.8 beats / second. The unique wing-beat frequency of Asian hornets provides an unambiguous method for detecting their presence.

Optimising the placement of yellow sticky traps for effective field monitoring of chicory leaf miner (*Phytomyza cichorii*) in witloof chicory (*Cichorium intybus* var. *foliosum*)

Klaartje BUNKENS (Researcher, Klaartje.bunkens@vlaamsbrabant.be)

Rana YURDUSEVEN, Tim DE CLERCQ, Emma VANDENBOGARDE, Bart DE KETELAERE, Wannes DERMAUW, Francine VAN NEERBOS

Abstract

The chicory leaf miner, *Phytomyza cichorii*, is one of the most important threats to witloof chicory (Belgian endive) production. In order to support timely management decisions, reliable monitoring strategies are crucial. Recently, the old monitoring method using water traps have been replaced by yellow sticky traps. While these sticky traps are more efficient, further optimization is necessary, particularly the optimal placement in the field remained unknown. Therefore, we analyzed the effect of trap orientation, height and spatial positioning in field trials conducted in 2018-2025. Further, this data was used to determine new economic damage thresholds.

Results indicated that trap orientation relative to prevailing wind direction is not a determining factor, whereas placement close to the ground significantly improved capture efficiency. A density of three traps per field proved statistically equivalent to four traps, supporting a reduced monitoring effort without loss of accuracy. Optimal positioning was identified between 30% and 60% of the field's centroid zone. An average of three flies on three sticky plates, per field, was determined as a critical threshold, supported by both field and semi-field (tent) experiments. Ongoing research investigates whether thresholds should be adjusted per flight period and potentially differentiated by sex.

These results contribute to the development of practical, evidence-based guidelines for monitoring *P. cichorii* using sticky plates, supporting integrated pest management strategies in witloof cultivation.

Kinematic reconstruction and dynamical analysis of micro-insect flight: High-speed videography and tracking.

Sergey FARISENKOV (Department of Entomology, Faculty of Biology, Lomonosov Moscow State University, Farisenkov@entomology.bio.msu.ru)

Fyodor BOLSHAKOV, Evgeny SHCHERBAKOV, Nadezhda LAPINA, Georgy NIKOLAEV, Alexey POLILOV

Abstract

The study of the locomotion of miniature animals has been developed significantly only in the last decade due to the technical challenges associated with working on submillimeter-sized specimens: maintaining animals in a normal physiological state throughout the experiment; high-speed macro video recording; kinematic reconstruction; CFD modeling of bristled appendages. The existing data processing framework allows for a general understanding of the mechanics in model species (Lyu et al. 2019; Cheng and Sun 2021; Farisenkov et al. 2022). However, to study a wider range of species and movement control mechanics we need methods that will enable the accurate and efficient collecting and processing the significantly larger data.

To solve this problem, we are developing the new universal high-speed videography setup with four cameras which allow to shoot untethered flying and swimming animals of sizes from 100 micrometers to 10 centimeters. Cameras are placed on rigid frame and have three degrees of freedom which is necessary for precise positioning during macro videography. Animals are placed in the closed chamber with temperature control. The lighting system includes focused sources of transmitted and incident infrared light.

The quality of the resulting videos is sufficient for automatic tracking based on deep machine learning using DeepLabCut environment. We chose one of the smallest flying species *Megaphragma viggianii* with a body length of 250 micrometers as a model object for optimizing the training parameters of neural networks. The training set consists of 300 frames with 22 landmarks on the wings and body. The best model is based on the Resnet50 neural network (He et al. 2015) and includes optimized skeleton. The average accuracy of the model is comparable with manual tracking.

This work was supported by the Russian Science Foundation (Project 25-14-00051).

#10823

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Density-dependence and inter-individual variation of movement strategies in the biocontrol agent *Trichogramma brassicae*

Yuan GAO (INRAE Provence-Alpes Côte d'Azur, Yuan.gao@inrae.fr)

Abstract

Parasitic micro-wasps of the genus *Trichogramma* are widely used as biocontrol agents for pest suppression, for instance against the European corn borer. Biocontrol practice involves the mass release of individuals in protected fields. At such high densities, it is expected that inter-individual interactions may play a significant role in the spatial propagation of the insects. However, studying the movement in groups of such tiny organisms has remained a challenge. Using automated video-tracking methods such as MultiObject Tracking (MOT) and subject ReIDentification (ReID), we could track individuals within large groups, maintaining identities over long period of time. We analysed the movements of groups of females in experimental arenas, contrasting two levels of density (15 versus 100 individuals). From tracking data, we obtained individual-level movement metrics, then we quantified how inter-individual variations and inter-individual interactions contribute to the total quantity of movement. This illuminates the consequences of population density for the rate of spatial spread and the behavioral underpinnings of density-dependent dispersal.

New optical measurement method for egg geometry and volume of microscopic ovoids

Sophie LE HESRAN (Wageningen University & Research, Sophielehesran@gmail.com)

Antonio MORENO-RODENAS

Abstract

Egg size is a determining factor in the survival of offspring in arthropods. It is also a particularly interesting trait, being simultaneously a maternal and offspring character. Progeny hatching from larger eggs can better withstand environmental stresses, while the age and physiological state of a female, as well as the environmental conditions she is exposed to, can affect the size of her eggs. However, the current scientific literature lacks a reliable and automatic measurement method for tiny arthropod eggs, as most methods have been developed for macroscopic bird eggs. We propose a new optical method for retrieving ovoid-shaped egg geometries, consisting in optimizing a parametric virtual model from a limited number of camera views (N-Views method). We first tested the N-Views method on chicken (*Gallus gallus domesticus*) and quail (*Coturnix coturnix*) eggs, comparing its accuracy with two other existing optical measurement methods (Photogrammetry and Silhouette). Across all tested methods, N-Views provided the best estimate of egg volume when compared with the reference manual measurements (Archimedean buoyancy force). We further tested the N-Views method on mite eggs (*Amblyseius swirskii*), confirming its transferability to microscopic ovoids. We are currently further developing the N-Views method to make it non-intrusive. This novel approach opens new research possibilities for the exploration of relationships between egg size and life history traits in arthropod species.

Evaluation of field dispersal of the alfalfa weevil adults using albumin as a marking agent

Alexandre LEVI-MOURAO (University of Lleida, Agrotecnio Centre, Lleida, Spain; Santarém Polytechnic University, Santarém, Portugal, Alexandrelevi.garcia@udl.cat)

Roberto MESEGUER, Xavier PONS

Abstract

The alfalfa weevil, *Hypera postica* Gyllenhal (Coleoptera: Curculionidae), is among the most destructive pests of alfalfa worldwide. Although limited information exists regarding adult dispersal, *H. postica* is thought to have poor natural mobility, making it essential to clarify how it colonizes new alfalfa fields. Marking and recapture is a useful tool for determining the insect movement. The egg white protein (albumin) is an external marking method inexpensive, environmentally safe, and easily detectable that may be useful for detecting insect movement under field conditions. In this study, we evaluated the usefulness of albumin for tracking the field movement of adult alfalfa weevils. Protein detection was performed using an indirect ELISA. To examine the persistence of the marker after direct contact, adults were individually treated with albumin and tested over time. All individuals remained positive during the first four days, and up to 86% continued to test positive through day 26, demonstrating strong durability of the protein on the cuticle. Indirect marking was also assessed by applying albumin to plants prior to releasing adults. Although marking efficiency was high during the first hour, it declined rapidly and became undetectable after 48 hours, thereby reducing the risk of unintended marking of non-target insects. Finally, adult dispersal was evaluated in two alfalfa fields during spring. An area of 2.38 ha was sprayed with a 10% albumin solution using a tractor-mounted insecticide sprayer, and periodic sampling was conducted at distances of 0, 20, 50, 100, 200, and 300 m from the treated area. Results showed that adults moved up to 100 m from the release point, providing new insight into the short-range dispersal behaviour of this pest.

Deep learning–assisted identification of the hazelnut mite *Phytoptus avellanae* for improved pest management

Roberto MASTURZI (University of Tuscia, Roberto.masturzi@unitus.it)

Domenico VALENZANO, Donato ROMANO, Stefano SPERANZA, Mario CONTARINI

Abstract

Hazelnut (*Corylus avellana* L.) is increasingly recognized as a major crop in Italy and worldwide. Despite its relatively high resilience, hazelnut production can be significantly affected by several insect and mite pests. Among these, the eriophyoid mite *Phytoptus avellanae* Nalepa has gained growing importance due to the severe yield reductions it causes in various hazelnut-producing regions. This small size mite (body length < 200 µm) colonizes both vegetative and reproductive buds, inducing irreversible tissue alterations that lead to the formation of swollen galls, commonly referred to as “big buds”. Infestation levels are typically assessed during winter by counting big buds on randomly selected plants, while mite dispersal, primarily wind-mediated, is monitored using sticky and water traps. However, sampling and identifying the mite fauna present in hazelnut orchards is extremely labor-intensive and time-consuming, requiring multiple steps such as washing, counting, slide preparation, and taxonomic identification.

This study, conducted in 2025 in the main hazelnut-growing area of Viterbo (central Italy), investigated the feasibility of streamlining and automating mite identification through the adoption of a single-stage, deep learning–based object detection framework (e.g. YOLO). Such architectures perform joint object localization and classification within a unified inference process, enabling high detection accuracy with low computational latency and making them well suited for the analysis of microarthropods. A dedicated image database of laboratory-acquired samples was constructed, processed, and manually labeled to support supervised model training. The trained system allows the automatic discrimination of phytophagous mites (further classified into vermiform and fusiform morphotypes) from predatory phytoseiid mites. The proposed approach also evaluates the contribution of data augmentation and image enhancement techniques to the detection of submillimetric objects, small-sized organisms such as microarthropods, providing a rapid, non-invasive, and low-cost diagnostic tool for the identification of hazelnut-associated mites.

#16383

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Real-time imaging and quantification of ant's trail pheromone deposits

Laure-Anne POISSONNIER (XLIM, Université de Limoges, Laure-anne.poissonnier@unilim.fr)

Abstract

Organisms have evolved diverse strategies to communicate. Beyond acoustic and visual signals, many species have also evolved different forms of chemical communication, for example through the use of pheromones. For instance, ant trail pheromones are volatile chemical signals deposited along routes connecting food sources to the nest. These pheromones facilitate collective navigation by establishing a scent-based trail, which is dynamically reinforced as additional foragers follow the path, thereby optimizing foraging efficiency. Although the chemical composition of many trail pheromones has been identified via gas chromatography, their direct visualization on the substrate has not yet been achieved. Deposit quantity is inferred indirectly, from ant counts, abdomen contacts to the ground, or speed drops while marking. Early visualization methods were never refined with modern optical tools, leaving pheromone quantification a crucial but unresolved aspect of ant foraging dynamics. We show the first direct observations and quantifications of ant pheromone trails. We have applied quantitative phase imaging using fast and high-sensitive quadriwave lateral shearing interferometry on a regular microscope. Our analysis shows for instance a fast evaporation of the pheromone solvent followed by a long-lasting solid residue, capable of being detected after several minutes. We also highlight differences in the size and shape of the deposits. This characterization paves the way for an enhanced understanding of communication in social insects by providing previously inaccessible information without requiring labeling or perturbing the insects.

#12002

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Automating area-wide insect monitoring

Matej STEFANCIC (Trapview, Matej.stefancic@trapview.com)

Abstract

Real-time understanding of insect population dynamics and its future development is crucial in today's agriculture and forestry. In the presentation we will showcase how such monitoring can be achieved with automated traps, why modern monitoring is data management problem and what are crucial steps needed for successful area-wide based projects.

In each step of the data management we will demonstrate what are key challenges, how technology can address them and what still requires human intervention.

We will also present some of the best practices in implementation real-time insect monitoring on local, regional or country level.

#12298

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Genetic components and transcriptomic basis of worker personality in the Argentine ant

Marco CAMGUILHEM (Insect Biology Research Institute (IRBI, UMR 7261) CNRS - University of Tours, Marco.camguilhem@utoulouse.fr)

Marina PSALTI, Romain LIBBRECHT

Abstract

Task specialization and behavioral division of labor are core components to the evolution and functioning of insect societies. Within social insect colonies, workers that specialize in performing distinct tasks have different individual personalities, in that they express robust behavioral differences that are consistent over time and across contexts. An important question in behavioral ecology and social insect biology is to understand the factors and mechanisms that regulate worker personality. In particular, there is a need for studies investigating the genetic and transcriptomic bases of worker behavior that explicitly test for individual behavioral consistency to address personality, while properly controlling for factors known to generate behavioral variation among individuals, such as age, experience, and social environment. To address this question, we used the Argentine ant *Linepithema humile* to experimentally produce 385 same-age workers from 15 single-queen colonies. For each worker, we conducted over several weeks three series of five behavioral assays (foraging, brood care, aggression, exploration and light affinity). We are in the process of assessing the individual repeatability of our behavioral measurements, and the effect of the colony of origin (and thus the genetic background) on worker behavior and/or personality. To further investigate the molecular mechanisms underlying behavioral variation, we extracted and sequenced the RNA from more than 120 individual brains, dissected from a selection of workers based on the behavioral analyses. Ongoing transcriptomic analyses will capture gene expression patterns associated with behavioral variation (both within and between genetic backgrounds) to identify candidate gene and/or pathways for the molecular regulation of worker personality. This study will improve our mechanistic understanding of worker behavior and division of labor in social insects.

#10897

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Ecological insights into *Vespa mandarinia*: dietary habits, nesting sites, natural enemies, and inquilines

Moon Bo CHOI (Kyungpook National University, Kosinchoi@hanmail.net)

Jaehee KIM

Abstract

Vespa mandarinia, the world's largest hornet, possesses potent venom and aggressive behavior, posing risks to humans and beekeeping. In Korea, autumn grass-cutting increases the likelihood of mass attack incidents, and the species threatens managed honeybee colonies. Its 2019 detection in North America raised ecological concerns, prompting eradication efforts in Washington State. This study examines *V. mandarinia*'s diet, nesting sites, natural enemies, and inquilines in Korea. DNA metabarcoding analysis revealed a broader diet than in North America, with social Hymenoptera as the primary prey. While most nests were found underground, some were located in tree cavities and rooftops. Additionally, six parasitoid and inquiline species were identified, providing insights into potential biological control strategies.

#10821

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Determinants of variability in the predatory stress responses of honey bees

Alice Mélusine DURAND (Research Center on Animal Cognition (CRCA), Center for Integrative Biology (CBI); CNRS, University of Toulouse, Toulouse 31062, France, Alice.durand@univ-tlse3.fr)

Ariane MARTY, Jean-Marc DEVAUD

Abstract

Honey bees are eusocial insects living in large colonies, where the workers tend to the colony needs. Their task allocation is mainly age-dependent (yet influenced by other factors): during spring and summer, younger bees carry in-hive tasks while older bees are allocated to outside tasks such as foraging. During winter, task allocation is much less clear, as workers remain within the hive for an extended period (up to six months). Whether an individual engages into a specific activity may depend on many factors, some of which remain unclear. Here, we focus on collective recruitment for the colony defense. When the colony is under predatory stress, especially from large predators, honey bees release a pheromone signal to recruit nestmates for colony defense. This alarm pheromone has multiple effects on recruited honey bees. In laboratory conditions, exposure to its main component, isopentyl acetate (IPA), leads to increased aggressiveness as well as decreased performances in a learning task related to foraging. However, preliminary results showed inter-individual variations in these responses to IPA, suggesting that not any bee can be recruited for colony defense. With the aim of identifying the determinants of such variability, we are currently investigating the respective roles of age, season, and current activity within the colony. For this, emerging honey bees were marked before being reintroduced in their colonies, then collected at different ages and while performing various tasks. These individuals were exposed to IPA and tested on either an aggressiveness assay, or an olfactory associative learning task. The results from this study will lead to a better understanding of honey bee task allocation under predatory stress, and are a first step in studying the behavioural and biological stress response of honey bees.

High-resolution tracking using machine-learning reveals the spatiotemporal dynamics of social immunity in *Reticulitermes flavipes*

Özge KILIC (Freie Universität Berlin, Ozge.klc.hms@gmail.com)

Abstract

Social immunity—the collective behavioural and organizational defences that reduce disease risk—is a defining feature of eusocial insects, yet its dynamics are difficult to quantify at the colony scale because interactions are dense, fast, and spatiotemporally variable. Here we present a high-resolution, multi-individual tracking and analysis pipeline that links pathogen exposure to changes in movement, contact network structure, and nest-use behaviour over time in the subterranean termite *Reticulitermes flavipes*. Colonies were recorded in custom arenas using a high-resolution multi-camera imaging setup, enabling continuous observation of >50 individuals over multiple hours. We applied a hybrid SLEAP workflow with a termite-specific anchor point set permitting reproducible and containerized processing for long videos and dense scenes. We extracted contact intensities, spatiotemporal dynamics and proximity-based interaction (social) networks from tracked individual trajectories and poses. Using a multi-camera high-resolution imaging setup and a hybrid SLEAP pipeline, we demonstrate an automated colony-wide tracking approach that can be integrated with downstream behavioural analysis. We apply our method to a pathogen-challenge experiment to explore the collective social immune responses of termites to fungal exposure. Together, this demonstrates how machine-learning analysis of insect tracking can convert complex colony activities into quantifiable output.

Predator loss (*Tamandua mexicana*) shapes colony-level defense investment in a neotropical termite (*Nasutitermes corniger*)

Emily MARPLE (Smithsonian Tropical Research Institute, Emilymeymarple@gmail.com)

Lara DOMINGUEZ, Dumas GALVEZ

Abstract

Predator-prey relationships are an important force in community composition, influencing population densities and structure. In the neotropics, termites are common prey items. In response to predation pressure, termites have evolved several defensive strategies. For example, in *Nasutitermes corniger*, an abundant species of arboreal termites, the soldier caste has evolved a specialized nasus that secretes a chemical defensive spray which deters predators and protects the colony. Yet, it remains unclear how the presence or absence of key predators alters colony-level investment into defense and, in turn, affects foraging and ecosystem processes such as wood decomposition. Recent research suggests strong top-down control of arboreal termites by *Tamandua mexicana*, making this system ideal for testing how predator threat shapes both colony defense strategies and foraging patterns.

This study combines two complementary approaches. First, a colony-level exclusion experiment in Gamboa, Panamá. Natural nests are selected to be either predator-present (exposed to natural *T. mexicana* and brief simulated attacks) or predator-excluded (protected from *T. mexicana* but allowing for normal termite movement) treatments. Across colonies, we assess multiple proxies for defense investment, including soldier proportion, response intensity and latency to attack, and potency of chemical secretions. After several months, nests are collected and caste composition is quantified. Secondly, to explore how predator threat influences foraging behavior and decomposition, we utilize vertical and horizontal transects of standardized wood baits across Panamá. These transects allow comparison of foraging activity and wood decomposition rates in areas with different levels of *Tamandua mexicana* presence.

Together, these studies clarify how predator loss alters colony defensive strategies and ecosystem-scale decomposition processes. By linking predator pressure to termite defense investment and foraging behavior, this work provides a novel perspective on how vertebrate predators shape the structure and functioning of tropical communities.

Characterizing the behavioral response of ant queens to larvae

Malo THÉVENIN (IRBI - CNRS - Univeristy of Tours, Malokoffi@gmail.com)

Christophe LUCAS, Romain LIBBRECHT

Abstract

Social insect colonies are characterized by a division of labor between queens, which are strictly specialized in egg production, and workers that fulfill all non-reproductive tasks. Notably, workers provide care to the brood to ensure its proper development. Recently, it has been reported that ant queens do express brood care – and thus lose their specialization – when isolated from their workers. One hypothesis to explain this finding is that queens and workers would differ in their response threshold to larval needs. Variation in larval needs results from any environmental or social cues that modify the physiological state of larvae, such as social isolation, food deprivation or temperature stress. This hypothesis makes two predictions. First, we expect that queens will exhibit a dose-dependent behavioral response to larval needs. Second, we predict that the behavioral response of queens will require a higher dose, while workers will need a lower dose. To test those predictions, we are currently developing an experimental protocol that allows for the filming of restrained ants from multiple angles when they are experimentally put in contact with a larva. In parallel, we are investigating the impact of various stressful conditions to experimentally produce larvae with different levels of needs. Together, these technical developments will allow us to (i) provide a precise and quantitative characterization of the behavioral response of ant queens to larvae, (ii) quantify changes in this behavioral response with increasing larval needs, and (iii) determine whether these dose-dependent changes differ between queens and workers. This project has the potential to shed light on the mechanistic basis of ant queen specialization and the regulation of division of labor in social insect colonies.

Why does he care? Repeatable differences of male behaviors and sexual conflict resolution in biparentally caring beetles

Max KÖRNER (University of Bayreuth, Maximilian.koerner@uni-bayreuth.de)

Marlena REINBOLD, Sandra STEIGER, Lena ZYWUCKI

Abstract

In some species, the high costs of parental care are shared by both parents during biparental care, which typically evolves if the male stays instead of seeking alternative mating opportunities. Biparental cooperation is only possible if sexual conflict over the often-opposing evolutionary interests of either parent is resolved. This dynamic is well-studied in evolutionarily derived family systems like altricial birds, but why and how it occurs in species with facultative care where neither parent must remain with the young — a state likely prevailing during the evolution of parental care — is poorly understood. We investigate this phenomenon by examining the resolution of sexual conflict over care behaviors in *Nicrophorus vespilloides*. These carrion-breeding beetles exhibit facultative biparental care comprising of multiple components exhibited by both sexes, with high variation in male efforts. This variation may be explained by a “negotiation”-tug-of-war over investments where one partner adjusts their efforts to the other but may also depend on repeatable individual differences in males, selected for by environmental gradients or different pace-of-life strategies. Here, we disentangle these mechanisms by testing repeatability of male care efforts over multiple reproductive bouts. By conducting these bouts with either the same or different female partners and taking female care contributions into account, we determined to what degree male care efforts depend on the accompanying female, or on the male itself. We found that male larval feeding was negatively correlated with female contributions and only repeatable in monogamous males, indicating that this behaviour is largely driven by the female partner. Conversely, maintenance of the carcass nursery was repeatable across males regardless of their partner, indicating little flexibility in this niche-constructing behaviour. Overall, our findings show that male repeatability and sexual conflict resolutions differ between care components, likely depending on different selective pressures shaping each behaviour in either sex.

#10770

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Heat stress disrupt maternal care through independent effects on mothers and eggs

Joël MEUNIER (IRBI, University of Tours, CNRS, Joel.meunier@univ-tours.fr)

Alice ROUX, Elfie PERDEREAU, Irene VILLALTA

Abstract

Parental care is often vital to offspring survival. However, its vulnerability to climate change and heat waves remains poorly understood, mostly because parental and offspring responses are rarely separated. Disentangling these sources of disruption is yet essential to reveal the targets of selection and predict the resilience of family-living species to intensifying climate changes. Using a cross-fostering design in the European earwig (*Forficula auricularia*), we independently manipulated maternal and egg exposure to heat stress and quantified maternal behaviours, egg development, and juvenile performance. We show that maternal and egg heat stress exert additive but independent effects. Heat-stressed mothers reduced egg collection, while heat-stressed eggs received more grooming. Both treatments altered embryonic development, hatching synchrony, juvenile production, and thermal tolerance. Strikingly, post-oviposition maternal heat stress accelerated egg development, while egg heat stress increased maternal weight gain. Heat exposure also modified egg morphology and chemical cues. Overall, our data show that earwig maternal care is largely independent of the partner's thermal stress (whether mother or eggs), limiting its buffering capacity. This decoupling suggests that the adaptive value of care may decline under intensifying heat waves, potentially constraining the evolutionary resilience of family living in fluctuating environments.

Body size responses of *Orius laevigatus* to maternal and transgenerational thermal history

Ana Belén ABELAIRA ROS (Universidad Politécnica de Cartagena, Anika95_ct@hotmail.com)

María del Carmen RECHE, Amador RODRÍGUEZ GÓMEZ, Virginia BALANZA, Pablo BIELZA

Abstract

Developmental temperature is a major determinant of insect body size, an essential trait influencing the effectiveness of predators employed in augmentative biological control. The anthocorid *Orius laevigatus* (Fieber) (Hemiptera: Anthocoridae) is extensively used to suppress thrips populations in greenhouse crops, and increased body size is associated with enhanced fecundity and predatory efficiency. In this study, we investigated how thermal conditions experienced across generations influence adult body size in this species, integrating effects of genetic selection and phenotypic plasticity. Two cold-tolerant lines of *O. laevigatus*, previously selected for improved performance at low temperatures, were compared with a commercial strain. Lineages were maintained for four consecutive generations under different combinations of 15 and 26 °C, and adult pronotum width in the final generation was used as an indicator of body size. Across all thermal treatments, cold-selected lines were significantly larger than the commercial strain, demonstrating a strong genetic basis for size differences. The rearing temperature of the final generation had the greatest impact, with individuals developing at 15 °C attaining larger sizes than those reared at 26 °C. Moreover, exposure of parents, grandparents, and great-grandparents to low temperature resulted in increased body size in descendants, indicating a distinct but progressively diminishing transgenerational effect. Nevertheless, extended exposure to low temperatures over multiple consecutive generations did not lead to further size increases and, in some cases, resulted in reduced size. Overall, our findings suggest that the combination of cold-adapted lines with carefully timed low-temperature rearing can enhance predator size without permanently compromising mass-rearing efficiency, whereas prolonged cold rearing may be detrimental.

#10633

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Frequencies of sex determination factors in Italian housefly populations

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Abstract

The housefly (*Musca domestica* L.) has a remarkable polymorphic sex determination system. It consists of various male and female determining genes with different alleles. Allelic frequencies of male and female determiners follow a latitudinal cline but can differ remarkably between populations. The male determining locus (M) can be present on the Y, X or any of the five autosomes. A dominant female determiner (WZ-system) is also found in some populations. In 2025, we resampled populations around Bologna (Italy) that were previously investigated in 1982 and 2006. Using back crosses and linkage analysis with strains carrying recessive visible mutations, we established hemizyosity and homozygosity of M factors, their chromosomal location and population frequencies. Presence of the dominant female determiner was determined by PCR. We compare the 2025 distribution of variants with the earlier samples to see whether population frequencies remained stable or shifted.

#11336

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Incomplete resistance of fall armyworm, *Spodoptera frugiperda* to dual-gene Bt maize

Jenny Paola CORREDOR PRADO (Programa de Biología. Facultad de Ciencias Matemáticas y Naturales. Universidad Distrital Francisco José de Caldas, Bogotá-Colombia, Jpcorredorp@udistrital.edu.co)

Juan HERNÁNDEZ-PLATA, Oscar F. SANTOS-AMAYA

Abstract

The fall armyworm, *Spodoptera frugiperda* (Lepidoptera: Noctuidae), is a major polyphagous pest in maize as well as in other crops and has evolved resistance to transgenic Bt maize producing Cry1/Cry2 Bt toxins. Transgenic crop “pyramids” producing two or more Bt toxins active against the same pest are used to delay evolution of resistance in fall armyworm populations. However, little is known about that evolutionary response from target species to the selective pressure imposed by two or more toxins with independent mechanisms of action. As part of our effort to improve the management of fall armyworm resistance to Bt crops, we studied incomplete resistance to Cry1A.105+Cry2Ab2+Cry3Bb1 Bt maize in a population of fall armyworm with practical resistance. Under laboratory conditions (12-hour photoperiod, 27 ± 3 °C temperature, and 70 ± 5 °C relative humidity), we compared the life history characteristics and population growth of the resistant population in Bt and non-Bt maize. The results show that the net reproductive rate (R_0) and intrinsic population growth rate (r_m) were significantly lower ($P < 0.05$) in individuals fed Bt maize. This indicates that the potential population growth of the resistant population is lower in transgenic maize. Additionally, pupal weight and survival rates were significantly lower ($P < 0.05$) in Bt maize. Taken together, our results support the hypothesis that fall armyworm resistance to Cry1A.105+Cry2Ab2+Cry3Bb1 maize is incomplete. This information is useful in designing strategies to reverse the resistance of fall armyworm populations resistant to Bt crops under field conditions.

Genetic Diversity Dynamics in Wild and Domesticated Populations of the Black Soldier Fly (*Hermetia illucens*)

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Alexandra GUIGUE, Céline COULOMBET, Erick SARNAY, Francesco BOATA, Romuald ROUGER

Abstract

The domestication process relies on isolating a subset of individuals from a natural population to establish a captive group exhibiting desirable traits. During this phase, three major evolutionary forces—inbreeding, genetic drift, and selection—act together to homogenize the domesticated population. In the black soldier fly (*Hermetia illucens*, BSF), a key species in insect farming, these dynamics remain poorly understood. This limited knowledge stems from an incomplete mastery of its biology combined with life history traits such as short generation times, high fecundity, and substantial larval mortality. These characteristics facilitate rapid losses of genetic diversity, potentially leading to inbreeding depression. In this study, several BSF populations were characterized using a 96 SNP KASPAR genotyping array to monitor temporal changes in genetic variability. The analyses focused on two domesticated commercial populations and one wild population, all genotyped and quality filtered prior to processing. A genetic clustering analysis using the Sparse Nonnegative Matrix Factorization (sNMF) algorithm enabled estimation of individual admixture coefficients and identification of genetic structure. The optimal model revealed the presence of two distinct genetic groups ($K=2$), corresponding to the two commercial populations, with the wild group clustering closely with one of them. At $K=3$, however, the three groups formed clearly differentiated clusters. Genetic diversity indices (allelic diversity, observed and expected heterozygosity H_O and H_E , and the inbreeding coefficient F_{IS}), along with genetic distance measures, showed that domesticated populations exhibit an excess of homozygotes, indicating an elevated risk of inbreeding within captive breeding lines.

#12501

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

How does genetic variation drive predator-prey dynamics?

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Raquel TOMÉ, Juan ADÁNEZ, Sofia HENRIQUES, Jéssica KING

Abstract

Predator–prey interactions are central to maintain systems stability and have received increasing attention in pest management. Understanding how genetic variation in key predator traits affects predator fitness and the stability of the predator-prey system is crucial in predicting species' persistence. Despite numerous theoretical predictions about which traits are most important for predator–prey dynamics, empirical evidence on how genetic variation in these traits affects the dynamics is still limited.

In this study, we used a system composed of the predatory mite *Amblyseius swirskii* and its prey *Tetranychus urticae*. Using functional response experiments and direct behavioral observations, we quantified genetic variation in several predator traits and incorporated these trait values into a predator-prey model to assess how different combinations of trait values affect predator–prey dynamics. Our results reveal substantial genetic variation in predator traits such as handling time, prey preference, and attack success rate. When predicting predator-prey dynamics with the trait values observed in our isofemale lines, we find that even small differences in parameters can strongly influence system persistence. These findings highlight the importance of integrating genetic variation into models of predator–prey interactions to improve long-term predictions of ecological stability and biological control efficiency.

Evaluation of the Population Genetic Parameters for Sterile Insect Technique Application of Mediterranean Fruit fly, *Ceratitis capitata* (Wiedemann, 1824) (Diptera:Tephritidae) in Türkiye

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Abstract

Evaluation of the Population Genetic Parameters for Sterile Insect Technique Application of Mediterranean Fruit fly, *Ceratitis capitata* (Wiedemann, 1824) (Diptera:Tephritidae) in Türkiye

Türkiye takes a prominent place in the world in terms of fruit cultivation potential and export. One of the most important factors negatively affecting food security and supply is economic losses caused by fruit flies. Mediterranean fruit fly which is highly invasive, is one of the most destructive polyphagous pest species. Since it is a quarantine pest, its economic impacts particularly to citrus varieties is considerable. Preventive cultural measures, biotechnical and chemical control has been carried out against *Ceratitis capitata* in line with Integrated Pest Management principles. Sterile insect technique (SIT) is an environment-friendly method that integrates into area-wide integrated pest management programmes to suppress Mediterranean fruit fly populations. In this research, the efficiency of the sterile insect technique (SIT) has been evaluated by mitochondrial and microsatellite and markers during 2023-2026 in Menderes, İzmir province before and after SIT application. As a result of phylogenetic analysis, some localities at SIT application area and VIENNA 8 strain were distinctly diverged from the other SIT localities (Menderes, İzmir). Number of polymorphic sites (S:39), total number of mutations (Eta:41), number of haplotypes (h:42), haplotype diversity (Hd: 0,795) were computed using DNA Sequence Polymorphism (DnaSP 6) software. Microsatellite multiplex PCR with 8 microsatellite loci has also been carried out to estimate the genetic diversity in SIT localities. After SIT application, the success of the sterile insect technique application will be evaluated by comparing bioinformatics data generated during the pre- and post-release of sterile insects.

Keywords: Medfly, IPM, sterile insect technique, molecular markers, genetic diversity

Same Species, Different Colors: Insights into *Bombus niveatus* Kriechbaumer, 1870 Morphological and Genetic Concordance

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Tuana ÖĞRETICI, Fatih DIKMEN, Vahap ELDEM, Çiğdem ÖZENIRLER, Ahmet Murat AYTEKIN

Abstract

This study investigates the controversial taxonomic status of the sympatric subspecies *Bombus niveatus niveatus* and *Bombus niveatus vorticatus* using mitochondrial COI and 16S rRNA and nuclear PEPCK and EF1- α gene regions. We aim to resolve whether the observed morphological divergences reflect true speciation or intraspecific variation through a multi-locus phylogenetic analysis.

High-quality genomic DNA was obtained from specimens collected from the Beytepe region of Ankara (Türkiye). The targeted mitochondrial (16S and COI) and nuclear (PEPCK, EF1- α) gene regions were successfully amplified and sequenced, including newly optimized primers for the PEPCK locus. After sequence quality control, alignment, and data refinement, datasets were subjected to three different species-delimitation tests (ABGD, GMYC, bPTP) and phylogenetic analyses. All species-delimitation analyses consistently grouped all individuals into a single lineage. Likewise, phylogenetic reconstruction based on both Maximum Likelihood and Bayesian approaches revealed no significant genetic differentiation between the two morphotypes.

Consequently, our findings reject the hypothesis of separate species status. We conclude that *B. n. niveatus* and *B. n. vorticatus* represent color polymorphs of a single biological species and recommend that both taxa be classified under *Bombus niveatus*, attributing the observed phenotypic differences to ecological plasticity rather than evolutionary divergence.

Evolutionary genome dynamics in malaria vector *Anopheles coluzzii* during laboratory colonization

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Giuseppe CONDORELLI, Chiara LEO, Anna ROCCHI, Alessandro TRUSSO, Rocco D'AMATO, Alekos SIMONI, Ruth MÜLLER, Andrea CRISANTI, Paula POLLEGIONI

Abstract

Laboratory-reared organisms are assumed to be accurate representations of their wild counterparts. However, the process of establishing a colony from a small number of founders under conditions that significantly differ from the natural environment may dramatically influence genetic composition of the colonized population. As a result, various aspects of physiology, fitness, and behavior may also be affected.

Here we investigated genomic changes occurring during laboratory adaptation in the malaria vector *Anopheles coluzzii*. The newly colonized progenies of indoor-resting blood-fed females collected from a field population in Mali were sampled across multiple generations and allele frequency changes were tracked through whole-genome sequencing of pools of 50 females. Our analysis revealed a marked decline in genetic diversity, most likely driven by a combined effect of small effective population size and strong selection. We observed dramatic allele shifts at multiple loci, occurring primarily in the earliest generations post-colonization. Among the most affected were (i) the voltage-gated sodium channel gene, with alleles conferring knock-down resistance (kdr) to pyrethroids and DDT highly advantageous in the field under insecticide pressure, but associated with high fitness costs in the absence of insecticides, (ii) paracentric inversions on chromosome 2, in particular inversion 2La, and (iii) a cluster of thioester-containing protein (TEP) genes on chromosomal arm 3L. Collectively, these results illustrate how stochastic processes and selective pressures rapidly reshape the genomic architecture of *A. coluzzii* during early laboratory colonization. Understanding these dynamics is essential not only to elucidating general patterns of population evolutionary trajectories, but also for accurately interpreting the ecological relevance of experimental outcomes in various mosquito studies.

#16517

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Phylogeography and local adaptation of a widespread butterfly

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Freerk MOLLEMAN, Vicencio OOSTRA

Abstract

Widespread species may have repeatedly adapted to various environments and habitats. The common evening brown butterfly (*Melanitis leda*) occurs in open and closed-canopy habitats in Africa, Asia, and Australia. To reconstruct (1) the phylogeography, (2) demographic history, and (3) the genomic regions associated with open vs closed-canopy habitats and latitude, we used whole-genome resequencing data of 212 *M. leda* samples and 3 outgroup samples from across its range. The results indicate 4 clades of *M. leda* in the phylogeny: Africa, mainland Asia, south-east Indonesia, and Australia. The species originated in mainland Asia and reached Indonesia and then Australia a long time ago, while Africa was reached only recently. In ongoing analyses, we expect to track changes in population size for each of these clades and identify genomic regions responsible for habitat adaptation.

#11049

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Genetic basis of resistance to dual-gene Bt maize in fall armyworm, *Spodoptera frugiperda*

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Juan Enrique HERNANDEZ-PLATA, Jenny Paola CORREDOR-PRADO

Abstract

Large-scale adoption of transgenic crops expressing genes from *Bacillus thuringiensis* (Bt) imposes strong selection pressure for evolution of field-relevant resistance that can reduce pest control efficacy, such as reported for Bt maize in *Spodoptera frugiperda* (J.E. Smith, 1797) (Lepidoptera: Noctuidae) in Colombia, Argentina, Brazil, and the United States. Theoretically, this field-evolved resistance could be linked to a genetic basis of resistance in *S. frugiperda* that do not meet some of the assumptions required for proper function of the “high dose/refuge” strategy. To improve the management of resistance to Bt crops, we conducted under laboratory conditions (27 ± 2 °C, $70 \pm 10\%$ r.h., and 12L: 12D photoperiod) experiments to determine the genetic basis of resistance to Cry1A.105+Cry2Ab2+Cry3Bb1 in a resistant *S. frugiperda* population. Genetic analyses using plant leaf tissue bioassays with progenies from reciprocal crosses between resistant and susceptible insects indicated that the inheritance of the resistance is completely recessive ($Dx = 0$), autosomal, and without maternal effects. This profile of resistance inheritance observed in the resistant *S. frugiperda* population supports some of the assumptions of the pyramid strategy for resistance management.

#16375

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Expanding the Field of View : Region-Specific Extraction for Target-Site Resistance Discovery in Insects

Christoph ZIMMER (Syngenta Crop Protection AG, Muenchwilen, Christoph.zimmer@syngenta.com)

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Abstract

Insecticide target proteins are encoded by one or a few genes. Target-site resistance is commonly observed across insect taxa and diverse molecular targets. This resistance frequently arises from single or few single nucleotide polymorphisms (SNPs), prompting many studies to employ biased sequencing approaches focused on suspected "hot-spot" regions within target genes. However, whole genome sequencing remains cost-prohibitive when investigating only a few genes, while uneven coverage often prevents high-resolution sequencing without substantial investment in sequencing depth, technology, and DNA input material.

We piloted a Region Specific Extraction (RSE) enrichment approach designed to reduce DNA input requirements while increasing sequencing depth compared to whole genome sequencing and expanding genomic coverage beyond traditional PCR-based amplicon sequencing. This method aims to enhance our understanding of target-site resistance complexity by broadening the analytical field of view beyond known hot-spots, potentially revealing novel resistance mechanisms and previously undetected variants.

Characterization of piRNA pathway in the parasitoid wasp *Cotesia congregata* and impact on its endogenous bracovirus

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Camille HEISSERER, Silke JENSEN, Elisabeth HUGUET, Johann CONFAIS, Karen KESTER, Emilie BRASSET, Jean-Michel DREZEN

Abstract

Tens of thousands of parasitoid wasp species of the braconid family are associated with bracoviruses that are integrated into their genome and produce virus particles injected into the parasitized host during wasp oviposition. The genes encoded by the viral DNAs packaged in these particles are expressed by host cells and produce virulence factors, ensuring successful wasp larvae development by altering host immune defenses. Bracoviruses originate from the endogenization of a large double-stranded DNA virus ~100 million years ago in a common ancestor of these braconid wasps. A previous study reported no overexpression of immune genes during particle production, suggesting that virus particles might now be considered as “self” by the wasp after 100 million years of virus evolution within the wasp genome. This observation supported the idea that no residual conflict remains between the wasp and the virus, unlike what is commonly observed in many symbiotic relationships. However, another antiviral strategy relies on specialized small non-coding RNAs, the piRNAs, as previously shown in mosquitoes. We undertook the characterization of the piRNA pathway in the parasitoid wasp *Cotesia congregata* and examined whether piRNAs might contribute to bracovirus regulation. We identified the presence of piRNAs in the ovaries, testis and head of both sexes with clear signatures of Transposable Elements (TEs) repression in all tissues, as indicated by ping-pong amplification patterns. Mapping piRNA-producing genomic loci revealed a 850 kb pericentromeric region on the short arm of chromosome 8 that concentrates more than 40% of piRNA production in *C. congregata* ovaries. We also detected a piRNA response covering bracovirus sequences located within the “macrolocus”, a large genomic region encoding 80% of the virulence genes. This piRNA-mediated regulation might trigger degradation of virulence genes transcripts, thereby limiting the production of parasitism-related proteins that could be harmful to the wasp if expressed in the ovaries.

The Endosymbiont Consortia of Two Cixiidae Planthoppers Reveal an Ancient Symbiosis With 'Candidatus Mirabilia Symbiotica'

Bessem CHOUAIA (INRAE, Bessem.chouaia@inrae.fr)

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Abstract

Insects of the suborder Auchenorrhyncha harbour multiple ancient endosymbionts that jointly produce essential nutrients lacking from the host's diet. Compared to cicadas, leafhoppers, and spittlebugs, our understanding of the multipartite symbioses among planthoppers, an extremely diverse insect group, remains very limited. Herein, we assembled the genomes of the primary endosymbionts of two planthopper species from the Cixiidae family, *Cixius wagneri* and *Pentastiridius leporinus*, both vectors of the phytopathogenic bacterium *Arsenophonus* in Europe. Each species harboured a different tripartite endosymbiont consortium: while *P. leporinus* carried the well-known combination 'Candidatus Karelulcia muelleri', 'Ca. Vidania fulgoroideae', and 'Ca. Purcelliella pentastiridiorum', *C. wagneri* harboured an unknown Gammaproteobacterium in addition to *Karelulcia* and *Vidania*. This new endosymbiont, 'Ca. Mirabilia symbiotica' is likely much older than *Purcelliella*, considering its extremely reduced genome. In both species, *Karelulcia* and *Vidania* jointly produce the 10 essential amino acids, whereas *Purcelliella* and *Mirabilia* provide the non-essential amino acid cysteine and slightly different gene sets encoding B vitamins. Our findings confirm the functional stability of multipartite planthopper endosymbiont consortia despite changing partners over evolutionary time.

Assessing Supply and Demand Within Symbiosis: Metabolic Economics in the Pea Aphid–Buchnera Interaction

Léo GERLIN (INRAE, INSA Lyon, UMR0203 BF2i, Leo.gerlin@inrae.fr)

Karen GAGET, Garance LAPETOULE, Yohann QUIVET, Patrice BAA-PUYOULET, Isabelle RAHIOUI, Mélanie RIBEIRO LOPES, Pedro DA SILVA, Federica CALEVRO, Hubert CHARLES

Abstract

Many herbivorous insects feed on unbalanced diets and rely on bacterial endosymbionts to meet their complete nutritional needs. This is the case for the pea aphid (*Acyrtosiphon pisum*), a plant pest whose remarkable growth and reproductive capacities cannot be sustained by its sole nutritional resource, the plant phloem sap. Instead, it depends on a symbiotic relationship maintained over millions of years with the intracellular bacterium *Buchnera aphidicola* for the biosynthesis of amino acids and vitamins. Using original experimental data and metabolic reconstructions, we have built the first quantitative genome-scale metabolic model of *B. aphidicola* and used it to quantify amino acid supply from the bacterium to the host. First, we identified metabolites supplied by *A. pisum* that can allow rewiring metabolic fluxes and influence the balance between selfish (growth-focused) and mutualistic (amino acid supplying) behaviors. Among the total amino acid flux from *Buchnera* to *A. pisum*, phenylalanine, tyrosine and leucine represent the main matter sinks and consume more than 60 % of glucose and serine provided by the host. Finally, we compared the predicted bacterial supply to the aphid's amino acid demand. We found that the pea aphid may efficiently regulate symbiont population density according to its metabolic requirements, but that embryos are not quantitatively self-sustaining, with embryonic bacterial supply falling short of demand by 50 %. Overall, by incorporating the quantitative dimension of supply and demand within this symbiosis, we highlight novel candidate compounds and pathways that could be targeted to destabilize this obligatory interaction and allow better predictions of its resilience to environmental or nutritional perturbations.

#12398

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Molecular mechanisms of thermal plasticity and acclimation in aphid holobionts

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Abstract

Aphids are very well adapted to their environment, thanks to their co-evolution with endosymbiotic bacteria. The involvement of the facultative endosymbiont *Serratia symbiotica* in resistance to heat shock is well known, although the underlying molecular mechanisms remain unclear. The involvement of other facultative endosymbionts such as *Hamiltonella defensa* and *Regiella insecticola* in this resistance is also poorly documented. To determine the role of endosymbionts in the response of aphids to environmental stress, and more specifically how these endosymbionts affect the host's response to temperature, we first determined the thermoregulatory behaviour of aphids by identifying their thermal preferences on leaf surfaces and their thermal limits. We then measured the thermal tolerance of aphids exposed to a series of temperatures. To achieve this, firstly we determined the thermoregulatory behaviour of aphids by measuring their thermal preferences on leaf surfaces and their thermal limits. Secondly, we characterised the molecular mechanisms involved in the thermal acclimation of aphids using a DualRNA-seq approach. Sequencing was performed on pea aphids with a single genotype and a single genotype for their obligate endosymbiont *Buchnera aphidicola*. In the samples, only the presence or absence of the facultative endosymbionts *S. symbiotica*, *H. defensa*, and *R. insecticola* discriminates between samples, which allowed for the identification of candidate genes in both the aphid and the endosymbionts that are likely involved in the host's resistance to rising temperatures.

Viral spillover and strain turnover in a parasitoid biocontrol agent

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Abstract

Microbiomes of insect biocontrol agents remain poorly characterised, despite their potential to influence biocontrol efficacy. Using a unique archival collection of the parasitoid wasp *Microctonus hyperodae*, a biocontrol agent released throughout Aotearoa New Zealand in the 1990s, we are examining how a DNA virus, *Microctonus hyperodae* filamentous virus (MhFV), spread and evolved within this system.

Using samples collected during the eight-year mass-rearing programme and from the field after the establishment of biocontrol, we have tracked MhFV prevalence in asexual isofemale lines of *M. hyperodae* collected from South America. Lineages from East and West of the Andes are genetically distinct, with MhFV initially restricted to Eastern wasp lines; however, during mass-rearing, spillover of MhFV into Western lines resulted in all wasp lines carrying MhFV.

Although equal proportions of wasps from each collection location were released, field collections from the 1990s and 2020s show consistently lower than expected proportions of West Andean wasps. All field samples also carry MhFV, despite initial releases including uninfected West Andean wasps. This high MhFV prevalence suggests that infected wasps may have outcompeted uninfected wasps, and/or that additional spillover was occurring in the field after release.

Population resequencing has revealed that certain strains of MhFV are predominant, though the strains are no longer as distinct in contemporary samples as they were initially. We are currently investigating whether MhFV spillover resulted in wasps co-infected with multiple strains and whether that resulted in recombinant MhFV strains. With recent declines in the efficacy of this biocontrol programme, we are interested in how viral evolution may have impacted long-term biocontrol success.

Together, these findings demonstrate how symbiont spillover and evolution might shape the composition and efficacy of biocontrol agents. Considering parasitoids as holobionts is essential for understanding the evolutionary trajectories and long-term efficacy of biocontrol programmes.

#11178

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Functional Prediction of the Gut Microbiome in *Vespa mandarinia* Based on Long-Read 16S rRNA Sequencing

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Abstract

Vespa mandarinia, a eusocial insect, maintains diverse symbiotic relationships with gut-associated microorganisms that contribute to host nutrition and immune regulation. In this study, the functional potential of the gut microbiome of *V. mandarinia* was inferred using PacBio full-length 16S sequencing data in combination with QIIME2 and PICRUSt2. Taxonomic classification based on the SILVA database (version 138.2) revealed that the dominant bacterial genera included *Lactobacillus*, *Gilliamella*, and *Snodgrassella*.

Functional prediction using PICRUSt2 indicated that the most abundant metabolic pathways among the top 20 MetaCyc categories were coenzyme A biosynthesis (PWY-7663), L-lysine biosynthesis (PWY-5973), and peptidoglycan biosynthesis (PWY-5100). These predictions were supported by low NSTI values ($\text{NSTI} < 0.02$), indicating high prediction accuracy and suggesting active microbial growth and a strong capacity for essential biomolecule synthesis. Furthermore, KEGG Orthology-based functional analysis revealed a predominance of genes associated with ATP-binding cassette (ABC) transport systems, with nutrient acquisition-related genes such as sucrose-6-phosphatase (K07024) being highly represented.

These results suggest that the gut microbiome of *V. mandarinia* may play a crucial role in host energy supply and metabolic homeostasis through essential nutrient biosynthesis and efficient substrate transport. This study provides fundamental insights into the functional landscape of the gut-associated microbial community in *V. mandarinia* and establishes a basis for future integrative investigations of host-microbiome interactions.

Until death do us not part: microbiota-pathogen interactions beyond host death

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Alexandra VON BISMARCK, Mathias FRANZ

Abstract

The host microbiota can interact with pathogens, providing protection against infection and impacting the evolution of pathogen virulence, i.e., the infection-induced reduction in host fitness. We are interested in investigating whether such microbiota-pathogen interactions can also occur after the host's death and what the implications would be for the evolution of pathogen virulence. Such interactions could be particularly relevant for insect pathogens that can utilize tissues of dead hosts for their growth and reproduction. We performed experiments using *Tenebrio molitor* and the bacterial pathogen *Pseudomonas entomophila* to test whether microbiota-pathogen interactions occur after host death. As a baseline, we first confirmed that in the absence of infection, the resident host microbiota grows after host death. Accordingly, the microbiota seems to grow on dead host tissue and therefore potentially act as a competitor for pathogens after they kill their host. We then infected both larvae with intact gut microbiota (CR-treated) and antibiotic-treated larvae (AB-treated) with *P. entomophila*. In AB-treated larvae, we found that the pathogen load increases after host death. In contrast, this was not the case in CR-treated larvae. Accordingly, in this system we found support for the hypothesis that the host microbiota competes with the pathogen after host death. This competitive effect could limit pathogen fitness and thus influence pathogen evolution. More generally, we hypothesize that such microbiota-pathogen interactions beyond host death could critically influence virulence evolution in pathogens by limiting the benefits of killing the host and exploiting dead host tissue. In future experiments we aim to test this hypothesis more directly.

#10791

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Bee-yond genomes: reusing large-scale sequencing data to metagenomically explore the honey bee holobiont

Thibault LEROY (GenPhySE, Université de Toulouse, INRAE, ENVT, 31326, Castanet Tolosan, France, Thibault.leroy@inrae.fr)

Julie BIRGEL, Claire HOEDE

Abstract

To date, our BeeGEES lab from the GenPhySE research unit at INRAE Toulouse, France, has resequenced more than 2,700 complete honey bee genomes. This includes about 1,200 haploid drones and around 1,500 queen genomes reconstructed from pools of workers using a pooled sequencing approach. With this large dataset, our team has gained important insights into honey bee evolution and into the genomic architecture of varroa mite resistance. In this poster, we will also present early results from a broad reanalysis of genomic data from hundreds of colonies with the objective to better describe the bee microbiome and its role in shaping bee health and resilience.

In practice, we carried out a metagenomic study using the reads that did not map to any of three high-quality honey bee reference genomes, then assuming these unmapped reads as non-bee DNA. We then applied metagenomic methods, including taxonomic assignment, based on several hundred million non-bee reads. Overall, we detected roughly two hundred bacterial families, with five of them forming most of the core microbiome and representing about two thirds of all assigned non-bee reads. The alpha diversity of the bee microbiome shows a strong correlation with the health status of the colony, more precisely the abundance of the varroa mites, raising questions about the direct or indirect impact of the parasite on bee-associated bacterial communities. In contrast, beta diversity appears more linked to the bees' genetic background, suggesting that the host genome may influence the structure of the bee microbiome. Finally, we will present perspectives on the host genetic factors that may influence microbiota control, as well as on the functional roles of the assembled genes from the reconstructed microbial genomes (MAGs).

Microbiota changes in the Olive Fruit Fly *Bactrocera oleae* driven by antimicrobial treatments of egg-infested olives

Laura MARETTO (University of Padova, DAFNAE Department, Laura.maretto@unipd.it)

Ivana CAROFANO, Isabel MARTINEZ-SAÑUDO, Marco FALASCO, Giacomo SANTOIEEMMA, Corrado PERIN, Hannes SCHULER, Markus RIEGLER, Jennifer MORROW, Luca MAZZON

Abstract

The olive fruit fly, *Bactrocera oleae* (Diptera: Tephritidae), is one of the most damaging pests of olive cultivation, and its management still largely depends on chemical insecticides. Increasing regulatory constraints and environmental concerns have shifted attention toward alternative strategies that target key biological processes of the pest. A central biological dependency is the obligate association with *Candidatus* *Erwinia dadicola*, which enables larval development within olives through its nutritional and detoxification functions and contributes to adult fitness. In a first study, the symbiotic association was challenged using five antimicrobial compounds (copper oxychloride, dodine, tannins, flavonoids, and a Zn-Cu-citric acid biocomplex) applied to egg-infested olives. Treatments resulted in a marked reduction of *E. dadicola* abundance in larvae, with dodine and the Zn-Cu-citric acid biocomplex producing the strongest effects. Symbiont depletion was consistently associated with impaired pest performance, as reflected by reduced pupation success. Based on these results, a second study focused on the effect of the antimicrobial treatment on the microbiota across pest development. Using 16S rRNA gene metabarcoding combined with qPCR, bacterial communities were characterized in larvae, pupae, and adults emerging from treated infested olives. The antimicrobial exposure caused a pronounced reduction in bacterial richness at the larval stage and induced shifts in community composition that persisted through pupation into adulthood. Alongside *E. dadicola*, four recurrent bacterial taxa involved in nutrient metabolism and detoxification (*Acinetobacter*, *Bacillus*, *Flavobacterium*, and *Corynebacterium*) were consistently depleted, with effects varying across developmental stages. Together, these studies show that antimicrobial treatments targeting egg-infested olives can disrupt a key symbiotic relationship and reshape the associated microbiota, imposing an early microbial bottleneck that affects both the primary symbiont and the broader bacterial community. The resulting microbiota alterations persist across development and are translated into reduced host performance, supporting microbial symbiosis as a viable target within integrated pest management programs.

Microbial Abundance and Diversity in Parasitic Hymenoptera

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Piotr ŁUKASIK

Abstract

Symbiotic microorganisms can shape insects' nutrition, reproduction, defense, and other traits, yet we know little about their diversity beyond a few model clades. For example, in Hymenoptera, microbiota research has strongly focused on two clades, bees and ants, while the remainder of the order's diversity, which primarily comprises parasitoids, remains poorly studied. These hyper-diverse and understudied insects play tremendously important roles in shaping host arthropod populations and multispecies communities and have been postulated as vectors of facultative endosymbionts among host species. Alternatively, because of their biology, they may have limited opportunities to develop specialized gut microbiota. However, systematic data on how microbial abundance and diversity vary among host lineages are lacking.

We aim to characterize bacterial and fungal symbioses across hymenopteran parasitoid taxa comprehensively. Specifically, we asked (1) how bacterial diversity and abundance vary across hymenopteran parasitoid taxa; (2) how geography shapes microbiota within and among species; and (3) whether we may identify common and region-specific partners that might influence host nutrition, immunity, or reproduction. To do this, we used an innovative approach – the simultaneous sequencing of insect, bacterial, and fungal genes, including microbiota quantification – applied to a collection of more than 3,000 diverse parasitic Hymenoptera collected from Greenland, Poland, and Madagascar, and analyzed several individuals from different habitats.

Our data reveals massive variation in bacterial abundance and community composition among the surveyed wasps. Many species harbor very low bacterial loads – are virtually sterile. On the other hand, the microbiota of others is dominated by abundant facultative endosymbiotic bacteria such as *Wolbachia*. Broadly, we found little evidence for the common presence of abundant, specialized microbial communities comprising taxa other than endosymbionts. In my presentation, I will explain how these patterns vary among taxonomic groups and biogeographic regions.

Symbiotic communities of *Planococcus ficus* (vine mealybug) from two vineyards varieties

Diego SANTOS GARCIA (Centre de Biologie pour la Gestion des Populations - UMR CIRAD, IRD, SupAgro, Université de Montpellier, INRAE – France,
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Guénaëlle GENSON, Netta MOZES-DAUBE, Lilach IASUR KRUH, Einat ZCHORI-FEIN

Abstract

The vine mealybug (*Planococcus ficus*) is a phloem-feeding insect, a major pest of grapevines (*Vitis vinifera*), and the principal vector of Grapevine leafroll-associated virus 3 (GLRaV-3). As insect symbionts may interfere with virus transmission, we investigated the biodiversity and dynamics of its gut symbionts, sampling mealybugs from low and high GLRaV-3-symptomatic grapevines. We analyzed their associated microbial communities using 16S rRNA amplicon sequencing, cultivation, and whole-genome shotgun sequencing.

We collected mealybugs from two different vineyards. Both populations carried the obligate symbionts *Tremblaya princeps* and *Moranella endobia*. However, mealybugs from Dalton vineyard had high loads of *Serratia symbiotica*, while those from En Zeitim harbored an abundant, previously undescribed *Acetobacteraceae* species. Both facultative bacteria were nearly absent after one laboratory generation, suggesting they are environmentally acquired; their detection in grapevine leaves supports this. We successfully cultured *S. symbiotica* and the novel *Acetobacteraceae* isolate. Comparative genomics show both cluster with facultative insect symbionts and possess pathways for riboflavin, biotin, thiamine, and pantothenate synthesis, a set of vitamins absent from vine phloem.

We suggest that *S. symbiotica* and the novel *Acetobacteraceae* species are environmentally acquired, plant-associated bacteria capable of colonizing *P. ficus*. Their potential role in supplementing biotin suggests a potential fitness benefit to the insect. Moreover, the colonization capacity of *S. symbiotica* opens promising avenues for microbiome-based pest control strategies.

Temporal and spatial dynamics of Wolbachia prevalence in *Drosophila suzukii* populations from France

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Dimitri CHOUEIRY, Nicolas BOROWIEC, Adrien LE-NAVENANT, Léa DARMEDRU, Benjamin COELHO, Mélanie HUGUET, David MONNIN, Capucine PERREY, Jeanne MONNIER, Ghais ZRIKI, Nicolas RODE

Abstract

The incompatible insect technique (IIT) is promising eco-friendly strategy for suppressing populations of vector and pest insects, which is based on the induction of male sterility by the endosymbiont Wolbachia. This phenomenon, known as cytoplasmic incompatibility, results in embryonic mortality when Wolbachia-infected males mate with uninfected females. In contrast, infected females can rescue this incompatibility, allowing normal embryo development. Therefore, the initial frequency of infected females in target populations critically determines the efficiency of IIT releases. *Drosophila suzukii*, an invasive agricultural pest, has caused major economic losses and is a strong candidate for IIT-based control. Wolbachia prevalence varied from 0 till 100% among natural populations (2010-2016), making it essential to understand its dynamics for the successful application of IIT.

We investigated the temporal and spatial dynamics of Wolbachia infection frequencies in *D. suzukii* populations from France, where IIT could potentially be implemented. By screening multiple populations sampled across different regions and time periods (n=59), we detected a pronounced decline in Wolbachia prevalence over a ten-year period (2016-2025), from 41% to 8%. This decline is likely due to selective processes (i.e. fitness effects influencing host survival and reproduction). At one location, we further compared two sampling sites separated by only 600 m and observed a persistent difference in Wolbachia prevalence between them, highlighting the importance of local environmental conditions in shaping infection dynamics.

We discuss the evolutionary and ecological mechanisms underlying these patterns, including, genetic drift, fitness effects, maternal transmission efficiency, and fluctuating selection due to temporal environmental variation. Importantly, our results provide critical insights into the feasibility of using a natural Wolbachia strain for IIT-based control of *D. suzukii* in France. However, accurate location-specific estimates of Wolbachia prevalence are essential, as the release of flies infected with natural strain may remain risky even in populations with low infection frequencies.

Wolbachia as a key player in a model butterfly for research on speciation and chromosomal evolution

Eric TORO DELGADO (Institut de Biologia Evolutiva (CSIC-UPF), Universitat de Barcelona (UB), Eric.toro@ibe.upf-csic.es)

Vlad DINĂ, Emily HORNETT, Vladimir LUKHTANOV, Niclas BACKSTRÖM, Magne FRIBERG, Christer WIKLUND, Roger VILA

Abstract

Wolbachia is a highly frequent bacterial endosymbiont of arthropods. Many of its strains can induce cytoplasmic incompatibility (CI), a phenomenon in which matings between infected males and uninfected females present substantially reduced fecundity. Despite being frequent in Lepidoptera, one of the most ecologically and economically relevant insect orders, our understanding of the distribution and consequences of *Wolbachia* in this insect order are limited. In this study, we investigated the prevalence, diversity and CI potential of *Wolbachia* strains in the butterfly genus *Leptidea*, an important research model on speciation and chromosomal evolution. Using PCR, we screened a total of 422 specimens across seven species, distributed from Western Europe to China, using *wsp* and *coxA* markers and/or multi-locus sequence typing (MLST). We found *Wolbachia* infection in five species, with prevalence ranging from 70% up to 100%. MLST revealed four different strains, with several species being infected by the same strain, suggesting recent horizontal transfer of the symbiont. In addition, we also conducted crosses of infected and uninfected *Leptidea juvernica* specimens, obtaining the first experimental evidence for cytoplasmic incompatibility within European butterfly populations. Lastly, we also screened whole-genome sequencing data of the *L. sinapis* complex, finding putative CI loci in all infected populations. This study illustrates how advances in genomics facilitate the study of *Wolbachia* phenotypes and evolutionary history.

#12094

Poster Session 1 - Ice breaker party
29/06/2026 at 16:00, Exhibition area

Recovering plant-associated arthropod communities by eDNA metabarcoding historical herbarium specimens

Manuel STOTHUT (Trier University, Stothut@uni-trier.de)

Henrik KREHENWINKEL, Lisa MAHLA, Lennart BACKES, Sven WEBER, Amirmohammad AVAZZADEH, Majid MORADMAND

Abstract

Natural history collections are a priceless resource for understanding patterns and processes of biodiversity change in the Anthropocene. Herbaria, which house millions of historical plant records from all over the globe, are particularly valuable to study population genetics of the plants themselves and to understand the assembly of plant-associated microbial communities. Here we test if herbaria can serve yet another essential purpose, namely to provide information on the historical assembly of plant-arthropod interactions. The specificity and temporal stability of these associations are poorly known. Considering their pivotal role in the assembly of terrestrial food webs, this knowledge is paramount to understanding the consequences of global change. We use environmental DNA (eDNA) metabarcoding to characterize communities of plant-associated arthropods from archived herbarium specimens of different ages and origins. The herbarium specimens yield arthropod DNA across various ecological guilds and trophic levels over multiple decades. In an experiment, we also show that the typical dry storage of plants in herbaria does not alter the recovered arthropod diversity and community composition. By analyzing a time series of leaf samples from a forest monitoring project, we then characterize changes in arthropod biodiversity over two decades, showing that archived plants can also provide the time series data that are urgently needed to understand arthropod declines. This use of herbaria and plant archives promises unprecedented insights into plant-arthropod interactions and revolutionizes our ability to monitor spatiotemporal changes in interaction diversity.

Ornamental plant trade: an active pathway for alien ant introductions in France

Romane BLAYA (Avignon Université, IMBE, Romane.blaya@gmail.com)

Marine NICOLAS, Ludivine PONS, Eline HIRON, Jérémy MIGLIORE, Olivier BLIGHT

Abstract

Invasive alien species represent a major threat to the functioning of ecosystems. More than 500 species of ants have been introduced outside their native ranges, some with major impacts on the biodiversity and economy of the invaded areas. The spread of these species at different spatial scales is mainly caused by human activities. One of the main routes of introduction for these exotic species appears to be the ornamental plant trade. Despite the increase in introductions and the recent arrival in Europe of species of particular concern, such as *Solenopsis invicta* and *Wasmannia auropunctata*, little information is available on this route of introduction to the continent. By studying the myrmecofauna of nurseries in the South of France (Vaucluse and Var), the aim is to identify the role of the plant trade in the introduction of invasive alien species in the region, and particularly *Wasmannia auropunctata*. In 2024 and 2025, initial results from 22 nurseries showed that this route of introduction is particularly active, with around five new species identified for mainland France and 2 new species for Europe. The diversity of origins of the identified species also reflects a process of assisted dispersal operating at different spatial scales. The plant trade thus plays a role at the global level, through the presence of species from other continents, at the European level, by promoting the dispersal of species native to neighboring countries, but also at the metropolitan level, by assisting in the spread of already highly dominant species, particularly those of the genus *Tapinoma*. The potential of establishment of some key exotic ants outside the greenhouses will be assessed using Species Distribution Models (SDM).

Reassessing the Parasitoid Assemblage of *Rhagoletis cerasi* in Europe to Support Proactive Classical Biological Control in the U.S.A.

Marie-Claude BON (European Biological Control Laboratory-USDA-ARS, Mcbon@ars-ebcl.org)

Gaylord DESURMONT, Javid KASHEFI, Nicholas MANOUKIS, Marie ROCHE

Abstract

Rhagoletis cerasi (Diptera: Tephritidae), the “European cherry fruit fly” (ECFF), is a major pest of cherries across Europe together with the spotted wing drosophila, *Drosophila suzukii* (Diptera, Drosophilidae). Larval feeding causes fruit breakdown and substantial reductions in marketable yield. Although native to Southern and Central Europe, ECFF was first detected in Ontario, Canada in 2016 and in New York State in 2017. To date, ECFF has not been reported from other U.S. cherry-producing states, but its establishment in New York increases the risk of further spread. To mitigate this threat, proactive development of classical biological control strategies is needed to support growers and help prevent the pest’s expansion into major production states.

Historical literature indicates a diverse assemblage of natural enemies—primarily parasitoids—associated with ECFF in its native range. Of the 21 parasitoid species recorded, three appear especially promising for biological control: the larval braconids *Utetes magnus* and *Psytalia rhagoleticola*, which have been reported to parasitize up to 32% of host larvae, and the ichneumonid *Phygadeuon wiesmanni*, which can induce pupal mortality of up to 72%. However, these studies are decades old, and European cherry orchards have undergone major ecological changes since that time, including dominance by the invasive *D. suzukii*, which may outcompete or disrupt ECFF and its parasitoid guild.

As a first step toward evaluating classical biological control options for North America, we initiated a contemporary survey of the parasitoid assemblage associated with ECFF in Southern France, Switzerland, and Greece. Our aim is to determine whether previously documented parasitoids persist and whether they remain viable candidates for introduction. We present the findings from the first year of this effort and discuss future work possibilities to develop effective classical biological control against ECFF.

#12542

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Integrated Pest Management for Wood-Boring Beetles Introduced into Europe

Alicia BRAY (Central Connecticut State University, Aliciabr@ccsu.edu)

Abstract

Wood-boring beetles are an increasing global problem due to international trade and travel. Beetles native to North America or Asia, including the walnut twig beetle (*Pityophthorus juglandis*) and black timber bark beetle (*Xylosandrus germanus*), are found in various countries in Europe. Integrated pest management strategies will be presented to control these and other wood-boring beetles

Monitoring of invasive Auchenorrhyncha species in Romanian vineyards

CONSTANTINA CHIRECEANU (Research & Development Institute for Plant Protection Bucharest, Romania, Cchireceanu@yahoo.com)

ANDREI TEODORU, Marioara PUSCALAU, Teodor PODRUMAR, Ionica DINA, Bogdan RADU, Ruxandra STOICA, Camelia DIRLOMAN, Daniela DOBROMIR

Abstract

Invasive insect pests are one of the main factors affecting the viticultural ecosystems worldwide. Their invasion can be effectively managed when their detection is carried out at an early stage within surveillance and monitoring programs. The aim of this study was to bring new knowledge on the current situation of invasive Auchenorrhyncha species inhabiting Romanian vineyards, obtained through the surveillance and early detection program within the ADER 6.3.16 research project. The study was performed on a network of forty vine plantations distributed in six vineyards, Miniș-Măderat, Dealu Mare, Odobești, Cotești, Panciu and Murfatlar in four viticultural regions: Crișana and Maramureș Hills, Muntenia and Oltenia Hills, Moldova Hills and Dobrogea Hills located in the country in NW, S, E and SE, respectively. The vine plots were planted with local and international varieties and managed in conventional or organic system. The plots were surveyed in 2024 and 2025, and insects were monitored using yellow sticky traps, four traps per plot, replaced every ten days from May to October. Nine species of invasive Auchenorrhyncha were identified, species entered into the country after 2000y such as *Erasmoneura vulnerata*, *Arboridia kakogawana*, *Orientus ishidae*, *Acanalonia conica*, *Metcalfa pruinosa*, *Scaphoideus titanus*, and species already present in the native entomofauna such as *Stictocephala bisonia*, *Japananus hyalinus* and *Phlogotettix cyclops*, classified to four families, namely Cicadellidae (six species), Membracidae, Flatidae and Acanaloniidae (one species each). The Japanese and N American Typhlocybinae leafhoppers, *A. kakogawana* and *E. vulnerata*, in continuous territorial expansion, have registered the largest populations. The N American leafhopper *S. titanus* has been present with constant annual populations, except in the Murfatlar Vineyard. The presence of three species, the Asian mosaic leafhopper *O. ishidae* (Deltocephalinae), the citrus honey leafhopper *M. pruinosa* (Flatidae) and the green cone-headed leafhopper *A. conica* (Acanaloniidae) was noted in the Dealu Mare Vineyard.

#11276

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Alien invasion threatens pollinator refuge

Florian COSA (Laboratory of Zoology, Research Institute for Biosciences, University of Mons, Mons, Belgium, Florian.COSA@umons.ac.be)

Denis MICHEZ, Guillaume GHISBAIN, Clément TOURBEZ

Abstract

Alien species invasions are major drivers of biodiversity loss and ecosystem disruption. Among them, alien invasive plants (AIPs) compete with native flora, reshaping the availability of resources for pollinators. In a context of global pollinator decline, such invasions represent a serious potential threat, particularly when occurring in habitats of high conservation value. Quarry grasslands are examples of such habitats that serve as refuges for many threatened species (e.g. plant specialist species) but are increasingly exposed to AIP invasion. Ranked among Europe's most detrimental plant invaders, the butterfly-bush *Buddleja davidii* has widely colonised quarry grasslands, yet its impacts on native plant-pollinator communities remain poorly quantified. We surveyed 26 quarry grasslands in the province of Hainaut (Belgium) presenting invasion gradient of *B. davidii*. We analysed the correlation between AIP gradient and : (i) floral resource availability (estimated based on floral units, FU), (ii) species richness and abundance of bees, hoverflies, and butterflies, and (iii) species-level abundance of dominant pollinator species. We further examined which pollinator species benefited from *B. davidii* as foraging resource. FU surveys revealed that *B. davidii* invasion markedly reduced non-*B. davidii* FU abundance without compensating for their loss. *B. davidii* flowers attracted few visitors (33 species on the 146 recorded species), suggesting that invasion may increase floral resource deficit for most pollinator species. Although overall pollinator species richness remained stable at the site level, species-level analyses revealed losses hidden by these general trends, with half of the most widespread pollinator species showing significant declines along the invasion gradient. These findings reveal that AIPs can deplete floral resources and erode populations of common pollinator species, even when community-level responses appear stable. This pattern underscores that biodiversity refuges, though sheltered from many anthropogenic pressures, remain vulnerable to biological invasions capable of pushing even common pollinator species toward local extinction.

SAFEGRAPE: leveraging citizen science to monitor endemic and emerging pests in French Vineyards

Lionel DELBAC (INRAE SAVE, Lionel.delbac@inrae.fr)

Rahil AMIN, Xavier BURGUN, Christian DEBORD, Lucile MARESCOT, Christine MEYNARD, Adrien RUSCH

Abstract

Endemic and invasive insect pests (e.g., Drosophilidae, Cicadellidae, Lepidoptera) pose potential risks to French vineyards, yet little is known about what factors drive their population dynamics. A key challenge is identifying the multi-scale environmental variables (farming practices, landscape structure, climate context) that explain their occurrence and population fluctuations. To anticipate future risks, we need hierarchical statistical modelling approaches that incorporate spatio-temporal dynamics and traits of species that are both already established or threatening to emerge. This will enable us to (i) produce knowledge on the ecology of key pests, and (ii) help practitioners to assess, anticipate and manage risks. However, robust predictions require high-quality *in situ* data from large-scale monitoring networks. To achieve this, we established a citizen-science monitoring network across French vineyards since 2022. The design creates a seamless feedback loop where: i) we provide each partner with a trapping kit and standardized protocol, ii) the partners implement the protocol and send us the trapped specimens, iii) we identify the target species, iv) we inform the partners of the results obtained, and v) we compile our database for analysis. Our network currently involves 60 partners (wine consultants, winegrowers, technical institutes and agricultural cooperatives) and consists of 158 vine fields covering the different French wine-growing regions, from Brittany to Alsace and from Corsica to Champagne. Since 2022, we have collected 2,500 traps and identified over 50,000 insects, enabling us to detect first emergence of serious invasive pest species such as the leafhopper *Jacobiasca lybica* and the fruit fly *Zaprionus tuberculatus* in the French vineyard. We are now coupling this monitoring effort with multi-scale Joint Species Distribution Modelling (JSDM) to provide practitioners with the predictive tools needed to assess and manage emerging risks.

Southern French winegrowers 'contribution in monitoring an invasive vine moth

Lionel DELBAC (INRAE SAVE, Lionel.delbac@inrae.fr)

Julia FERRÉOL, Nicolas CONSTANT

Abstract

Among the invasive pests of grapevines, the honeydew moth, *Cryptoblabes gnidiella* (Lepidoptera: Pyralidae), represents the main phytosanitary problem for vineyards in southern France. First detected 25 years ago, the species now causes rapidly increasing damage, surpassing that caused by grape moths. Mapping its spread and impact on one of France's largest vineyard regions requires significant resources. One of the solutions we considered was to ask the stakeholders directly—namely, the winegrowers—to help us obtain this essential information. We therefore took a participatory science approach, conducting a survey over two consecutive years and sending it to thousands of winegrowers via professionals (e.g., advisers, cooperative wineries, technical institutes) who work with them. We collected more than two hundred responses per year. These responses enabled us to draw up an accurate map of the geographical spread of the species, which extends more than 100 km north of the vineyards where it was first detected, near the Mediterranean coast. The extent of the damage and the resulting management measures highlighted gaps in our knowledge, particularly regarding the factors explaining the presence and abundance of the species in the plots. Some volunteer winegrowers were contacted again to explore this aspect in more depth through a more detailed questionnaire. This shows that crop practices such as grass cover on plots and mechanical harvesting are favourable factors for the species. Similarly, the environment surrounding the vineyard plot, such as urban habitat or other vineyard, has a significant impact on its susceptibility. These results provide clues for developing better in situ management of the species.

Integrated Post-Entry Surveillance of the Oriental Fruit Fly: Pathway Analysis and Targeted Trapping Approaches in a European Quarantine Context

Wannes DERMAUW (Plant Sciences Unit, Flanders Research Institute for Agriculture, Fisheries and Food (ILVO), Belgium, Wannes.dermauw@ilvo.vlaanderen.be)

Jochem BONTE, Lore ESSELENS, Luiza MITRACHE, Fanny KRATZ, Alexandre KUHN, Louis HAUTIER, Marc DE MEYER, Massimiliano VIRGILIO

Abstract

The oriental fruit fly, *Bactrocera dorsalis*, is a tephritid species predominantly inhabiting (sub)tropical regions and is classified as a priority quarantine pest within the European Union (EU). Recent EU-mandated annual surveys have documented the presence of *B. dorsalis* at multiple sites across several EU member states, including Belgium. The PESTFLY project aims to prevent the introduction and establishment of *B. dorsalis* in the EU via Belgian trade or intra-EU spread. To achieve this, the project integrates three core strategies: (1) elucidating the pathways of potentially infested fruit by combining genomic analyses of adult *B. dorsalis* detected in Belgium with trade data on high-risk exotic fruits and associated waste management practices; (2) optimizing surveillance through targeted deployment of traps and intensified sampling at high-risk locations, particularly those linked to exotic fruit waste; and (3) engaging citizen scientists to enhance pest monitoring efforts, thereby increasing both the volume and quality of surveillance data. This multidisciplinary strategy is anticipated to enhance early detection and prevention of *B. dorsalis* in Belgium and the wider EU, while supporting the efforts of the Belgian Plant Protection Organisation.

#10604

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Bulimulus bonariensis, a recent invasive pest in North America and beyond

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Abstract

The invasive land snail, *Bulimulus bonariensis*, has been wreaking havoc on multiple agricultural systems in the Southeastern United States. Due to its life history traits, this species is adept at finding its way into new regions/habitats. As such, it was discovered at the Port of Brisbane, Australia, in the summer of 2025. In the US, we find this species hitchhiking on equipment and vehicles to new locations and then becoming sources of new infestations.

Early impacts were noted in Florida citrus orchards in 2020, with *B. bonariensis* aggregating on irrigation, thereby blocking both water and fertilizer delivery to trees, removing critical resources from trees already afflicted with an incurable pathogen. Since then, direct damage to trees has been documented, as well as damage to other crops including vegetables, peanuts, cotton, and soybeans. Additionally, this species has become an urban nuisance pest, necessitating management options for both commercial and residential clientele.

Our research team has been monitoring *B. bonariensis* in commercial citrus orchards and evaluating available management options. From this, we have found seasonal cycles that roughly align with periods of high moisture. During wet, temperate periods, trap captures decrease, whereas in the dry/hot periods, trap capture increases as snails seek refuge from increasingly poor foraging environment. In laboratory assays, we have evaluated available bait products, all of which perform well in enclosed environments; however, this may not directly translate to field performance. Meanwhile, growers noted that some of the pesticides currently used in their orchards appeared to have impacted the snails. As such, we have been evaluating pesticides (molluscicides, insecticides, herbicides, and fungicides) currently used in Florida citrus orchards. To date, we have documented the efficacy of one insecticide and one herbicide towards the mortality of this species.

Laboratory evaluation of the predation effectiveness of *Chrysoperla lucasina* (Lacroix) against the invasive alien species *Cydalima perspectalis* (Walker)

Serena GALLIZIA (Department of Agricultural, Forest and Food Sciences, University of Turin, Grugliasco, Italy, Serena.gallizia@unito.it)

Chiara LAI, Laura LORU, Chiara FERRACINI

Abstract

Cydalima perspectalis (Walker) (Lepidoptera; Crambidae), commonly known as the box tree moth, is an invasive lepidopteran species native to Asia that has rapidly spread across Europe following its accidental introduction through the ornamental boxwood trade (*Buxus* sp.). Since its first record in Germany in 2006, *C. perspectalis* has colonised urban and natural environments throughout the continent, posing a serious threat to natural *Buxus* stands, including those within Natura 2000 Habitat 5110. In Europe, parasitism and predation by indigenous natural enemies are generally sporadic. Several generalist predators have been documented on *C. perspectalis* in natural conditions, including insectivorous birds, bats, spiders and insects belonging to the orders Thysanoptera, Hemiptera, and Neuroptera. In literature, preliminary laboratory assays, focusing on the predation rate by *Chrysoperla lucasina* (Lacroix) (Neuroptera; Chrysopidae), suggest a good potential of this native species as a biocontrol agent of *C. perspectalis*. In this context, we performed experiments in controlled conditions to test first, second, and third-instar *C. lucasina* larvae exposed to *C. perspectalis* eggs and larvae. Our results showed that all *C. lucasina* instars preyed on *C. perspectalis* eggs, with an average consumption of 3.33 ± 0.36 , 6.11 ± 0.96 , and 7.48 ± 1.10 eggs by first, second, and third-instar larvae, respectively. *C. lucasina* larvae also effectively preyed on *C. perspectalis* larvae of both early and advanced instars. First-instar *C. perspectalis* caterpillars were frequently attacked (> 90% of replicates), whereas larger larvae (5–7 mm) were preyed upon with frequencies ranging from 70% to 87%. Although further trials are needed to confirm these findings under broader experimental conditions, the current results demonstrate a strong predatory performance by *C. lucasina*, making it a promising biocontrol agent against *C. perspectalis*.

The Most Northerly Reported *Vespa velutina* nest, Belfast Northern Ireland

Joanna KIRBAS (Agri-Food and Biosciences Institute, Joanna.kirbas@afbini.gov.uk)

Florentine SPAANS, Archie MURCHIE, Andrew MCCLURE

Abstract

The first *Vespa velutina* nest in Northern Ireland, was found in October 2025. It was located and removed by the Northern Ireland Environment Agency (NIEA) and was analysed by the Agri-Food and Biosciences Institute (AFBI). The finding is of significant concern as this pest poses a major threat as an invasive species, reducing pollinator populations, destabilizing ecosystems, and impairing agricultural productivity through disrupted pollination services. The nest contained 6-7 combs with active brood and was estimated to have produced ca. 3,300 individuals. It is therefore a moderate sized nest, of average size for the time of year and stage of development. A total of 84 adults were found in the nest, including 51 males and 33 females. The queen was absent from the nest, likely having fled when the nest was destroyed. There was a marked dominance of males in the brood as well as the adult stage. Caste analysis of the females indicated that there were at least 25 gynes in the brood, while most of the adult females were workers, with 3-6 individuals being potential newly emerged gynes. The nest appears to be in the early reproductive phase, beginning production of reproductive females. While it is possible that the nest was taken down in the roughly two-week interval where reproductive males are produced before gynes emerge, it is not possible to say with certainty that no fertile gynes have left the nest, though it is unlikely that many would have been able to do so. It is therefore recommended that precautionary trapping for new queens takes place in spring 2026 to prevent the establishment of any subsequent nests and to monitor the area closely for sightings of individuals.

#12268

Poster Session 1 - Ice breaker party
29/06/2026 at 16:00, Exhibition area

Zaprionus tuberculatus (Diptera: Drosophilidae): a new threat for fruit crop production?

Laura LORU (National Research Council (CNR) Institute of Research on Terrestrial Ecosystems (IRET); National Biodiversity Future Center (NBFC), 90133, Palermo, Italy, Laura.loru@cnr.it)

Sandro FLORE, Francesco FODDI, Chiara LAI, Piera Maria MARRAS

Abstract

Zaprionus tuberculatus (Diptera: Drosophilidae), native to tropical Africa, is an invasive fruit fly spreading worldwide including Europe. The species is highly polyphagous and can attack damaged or decaying fruits or ripening fruits, particularly those having an ostiole (e.g. fig) or thin skin (e.g. strawberry). Recorded in Italy since 2013, *Z. tuberculatus* was detected across Sardinia Island in 2024 during a monitoring program targeting the Spotted Wing Drosophila (SWD) *Drosophila suzukii* (Diptera: Drosophilidae). From May to November cultivated (e.g. cherries, peaches, figs, apples, strawberries) and wild (e.g. *Arbutus* berries, elderberries) fruits were collected and maintained in laboratory under controlled conditions to check for emerging pest and parasitoid species. About 39% sampled fruits resulted infested by *Z. tuberculatus* of which 34% and 15% also hosted *D. suzukii* and *Ceratitis capitata* (Diptera: Tefritidae) respectively. Only one fruit sample was shared by the three pest species. No parasitoids emerged from *Z. tuberculatus* pupae. These results prompted a specific monitoring program targeting the invasive *Z. tuberculatus* to assess its impact on fruit crop production in Sardinia.

Spread of Pine Processionary Moth (*Thaumetopea pityocampa* Lepidoptera; Notodontidae) in Continental Urban Areas in Croatia: Monitoring, Risk Mapping and Early Warning System

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Andrija JUKIC, Nikola ZORIC, Martina KICIC, Ivan BALENOVIC

Abstract

Pine processionary moth (*Thaumetopea pityocampa* Lepidoptera; Notodontidae) (PPM) has historically been restricted to Mediterranean regions in Croatia due to its requirement for mild winters to complete its life cycle. However, the species is now exhibiting northward and altitudinal range expansion, a phenomenon increasingly attributed to climate change. In recent years, this expansion has been documented in continental parts of Croatia, notably the Lika region, area previously considered climatically unsuitable due to its harsh winter. Most recently, in early 2025, an outbreak of PPM was recorded in Sveta Nedelja, urban municipality within Zagreb County.

The spread of PPM from Mediterranean regions into continental parts of Croatia, especially urban areas where pines are often planted on private land, marks a significant ecological shift driven by climate change. This poses great public and animal health risk. This expansion highlights the need for early detection and risk assessment in environments not traditionally monitored for forest pests. As the species continues to establish in previously unaffected areas, practical, accessible monitoring approaches and early warning system will become increasingly important for protecting both public and urban tree health.

The project „Expansion of the distribution of pine processionary moth in continental urban areas in Croatia due to the impact of climate change: risk mapping and early warning system“ will monitor its spread, map the risk for urban areas in continental Croatia and develop early warning system for citizens in affected areas. The methods will include field observations, and citizen reports to assess the extent, dynamics, and drivers of its urban spread. Spread will be monitored with unmanned aerial vehicle (UAV) equipped with RGB and thermal sensors.

#12441

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Establishment of a monitoring network for invasive ant species in the Loire Valley regions.

Jean-Luc MERCIER (IRBI - CNRS / University of Tours, Jean-luc.mercier@univ-tours.fr)

Simon DUPONT, Elfie PERDEREAU, Fabrice VANIER, Esteban MOYER, Eline HIRON, Justine CELIS, Antonin GRIMAUTL-FREMY, Louise BELAMY, Fanny CHAUVIRE, Colleen BADE-VRAIE, Romain LIBBRECHT

Abstract

The Loire Valley region has seen the establishment of several invasive ant species in recent years, but currently no monitoring network exists to track their presence and geographic expansion. This is due to the recent nature of these invasions and the difficulty in identifying the problematic species. The FIVALO project, co-financed by the French Office for Biodiversity (OFB), aims to establish a monitoring network to collect, identify, map, and characterize the level of invasion of invasive ant species in the Loire Valley. The project's primary objective is to develop effective methods for sampling individuals and identifying species, based on morphology, chemical ecology, and molecular biology. The data collected over the past two years has enabled the identification and mapping of seven ant species considered invasive in France. Of particular interest is the critical expansion of the ant *Tapinoma magnum*, which we have detected in 86 new cities since the start of the project. Ongoing investigations of invasion history will help assessing the origin, rate of expansion and impact of the invasions.

Current status of the fall armyworm *Spodoptera frugiperda* (J.E. Smith, 1797) (Lepidoptera: Noctuidae) and its natural enemy complex in Türkiye

Serkan PEHLIVAN (Çukurova University, Department of Plant Protection, Spehlivan@cu.edu.tr)

Mahmut Mete KARACA, Başak ULAŞLI, Kamuran KAYA, Ekrem ATAKAN, Hogir CEYLAN, Şebnem TIRENG KARUT, Kamil KARUT

Abstract

The fall armyworm, *Spodoptera frugiperda* continues to expand its distribution across Eurasia, raising concerns for maize production in Türkiye. This study provides a two-year assessment (2024-2025) of its distribution and associated natural enemies in major maize-growing areas of the eastern Mediterranean Region (Adana, Osmaniye, Hatay). Surveys were conducted during both first and second crop seasons, examining 100 maize plants per field. Collected immature stages were reared under controlled laboratory conditions to obtain parasitoids, and predatory insects were sampled for identification.

Infestation levels exhibited strong seasonal and interannual variation. In 2024, low infestation occurred during the first crop (10% overall), whereas the second crop showed a dramatic increase, with 91% of fields infested in Adana, 75% in Osmaniye, and 71% in Hatay, reaching up to 100% infestation at the field level. In 2025, early-season infestations remained minimal (0–1.5%), but late-season infestations increased again, particularly in Adana (34.6%) and Osmaniye (28.6%). These trends confirm that *S. frugiperda* is now established and capable of building high-density populations late in the season.

A diverse natural enemy complex was documented. In 2024, parasitoids were dominated by Braconidae (n = 326), followed by Ichneumonidae (n = 47) and Trichogrammatidae (n = 7), with activity concentrated in the second crop. In 2025, parasitoid emergence was lower but included Braconidae (n = 23) and Trichogrammatidae (n = 18) in Adana. Predatory insects were also abundant, particularly Anthocoridae (n = 102 across years) and Coccinellidae (n = 46), with smaller contributions from Chrysopidae, Geocoridae, Nabidae, and Dermaptera. Predator and parasitoid activity increased during periods of high FAW density.

These findings provide the most detailed evaluation to date of *S. frugiperda* spread and natural enemy communities in Türkiye and offer essential baseline information for developing biologically based integrated pest management strategies.

#16487

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Cryptoblabes gnidiella an emerging pest of grapevines in the southern region of France

JEAN-CLAUDE STREITO (CBGP, INRAE, CIRAD, IRD, Institut Agro Montpellier, Univ. Montpellier, Montpellier, France , Jean-claude.streito@inrae.fr)

Nicolas CONSTANT, Jean-Pierre ROSSI

Abstract

Cryptoblabes gnidiella (Millière, 1867) (Lepidoptera: Pyralidae: Phycitinae), commonly known as the honeydew moth, is a Palearctic species widely distributed across the Mediterranean region, where it is expanding northward. Climate warming has been suggested as the driver of this range shift but robust empirical evidence remains limited. Despite its growing impact on Mediterranean vineyards in France, *C. gnidiella* remains poorly understood. The first step of our research was to identify morphological characters allowing for the reliable identification of the adults, the pupae and the caterpillars. The second part of our study consisted in developing ecological niche models to assess the potential distribution of *C. gnidiella* in Europe according to recent, current and future climate conditions. The results indicated that climate suitability increased in the western Mediterranean region since the 1950s and that this trend is projected to persist under future climate scenarios.

#12486

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

What happens when bumblebees feed on alien food?

Clément TOURBEZ (Laboratory of Zoology, Research Institute for Biosciences, University of Mons, Mons, Belgium, Clement.tourbez@umons.ac.be)

Abstract

Biological invasions are increasingly recognised as major drivers of biodiversity loss. By competing with native plant species, alien invasive plants can alter floral resource availability, potentially triggering cascading effects on pollinator communities. Yet native pollinators often forage on these alien flowers, with largely unknown consequences for their fitness. Among alien invasive plants, *Robinia pseudoacacia* and *Impatiens glandulifera* provide abundant floral resources, with native bumble bees showing strong foraging fidelity to these invasive resources. Here, we investigate how such dietary shifts affect bumble bee (i) colony development, (ii) mortality, (iii) mating success, and (iv) parasite resilience. In May 2025, forty-five *Bombus terrestris* sentinel colonies were deployed across 15 spoil tips experiencing a gradient of invasion by *R. pseudoacacia*. In August 2025, thirty colonies were similarly placed across 10 wetlands gradually invaded by *I. glandulifera*. Colonies developed freely for 25 and 30 days, respectively, encompassing the main flowering period of each species. Following this field phase, colonies were returned to the laboratory to assess colony development, conduct mating experiments between reproductives from the same site, and screen for the trypanosome *Crithidia* spp., a common bumble bee parasite. Increasing invasion by *R. pseudoacacia* around colonies reduced queen and worker production and increased worker mortality. As *R. pseudoacacia* pollen was the second most abundant pollen type in the colony diet, these results may indicate a toxic effect of its floral resources. Conversely, a higher proportion of *I. glandulifera* pollen in the diet increased queen and male production as well as parasite occurrence, without affecting mortality. This suggests that *I. glandulifera* provides suitable resources enhancing colony fitness, while its populations potentially act as a parasite transmission hub. Neither species affected mating success. Overall, these findings demonstrate that invasive plants can become integrated into native bumble bee diets, with contrasting consequences for colony development and fitness.

Nanoparticle-mediated RNA interference for sustainable control of the red imported fire ant (*Solenopsis invicta*): Innovations in targeted gene silencing, colony transfer, and biocontrol enhancement

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Yisha LI

Abstract

The red imported fire ant (*Solenopsis invicta*) is a globally invasive pest that poses severe threats to agriculture, ecosystems, and human health. Conventional chemical control strategies are limited by environmental risks and the potential for pesticide resistance, highlighting the need for species-specific and sustainable alternatives. RNA interference (RNAi) represents a promising tool, yet its practical application in social insects is constrained by challenges in delivery, stability, and colony-wide dissemination. This study investigates the use of engineered nanocarriers to enhance RNAi efficacy in *S. invicta*. Two delivery platforms, chitosan nanoparticles and Lipofectamine 2000 (Lipo2000) liposomes, were evaluated for dsRNA encapsulation, nuclease protection, and gene-silencing efficiency. We further assessed the potential for RNAi transfer from worker ants to queens via trophallaxis and explored the synergistic effects of RNAi-mediated immune gene silencing on the biological control efficacy of *Beauveria bassiana*. Results demonstrated that Lipo2000 nanoparticles provided superior dsRNA stability and sustained release, achieving robust and long-lasting gene silencing. Chitosan nanoparticles offered rapid RNAi onset, suitable for immediate control needs. Importantly, RNAi-treated workers were capable of transmitting silencing effects to queens, and targeted gene knockdown enhanced *B. bassiana* pathogenicity. These findings highlight innovative strategies for precise, species-specific RNAi delivery, offering a foundation for sustainable, integrated pest management approaches against *S. invicta* that align with ecological and environmental safety goals.

Photoperiodic induction of reproductive diapause in *Corythucha arcuata* (Heteroptera: Tingidae)

Thomas ZANKL (BOKU University Vienna, Thomas.zankl@boku.ac.at)

Christa SCHAFELLNER

Abstract

The oak lace bug, *Corythucha arcuata* (Say, 1832), is native to North America but was accidentally introduced to Europe, likely via international trade. It was first discovered in Italy (Lombardy and Piedmont regions) in 2000 and has since spread rapidly throughout European oak forests, causing significant damage to various oak species by sucking on leaves. The multivoltine insect produces two to three generations per year. Adults overwinter in a state of reproductive diapause from late summer to spring. In the laboratory, we examined the effects of photoperiod on diapause induction and assessed the sensitivity of the preimaginal stages and newly emerged adults to diapause-inducing photoperiods. Eggs, newly ecdysed first- and second-instar nymphs, third- and fourth-instar nymphs, and adult females were exposed to decreasing photoperiods (16:8, 15:9, 14:10, 13:11, 12:12 L:D) at a constant temperature of 23°C. The critical photoperiod for initiating diapause lay between 14:10 and 13:11 L:D and was perceived by the nymphs, which responded to the diapause-inducing photoperiod, but the adults were the ultimate responsive stage as females did not lay eggs. Diapause was more pronounced in females exposed to short daylengths as young nymphs than in females that were transferred to short days as third- and fourth-instar nymphs or as adults. Mature females reared under daylengths near the critical threshold remained sensitive to diapause-inducing photoperiods for at least 20-30 days after emergence. Photoperiod also appears to play a role in diapause maintenance; females retransferred from a diapause-inducing photoperiod (14:10 or 13:11 L:D) to a diapause-averting photoperiod (16:8 L:D) after three weeks resumed oviposition. In the field, overwintered adults begin laying eggs from late May to early June, suggesting that – apart from temperature – photoperiod plays an important role in triggering post-overwintering oviposition in adult females.

The invasion of *Solenopsis invicta* in Sicily: distribution, ecological interactions and population genetics

Lucia ZAPPALA (Department of Agriculture, Food and Environment - University of Catania (Italy), Lzappala@unict.it)

Roberto CATANIA, Simone FONTANA, Antonio BIONDI, Giuseppe MASSIMINO COCUZZA, Michele RICUPERO

Abstract

The red imported fire ant *Solenopsis invicta* (Hymenoptera, Formicidae), native to South America, is among the world's worst invasive species, causing significant consequences on human health, natural and agricultural ecosystems. Recently, a mature European polygynous population of *S. invicta* was confirmed in eastern Sicily, prompting an ongoing eradication plan. Since *S. invicta* prefers to colonise ecologically disturbed areas and disrupts local fauna, its distribution and interaction with native ant communities require investigation. Population genetic analyses are also required to clarify the origin of the species and its potential dispersal capacity across the island. In this study, we mapped the distribution of *S. invicta* along the Sicilian eastern coast using nest surveys and baiting, and assessed its interaction with native ant species through pitfall traps and transects. In addition, the genetic structure of Sicilian populations was characterized through partial mtCOI sequencing and frequency distribution of Gp-9 alleles. *Solenopsis invicta* was found in approximately 19% of surveyed sites in Siracusa province, with an isolated outbreak in Catania. Preliminary results indicate a significant decline in native ant colony numbers correlated with the presence and density of *S. invicta* colonies. Phylogeographic analyses revealed different haplotypes. Analyses of the Gp-9 gene showed that most of the workers carried Gp-9bb genotype, typically associated with adult lethality after pupation. This investigation is crucial to support eradication efforts and raise public awareness, offering valuable insights about the ecological impact of *S. invicta* in Europe.

Unequal Risk: A Comparison of Pesticide Sensitivity of Wild and Managed Bees

Luca DORIO (Laboratory of Zoology, University of Mons, Luca.dorio@umons.ac.be)

Manon FIEVET, Antoine LEPRINCE, Marion SUSINI, Pierre-Louis CLOCHARD, Antoine GEKIÈRE, Kévin TOUGERON, Denis MICHEZ

Abstract

The rise of the Anthropocene has brought unprecedented disturbances to the Earth's ecosystems. Of these disturbances, the increased use of pesticides is identified as one of the primary drivers in the sharp decline of wild pollinators. Pesticide effects on bees have been extensively studied these last years, but these studies were almost exclusively focused on domesticated bee species (e.g. honey bees, bumble bees) completely ignoring wild species. Bees (Hymenoptera: Anthophilia) is a diverse clade where belong many species (around 20,000 worldwide) presenting various ecological traits (i.e. morphology, physiology, behaviour). This diversity is also reflected in their resilience to environmental stress.

Assessing and characterising these interspecific differences among pollinators exposed to pesticides is one of the main objectives of the European WildPosh project (Horizon program, 2024-2028). The first step was to describe the lethal and sub-lethal effects of pesticides, in controlled conditions, on different species of wild bees using innovative and new exposure protocols adapted for wild species.

Three pesticides, commonly detected as environmental residues and among the most widely used in Europe (i.e. acetamiprid, cypermethrin and tebuconazole) were tested on four eusocial species from the *Bombus* genus (i.e. *B.terrestris*, *B.hypnorum*, *B.lapidarius*, *B.pascuorum*) and two solitary species (i.e. *Andrena vaga* and *Colletes hederæ*). Wild bees were exposed to the weight-adapted LD50 of the commercial buff-tailed bumblebee (*Bombus terrestris* L.).

Exposure by both oral and topical routes revealed that wild species were more sensitive to pesticides than their domestic counterparts. The two solitary bees were the most sensitive species. *Bombus* species have also generally been more sensitive but higher sensitivity was compound- and species-dependent, revealing more complex mechanisms related to pesticide sensitivity.

#11171

Poster Session 1 - Ice breaker party
29/06/2026 at 16:00, Exhibition area

Regional variation in insecticide susceptibility and Point mutation detection in *Phthorimaea absoluta* populations from South Korea

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Seong KEONMOOK

Abstract

The tomato leafminer, *Phthorimaea absoluta*, a major pest of tomato production worldwide, was first reported in South Korea in 2023 and has since spread rapidly. Its management largely depends on chemical insecticides, raising concerns about resistance development, yet studies on resistance monitoring in South Korea remain limited. We evaluated six registered insecticides (metaflumizone, cyantraniliprole, spinetoram, emamectin benzoate, fluxametamide, and pyridalyl) through bioassays on the Gwangju population collected in 2025 and analyzed mutations at six insecticide target sites from ten regional strains. In bioassay results, Fluxametamide, spinetoram and cyantraniliprole showed the highest performance, causing complete mortality (100%) at the recommended concentrations, whereas pyridalyl, metaflumizone and emamectin benzoate exhibited reduced performance at the recommended concentrations, with mortality rates of 63.3%, 74.4% and 86.7%, respectively, in the Gwangju population. Mutation screening from ten regional strains detected known mutations in Ace1 (A201S), VGSC (M918T, T929I, L1014F), and RDL (A301S), whereas no mutations were detected in RyR, nAChR, and GluCl. These results provide the first baseline data on insecticide susceptibility and Point mutations in *P. absoluta* across South Korea and will contribute to the development of resistance management strategies. Additional insecticide bioassays and regional mutation screening are currently underway.

Detection and functional characterisation of striking insecticide resistance phenotypes in *F.occidentalis* populations from Crete

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Konstantinos MAVRIDIS, Christos ANDRONIS, Chrysoula NIKOLAOU, Dimitra TSAKIRELI, Anastasia A. NIKOLOUDI, Ioannis PIRGIANAKIS, Ioannis LIVADARAS, Thomas VAN LEEUWEN, John VONTAS

Abstract

Western Flower Thrips (WFT), *Frankliniella occidentalis*, is a globally significant pest that causes substantial economic losses due to its generalist feeding habits on high value crops, coupled with its ability to transmit plant diseases, especially tospoviruses. The widespread use of insecticides has led to the emergence of insecticide resistance (IR), which significantly impacts control efforts. This study investigates the status of IR in *F. occidentalis* populations in Crete, Greece. Bioassays were conducted to monitor resistance levels to key insecticides used in local agricultural practices. In addition, novel ddPCR-based molecular diagnostic tools were used to detect mutant allelic frequencies (MAF) of key target site mutations in the voltage-gated sodium channel (*VGSC*), chitin synthase 1 (*CHS1*), and nicotinic acetylcholine receptor (*nAChR*) genes, associated with resistance against pyrethroid, benzoylureas and spinosyns, respectively. The results revealed significant multiple resistance phenotypes (including abamectin and spinosad). To investigate additional molecular mechanisms underlying this resistance, RNAseq was performed. Transcriptomic analysis revealed the upregulation of cytochrome P450 (CYP) detoxification enzymes in the IR population, compared to both susceptible laboratory strain and field population. Functional validation through RNAi and *in vitro* assays using recombinant CYPs have been used to confirm the role of these genes in the striking resistance phenotype.

Resistance Dynamics of *Frankliniella occidentalis* Populations in Korean Pepper Houses: Implications for Integrated Pest Management

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Seoyul HWANG

Abstract

The western flower thrips, *Frankliniella occidentalis*, is known as a significant agricultural pest that causes substantial damage to vegetable, fruit, and ornamental crops through feeding and oviposition. They also transmit the tomato spotted wilt virus (TSWV) during feeding. Numerous insecticides have been applied to control *F. occidentalis*. Resistant populations have rapidly emerged due to their biological characteristics, such as a short life cycle and high reproductive capacity. To date, over 100 cases of insecticide resistance have been reported for various active ingredients worldwide, including Spain, Turkey, New Zealand, Japan, and China. In this study, field populations were collected from chili pepper greenhouses in eight regions in Gangwon Province, the Republic of Korea (Chuncheon, Hoengseong, Hongcheon, Hwacheon, Inje, Pyeongchang, Yanggu, and Yeongwol) to evaluate the level of insecticide resistance, which was measured using the leaf dipping assay against nine insecticides classified by different modes of action. Spinetoram, emamectin benzoate, and chlorfluazuron were highly effective against *F. occidentalis*, while acrinathrin and abamectin were less effective insecticides. Regional differences in mortality were also observed for acetamiprid, dinotefuran, chlorfenapyr, and cyclaniliprole. Taken together, these results highlight the necessity of continuous resistance monitoring and region-specific management strategies to ensure the sustainable control of *F. occidentalis* in Korea.

#11194

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Adverse sublethal effect of insecticides on spider locomotion in Mediterranean olive groves

Ilaria LATERZA (University of Bari, Ilaria.laterza@uniba.it)

Abstract

Spiders are important generalist predators in agricultural landscapes, yet their ecological role is threatened by pesticide use. Even indirect contact with residues on vegetation, can impair their movement and reduce their effectiveness in pest control. In this study, we investigated the sublethal effects of three commercial formulations — deltamethrin, flupyradifurone, and sweet orange essential oil, insecticides commonly applied in olive groves to control *Xylella fastidiosa* vectors, on the locomotory activity of four spider species: of *Oxyopes heterophthalmus*, *Neoscona athenia*, *Icius hamatus*, and *Philodromus lividus*. Adult spiders were collected from olive groves, exposed via tarsal contact to insecticide residues (maximum field concentration), then their locomotory activity was tracked using EthoVision software at 1 and 24 h after exposure, and their predatory activity was recorded at 24 h. Preliminary analyses showed species-specific responses, with a generally adverse effect of deltamethrin on locomotion after 1 h, while no effect was observed on their predatory capacity.

Role of detoxification in xenobiotic adaptation in *Drosophila suzukii*, the spotted wing

Mingjian LI (Université Côte d'Azur, INRAE, CNRS, ISA, Mingjian.li@inrae.fr)

Nicolas DESNEUX, Gaëlle LE GOFF

Abstract

Drosophila suzukii is an invasive drosophilid pest that attacks ripening, healthy fruits and has become a major pest of soft fruit crops worldwide. As a polyphagous species, *D. suzukii* is exposed to a wide diversity of plant defence compounds and synthetic insecticides, which creates a complex xenobiotic environment. In insects, xenobiotic detoxification is classically described as three phases: phase I functionalisation (cytochrome P450 monooxygenases, carboxylesterases), phase II conjugation (glutathione S-transferases, UDP-glycosyltransferases) and phase III excretion (ATP-binding cassette transporters). In this study, we specifically focus on phase I and phase II to investigate their contribution to the adaptation of *D. suzukii* to this chemically heterogeneous environment.

Our objectives are (i) to clarify the role of detoxification metabolism in xenobiotic adaptation of *D. suzukii*, with a particular focus on host-plant defence compounds; (ii) to determine whether adaptation to host plants can also confer pre-adaptation to chemical insecticides; (iii) to evaluate whether field populations have already evolved insecticide resistance. To address these objectives, flies were maintained for 48 h on fruit puree media differing in suitability (cherry, blueberry and grape), then toxicological tests and detoxification enzyme activities were performed, together with the expression of selected detoxification genes. Compared with the flies fed on standard cornmeal medium, flies reared on cherry, blueberry or grape puree exhibited increased tolerance to spinosad and lambda-cyhalothrin, consistent with differences in host secondary-metabolite profiles. For enzyme activity, there was no significant difference in glutathione S-transferases activity but a significant decrease in carboxylesterases activity. P450 activity showed a sex-specific pattern, with up-regulation in males and no significant change in females. Ongoing transcriptomic analyses will identify candidate detoxification genes for subsequent functional validation.

This project aims to clarify how detoxification metabolism contributes to xenobiotic adaptation in *D. suzukii* and to provide basic information for insecticide resistance risk management.

Transcriptomic insights into chlorantraniliprole resistance in *Spodoptera frugiperda*

Antonio Rogério Bezerra do NASCIMENTO (University of São Paulo, Arbnascimento@usp.br)

Carolina P. MONTEIRO, Rubens H. KANNO, Fernando F. CÔNSOLI, Celso OMOTO

Abstract

Insecticides of the diamide group have played a significant role in the control of defoliating insects, including *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae), which is considered one of the major pests in Brazilian agroecosystems. This species exhibits a high adaptive capacity, thereby resulting in the evolution of resistance to several insecticides, including the anthranilic diamide chlorantraniliprole. Previous large-scale genomic studies have associated resistance in *S. frugiperda* with mutations in the ryanodine receptor (RyR) gene, as well as with changes in gene expression levels in diamide-resistant strains. Given this context, the present study employed large-scale RNA sequencing (RNA-Seq) to identify gene expression changes associated with chlorantraniliprole resistance in *S. frugiperda*. Total RNA was extracted from fourth-instar larvae of susceptible (Sf-ss), resistant (Clor-R), and near-isogenic resistant (Clor-near-R) strains of *S. frugiperda*, followed by sequencing on an Illumina platform. Differentially expressed gene (DEG) analysis was conducted using the DESeq2 package. We identified a total of 2,286 DEGs in the comparison between susceptible and resistant strains, with 954 genes upregulated and 1,332 downregulated in the Clor-R strain. In the comparison between susceptible and near-isogenic resistant strains, 1,728 DEGs were identified, including 777 upregulated and 950 downregulated genes. Notably, a large number of detoxification-related enzymes were highly expressed in both resistant strains, including 70 cytochrome P450s, 15 esterases, 14 glutathione S-transferases, and 25 UDP-glycosyltransferases. These findings indicate that metabolic detoxification mechanisms play a major role in chlorantraniliprole resistance in *S. frugiperda*.

Translocation and Bioactivity of Root-applied dsRNA in Oilseed Rape Seedlings Targeting *Psylliodes chrysocephala*

Rahima Nusrat REMME (PhD student, Agricultural Entomology, Department of Crop Sciences, University of Göttingen, 37077 Göttingen, Germany & Agrotechnology Discipline, Khulna University, Khulna 9208, Bangladesh, Rahima-nusrat.remme@agr.uni-goettingen.de)

Catalina POSADA-VERGARA, Stefan SCHOLTEN, Michael ROSTÁS

Abstract

The cabbage stem flea beetle (*Psylliodes chrysocephala* (L.)) is a major pest to oilseed rape cultivation in Europe. Adult beetles aestivate for 1–2 months after early-summer emergence before migrating into newly sown fields, where feeding on cotyledons and young leaves causes severe seedling damage. Widespread resistance to pyrethroid insecticides, together with restrictions on neonicotinoid seed treatments in Europe, has increased the need for sustainable pest management strategies. RNA interference (RNAi), a natural gene-silencing mechanism mediated by sequence-specific double-stranded RNA (dsRNA), offers a promising alternative for targeted control. Proteasome subunit beta type-1 (Prosβ1), an essential enzyme for protein degradation and cellular homeostasis in adult beetles, represents a highly effective RNAi target; silencing this gene disrupts protein turnover, causing cellular failure and insect death. Oral delivery of 500 ng dsRNA targeting Prosβ1 via oilseed rape leaf discs previously resulted in complete mortality within 8 days. In this study, we investigated whether root-applied dsRNA is absorbed by oilseed rape seedlings, translocated to cotyledons, and retains functional activity against *P. chrysocephala*. Using qPCR, dsRNA was detected in cotyledons three days post-treatment, indicating successful systemic movement and short-term stability. Functional activity was confirmed in a feeding bioassay: ds-prosβ1 induced dose-dependent mortality, with the highest lethality at 1400 and 2800 ng, while lower doses (350–700 ng) did not differ from controls, indicating that effective knockdown requires high dsRNA concentrations. These results demonstrate that root-applied dsRNA can move systemically within oilseed rape seedlings and retain biological activity against *P. chrysocephala*. However, the long-term stability and persistence of dsRNA-mediated lethality remain unknown, highlighting the need for further research to optimize RNAi-based pest management strategies.

Interactive Effects of Drought and Endophytic Fungi on Soybean Performance and Fall Armyworm Development

Paolo SALAZAR-MENDOZA (University of São Paulo, Paolo.salazar@usp.br)

Italo DELALIBERA JR.

Abstract

While drought and insect pests are among the major constraints limiting soybean yield in Brazil, endophytic fungi represent a promising strategy to enhance plant fitness and reduce insect damage. However, their effectiveness under combined drought–herbivory stress remains poorly understood. This study evaluated the effects of endophytic entomopathogenic fungi and drought on fall armyworm (*Spodoptera frugiperda*) performance, soybean physiology, and yield under semi-field conditions. Soybean plants were grown in a greenhouse under three water regimes: severe drought (50% field capacity), moderate drought (70%), and well-watered conditions (100%), supplied via drip irrigation and adjusted based on daily soybean evapotranspiration estimates. Plants were inoculated with either *Beauveria bassiana*, *Cordyceps javanica*, or left untreated, with applications repeated every 15 days (four in total). Ten days after the first inoculation (V4 stage), second-instar *S. frugiperda* larvae were confined on plants for five days. Larval mass gain was recorded, after which larvae were transferred to an artificial diet to assess larval development time, pupal weight, and pupal development time. Leaf-level physiological responses (stomatal conductance, intercellular CO₂ concentration, photosynthetic rate, and transpiration) and yield components (pod number, grain weight, and 100-grain weight) were also measured. Overall, drought was the main factor shaping physiological and yield responses, whereas larval performance was only weakly affected. *C. javanica* improved photosynthetic traits under drought, and both endophytic fungi affected 100-grain weight. These findings provide preliminary evidence that endophytic fungi can partially mitigate drought impacts on soybean performance, with limited effects on *S. frugiperda* under the conditions tested.

Spatial structure and chemical heterogeneity of insect cuticular hydrocarbon layers: insights from different extraction methods and acclimation regimes

Sascha SCHLÜTER (Johannes Gutenberg University of Mainz (JGU Mainz), Institute of Organismic and Molecular Evolution (iomE), Sschluet@uni-mainz.de)

Florian MENZEL, Kiara MANGIN

Abstract

Insect cuticles are covered by a complex layer of cuticular hydrocarbons (CHCs) essential for chemical communication and desiccation resistance. Although CHC composition, and its variation within and across species, is well-studied, the physical structure of CHC layers remains poorly understood.

We extracted CHCs from five insect species (desert locusts, house crickets, American cockroaches, and two ant species) using different solvents and extraction durations, and insects from different temperature regimes. n-hexane preferentially extracted relatively solid CHCs (n-alkanes, terminally branched monomethylalkanes), while dichloromethane and dichloromethane-methanol favored more fluid compounds (internally branched monomethyl and dimethyl alkanes, unsaturated hydrocarbons). Moreover, more solid CHCs were obtained with shorter extraction times, whereas fluid ones required prolonged extractions. This supports a model of elevated solid domains surrounded by fluid regions.

CHCs of similar phase behaviour co-varied across treatments, indicating that they aggregated in the same domains. Warm acclimation increased solid compounds whereas fluctuating temperatures enhanced CHCs with intermediate phase behaviour.

Our results reveal spatial heterogeneity in the CHC layer, with CHCs clustering in domains of different phase behaviour. This likely facilitates CHC multifunctionality. Phase behaviour and cluster membership of each CHC depend on its biophysical properties relative to the remaining CHCs of the individual insect.

#11170

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Resistance Monitoring and Target-Site Mutation Analysis of *Ostrinia furnacalis* to Deltamethrin in Korea

Oh SHEUNG TAEK (Department of Applied Biology, Chungnam National University, Republic of Korea, Oho4902@naver.com)

Seong KEON MOOK

Abstract

The Asian corn borer, *Ostrinia furnacalis* (Guenée), is a major pest of maize that damages leaves, stems, and ears, causing yield loss and quality deterioration, particularly through ear rot when ear tissues are attacked. Effective and systematic management strategies are therefore required. To date, most studies on the control and resistance of *O. furnacalis* have focused on Bt-based products, whereas information on the efficacy and resistance status of chemical insecticides remains limited. In this study, resistance monitoring and target-site mutation analysis of *O. furnacalis* populations were conducted using the synthetic pyrethroid insecticide deltamethrin. Bioassays were performed using a leaf-dip method with deltamethrin 1% EC diluted 1,000-fold (recommended concentration, 10 ppm active ingredient). Mortality rates of populations collected from the Chungcheong region (Cheongju, Cheonan, and Nonsan) were 76.7%, 81.7%, and 73.3%, respectively, while those from the Yeongnam region (Gyeongju, Yeongcheon, Gumi, and Yecheon) showed mortalities of 86.7%, 61.7%, 58.3%, and 91.7%, respectively. In addition, the representative pyrethroid resistance-associated point mutation, L1014F, was analyzed across all seven field populations, and no mutation was detected. These results indicate variable susceptibility of *O. furnacalis* populations to deltamethrin and suggest that target-site resistance mediated by the L1014F mutation is not currently prevalent in the surveyed regions. This study provides baseline information for resistance monitoring and supports the development of effective management strategies for *O. furnacalis* in maize-growing areas.

#12479

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

How calcium pathways can modulate the mode of action of neonicotinoids and their new representatives : recent advance using american cockroach model

Emiliane TAILLEBOIS (P2E laboratory, University of Orleans, France, Emiliane.taillebois@univ-orleans.fr)

Steeve THANY, Maria TAHA, Alison CARTEREAU, Jean-Noël HOUCAT

Abstract

Neonicotinoids insecticides and their new representatives (sulfoximine and butenolide) are widely used as control strategy against insect pests. However, the long-term viability of their use is being questioned, particularly due to the emergence of resistance mechanisms in targeted species. It is crucial to improve our understanding of these mechanisms to implement alternative control methods and prevent the emergence of new resistances. In recent studies, we used the cockroach *Periplaneta americana* as a model to better understand the mode of action of these insecticides at molecular level. Using electrophysiological approach on dorsal impaired median (DUM) neurons, we identified how intracellular calcium pathways can modulate the activity of two insecticides, the butenolide flupyradifurone, and the neonicotinoid clothianidine. In particular, we explored the involvement of IP3 and ryanodin receptors in modulating DUM neuron nAChRs. We found that activation of nAChRs can induce a calcium release from endoplasmic reticulum which can affect insecticide mode of action. Overall these data add our understanding of the fine regulation of neurotoxic insecticides targeting nAChRs.

#11097

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Assessing Insect Vulnerability in a Rapidly Urbanising Tropics

Eunice TAN (National University of Singapore, Eunice.tan@nus.edu.sg)

Abstract

Urbanisation is accelerating worldwide, with 68% of the global population projected to reside in cities by 2050. The associated loss and fragmentation of natural habitats is now recognised as one of the most pervasive threats to biodiversity. Insects—key providers of pollination, nutrient cycling, and essential links in food webs—are particularly vulnerable, yet remain understudied in tropical systems where their diversity is highest and declines may be most consequential. Singapore presents an extreme example of long-term habitat loss. Since 1819, more than 95% of its original vegetation has been cleared, and only ~24 km² of forest remains, of which less than 10% is primary. Catastrophic local extinctions across taxa have followed, with approximately 73% of vertebrate and invertebrate species lost from historical records. Despite this, the ecological responses of tropical insects to contemporary environmental pressures remain poorly quantified.

We conducted a twelve-month survey of insects and environmental parameters—including temperature, ambient light levels, and airborne pollutants—across six primary forest sites. Environmental conditions differed significantly among sites. Insect abundances also varied across sites, suggesting that these environmental gradients may influence community structure. This dataset provides one of the first integrated, year-round baselines for Singapore's remaining primary forest insects and highlights how fine-scale environmental variation can shape tropical insect assemblages. Our findings underscore the urgent need to monitor insect communities in rapidly urbanising tropical landscapes, where biodiversity loss is both acute and poorly documented.

Transgenerational Hormesis in an Invasive Insect Herbivore Triggered by Sublethal Insecticides: Molecular and Biological Insights

Farman ULLAH (Institute of Bio-Interaction, Xianghu Laboratory, Hangzhou, 311258, China, Farmanullah787@gmail.com)

Ali GÜNCAN, Hina GUL, Xiaowei LI, Yaobin LU

Abstract

Hormesis, a biphasic dose-response phenomenon, is gaining recognition for its bioregulatory and practical implications. Invasive species present a critical context for studying hormesis, as sublethal population-level responses may facilitate establishment and spread, particularly when transgenerational effects are involved. The invasive South American tomato pinworm, *Tuta absoluta* Meyrick, a global agricultural pest, exemplifies this scenario. Despite its relevance, the role of hormesis, particularly in response to novel insecticides widely used against lepidopteran pests, remains underexplored. Thus, using age-stage, two-sex life table analyses and molecular approaches, we examined the sublethal and low-lethal effects of three insecticides—cyantraniliprole, tetraniliprole, and spinosad—on *T. absoluta*. While spinosad consistently caused toxicity and negative intergenerational effects on development and reproduction, cyantraniliprole and tetraniliprole induced a hormetic response. Exposure to LC10 concentrations of these two insecticides in the parental generation (F0) reduced longevity and fecundity, but paradoxically enhanced developmental rate, survival, and reproductive output in the F1 and F2 generations. Conversely, LC30 exposures caused detrimental effects across all generations. Gene expression analysis revealed that this transgenerational hormesis was associated with the upregulation of development and reproduction-related genes (*Vg*, *VgR*, *JHBP*) in progeny at LC10, alongside persistent overexpression of key detoxification P450 genes. Targeted silencing of these P450 genes via nanomaterial-dsRNA increased larval susceptibility. These findings demonstrate that sublethal exposure to diamide insecticides can trigger a transgenerational hormesis effect, potentially increasing the risk of population resurgence. The study underscores the critical need to incorporate hormesis and multigenerational assessments into insecticide resistance management strategies for the sustainable control of *T. absoluta*.

The effects of nesting location on the thermal ecology and greenhouse gas emissions of arboreal termites.

Lara DOMINGUEZ (Coiba AIP, Smithsonian Tropical Research Institute, and Global Sustainability Scholars, Lara.blair.dominguez@gmail.com)

Emily MARPLE, Dumas GALVEZ

Abstract

Arboreal termites are ubiquitous members of neotropical ecosystems, vital to nutrient cycling and decomposition in some of the world's most biodiverse regions. Additionally, tropical termites contribute to greenhouse gas emissions, and there is a growing interest in whether anthropogenic environmental changes may influence these emissions. However, the difficulties of observation have left arboreal termites relatively understudied, despite comprising a large subset of the population of tropical termites.

The termitaria, or termite nests, of arboreal termites are essential to the physiology, ecology, and functioning of termite colonies. Arboreal termitaria also serve as roosting locations for many species, making them essential components of tropical biodiversity. Members of *Nasutitermes*, the most abundant genus of neotropical arboreal termite, are known to construct nests at variable heights, from near-canopy to ground levels. We investigate how this variation affects the internal thermoregulatory function of nests and how these differences in nest temperature in turn affect foraging and emissions from termite colonies. An observational study of the internal nest temperatures of *Nasutitermes* nests shows how nest location variables such as height, light exposure, trunk angle, and tree species influence the thermoregulatory abilities of arboreal termitaria. Follow-up studies on the foraging behavior of termites in the lab under different temperature conditions reveal whether changes to the internal temperature of nests have downstream effects on the behavior of arboreal termites. Finally, the effects of internal nest temperature on the CO₂ and methane emissions of whole termite nests are investigated. This study supports the importance of augmenting fundamental understandings of termite behavior and ecology to understanding and predicting their ecosystem services.

The influence of heat stress on the parental control of microbial competition

Maja FLUCH (University of Bayreuth, Maja.fluch@gmail.com)

Sandra STEIGER, Jos KRAMER

Abstract

Animals almost continuously interact with a vast diversity of microbes, and some animals can leverage complex social strategies to manage their microbial interaction partners. However, it remains little understood how robust such social strategies of microbial control are to changing environmental conditions, including those expected under rapid anthropogenic climate change. Here, we tackle this question by investigating the influence of heat stress on microbial control in *Nicrophorus vespilloides*. These burying beetles provide parental care to their offspring on small vertebrate carcasses, an ephemeral resource heavily contested by microbes. While heat stress has been shown to reduce larval fitness and impair parental care, it remains unclear whether these negative effects arise from increased microbial competition. To tackle this question, we are assessing larval fitness, parental effort, and the carcass microbial community in a full-factorial experiment independently varying the occurrence of (i) heat stress, (ii) parental care, and (iii) an antimicrobial treatment reducing the density of microbes on the carcass. If heat stress reduces the efficacy of parental care in microbial control, we expect that reducing the density of microbes on the carcass mitigates at least some of the negative effects of an increased temperature. By unraveling the impact of heat stress on the efficacy of parental care as a strategy of microbial control, our experiment will contribute to a better understanding of the potential effects of climate change on animal-microbe interactions and the fitness effects of social life.

Using biochemical proxies to assess fitness along a range expansion gradient: physiological responses to thermal stress among populations of the Pine Processionary Moth

Pierre GOSSEAUME (INRAE, Pierre.gosseaume@inrae.fr)

Claire MELOT, Aurore MIGNAN, Lissette CORNEJO-ESPINOZA, Benoît NUSILLARD, Jérôme ROUSSELET, Mathieu LAPARIE

Abstract

Theoretical work suggests that organismal performance and fitness can change along range expansions gradients as a result of two opposing — yet non-exclusive — evolutionary mechanisms. On the one hand, positive selection near the advancing range front may concentrate best dispersers and individuals that best tolerate environmental stress in areas near the limit of the species' preferendum (spatial sorting). On the other hand, the balance between cumulating and purging deleterious mutations may be altered, potentially reducing fitness.

The pine processionary moth (*Thaumetopoea pityocampa*), a native defoliator expanding northward due to climate change, is an ideal model to investigate these dynamics, supported by well-documented histories across Europe. The LOADEXP ANR project combines population genomics with physiological and phenotypic approaches to compare proxies of fitness along the expansion gradient and test the genetic load hypothesis.

Larval colonies from the range core to the range front were exposed to thermal stress. We developed and optimized a set of biochemical assays to quantify energetic metabolites as proxies of physiological condition before stress, at its onset, and during recovery. Samples are analyzed for soluble sugars (glucose and trehalose) and lipid reserves (triglycerides), key components of insect energy metabolism and stress response.

Given the low biomass of some individuals and requirement to extract both the polar and apolar fractions from the same samples, protocols were adapted to micro-scale conditions. This included miniaturized enzymatic assays in microplates, optimized sample preparation and evaluation of extraction procedures to maximize recovery while limiting analytical losses.

Ongoing assays aim to capture any variation in energy reserves management and stress tolerance across populations along the expansion gradient. The results will provide insights into the physiological consequences of expansion-associated genetic load.

Overall, this work and methodological developments are a step towards explicitly integrating biochemical phenotypes into studies of eco-evolutionary dynamics during range expansions.

Nanocarrier-mediated RNAi of HSP83 and CP7 elucidates their roles in thermo-hygrometric adaptation in *Tuta absoluta*

HINA GUL (Zhejiang Academy of Agricultural Sciences, Farmanullah787@gmail.com)

Xiaowei LI, Nicolas DESNEUX, Yaobin LU

Abstract

The tomato leafminer, *Tuta absoluta*, is a global pest whose survival and adaptation under thermo-hygrometric stress are poorly understood. This study investigated transcriptomic responses and functional roles of two key stress-responsive genes, HSP83 and CP7, in 3rd instar larvae exposed to high temperature with low humidity (HT-LH: 38°C, 50% RH) and high temperature with high humidity (HT-HH: 38°C, 75% RH). RNA sequencing revealed substantial differential gene expression, with 882 upregulated and 868 downregulated genes under HT-LH, and 1158 upregulated and 1069 downregulated genes under HT-HH. Gene Ontology and KEGG pathway analyses highlighted enrichment in protein processing, metabolic pathways, cuticular structure, and detoxification processes. RT-qPCR validation confirmed significant upregulation of HSP83 (3.16-4.63-fold) and CP7 (3.55-5.85-fold) under non-stress conditions. Nanocarrier-mediated RNA interference effectively silenced these genes, resulting in a marked decrease in larval survival, demonstrating their critical role in stress tolerance. A conceptual model integrating transcriptomic and functional data illustrates CP7-mediated cuticle reinforcement and desiccation resistance, and HSP83-driven protein stabilization, with RNAi-mediated disruption compromising thermo-hygrometric tolerance. Overall, these findings indicate that although high temperature and humidity reduce survival, *T. absoluta* larvae indicate robust molecular mechanisms to withstand stress. Understanding these adaptive responses provides insights into pest dynamics under climate change and identifies HSP83 and CP7 as potential targets for RNAi-based pest management strategies.

#15536

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Interactive effects of developmental and adult thermal environments on lifespan in *Drosophila*

Emanuel Manfred MAKWISA (Institute of Zoology, Slovak Academy of Sciences, Emanuel.makwisa@savba.sk)

Malleswara DHARANIKOTA, Martina GÁLIKOVÁ, Peter KLEPSATEL

Abstract

Lifespan is shaped by temperatures experienced during both development and adulthood, but the combined effects of these thermal environments remain insufficiently understood. We examined how developmental and adult temperatures influence longevity in three *Drosophila* species: *Drosophila melanogaster* and *D. simulans*, represented by populations collected in temperate Slovakia, and *D. ananassae*, represented by a population collected in tropical India. *D. melanogaster* was reared at 10 developmental temperatures (13–31 °C), *D. simulans* at 9 (13–29 °C), and *D. ananassae* at 9 (15–31 °C). After eclosion, adults were distributed across three adult temperatures (19, 25, and 29 °C). Lifespan was measured in mixed-sex groups across all developmental-by-adult temperature combinations. This design allows us to characterize longevity reaction norms and assess the effects of mismatch between developmental and adult thermal environments. Preliminary analyses suggest that development under thermal extremes reduces adult lifespan in all three species. These results provide a high-resolution comparative view of how early thermal conditions shape adult longevity and may help predict population- and species-level vulnerability to climate change.

Phenology and thermal tolerance shape the biological control potential of *Aphelinus mali* against woolly apple aphid in Northern Italian orchards

Panizza SONIA (Laimburg Research Centre, Sonia.Panizza@laimburg.it)

Alessia CONCI, Urban SPITALER, Martina FALAGIARDA

Abstract

The woolly apple aphid (WAA), *Eriosoma lanigerum* (Hausmann), has become increasingly relevant for apple production in South Tyrol (Italy). Its host-specific parasitoid *Aphelinus mali* (Haldeman) is the main natural antagonist, yet its biological control effectiveness varies across locations. Understanding its field phenology and physiological constraints is essential for predicting and improving its biocontrol efficacy under climate warming. Therefore, we initiated a multi-annual study combining field monitoring with experimental assessments of thermal tolerance.

During 2025, WAA and *A. mali* dynamics were monitored in four apple orchards: two hillside sites and two lowland sites. WAA monitoring included migration dynamics using sticky bands and visual infestation assessments at two sites. *A. mali* activity was recorded using yellow sticky traps and sticky bands, and parasitism rate was evaluated on colonies in two sites. Concurrently, adult parasitoid longevity was tested under thermal stress (25–38 °C) using Kaplan–Meier survival analysis to identify critical temperature thresholds.

Preliminary results revealed marked site-specific differences. One lowland site showed the highest and most persistent WAA infestations, with parasitism reaching 85.6% but without a corresponding aphid decline; here, *A. mali* exhibited two distinct summer peaks. In the hillside sites, both species displayed a pronounced summer peak followed by a rapid decline, with parasitism reaching 95.3% where assessed. The second lowland orchard consistently showed low infestation levels.

Laboratory thermal tolerance trials demonstrated significant reductions in *A. mali* longevity above 32°C, with critical mortality increases at 36–38°C. The lowland site with the highest infestation experienced several days above 34°C in late June and August, whereas hillside sites rarely exceeded this threshold, likely contributing to differences in parasitoid performance.

Overall, the integration of field phenology and thermal biology suggests that summer temperature extremes may limit *A. mali* effectiveness in warmer lowland orchards, with important implications for biological control strategies under climate change.

Impact of high temperatures on Bumblebees' foraging behaviour.

Yoorana PEYRE (University of Stirling, Ybp1@stir.ac.uk)

Gema MARTIN-ORDAS, Sonia REY-PLANELLAS

Abstract

Despite being responsible for 75% of crop pollination and essential for ecosystem maintenance, insect pollinators are declining worldwide. Among other threats, climate change is known to play an important role in this decline, either through global warming, or by an increase in the occurrence of extreme climatic events. Several studies have shown the detrimental effect of climate change on pollinators, either indirectly through a plant pollinator mismatch, or directly, affecting their morphology, physiology, phenology, or even cognition.

Previous studies have shown that external stressors might impact negatively foraging activities in bees. For example, humoral immune response impairs foraging resource flexibility in bumblebee and exposure to pesticides has been linked to an increase in flower handling time. A recent study also showed that short exposures to heatwaves-like temperatures altered floral scent detection through a disruption of antennal responses in bumblebees. However, how high temperatures might affect pollinators foraging behaviour, such as resources specialisation, quality discernment and flower handling abilities is still unknown.

In 3 experiments, we aimed to assess how, in comparison with bees exposed to 22°C, an acute as well as a chronic exposure to heat (32°C) impact several aspects of bumblebees' foraging. Specifically, we assessed if preferences for (a) pollen or nectar; b) quality of the rewards and (c) reward accessibility were impacted by either short or chronic exposures to high temperatures. Preliminary results show that bumblebees chronically exposed to 32°C appear to have a severe preference for nectar rewards, lower foraging flexibility and overall, lower flower visitation and participation rate. If confirmed, our results would suggest that heatwaves events and global warming might impact negatively how bumblebees forage and therefore their survival, fitness, and the pollination ecosystemic service they provide.

Determining the thermal conditions of underground nests of *Bombus terrestris*

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Beth NICHOLLS, Jeremy NIVEN

Abstract

Empirical data on the thermal conditions experienced by bumblebees inside underground nests remain extremely limited, despite their importance for predicting responses to climate warming. We conducted a field experiment to quantify ambient, nest, and brood temperatures in 12 buried *Bombus terrestris* nests. Half of the nests were placed in shaded conditions and half in full sun, and included both commercial colonies and empty control nests. Temperature loggers continuously recorded thermal conditions inside and outside the nests.

Preliminary results indicate strong thermal buffering within underground nests. While ambient temperatures in full-sun sites frequently exceeded 40 °C, internal nest temperatures remained relatively stable, with mean values between ~17–20 °C across shaded and sun-exposed treatments. Nest temperature ranges overlapped between shaded and full-sun nests, suggesting that soil insulation and nest structure decouple nest microclimates from external thermal extremes. In contrast, brood temperatures were consistently higher than surrounding nest temperatures, reaching mean values above 30 °C, indicating active worker-mediated thermoregulation.

These findings provide rare field-based measurements of the thermal environments inside *B. terrestris* nests and highlight the importance of nesting ecology and behavioural thermoregulation in buffering colonies against extreme temperatures. Ongoing analyses and additional replicates will further refine these patterns and improve predictions of bumblebee vulnerability to increasing heatwave intensity.

Evolutionary insights from complete mitochondrial genomes of *Aedes albopictus* and *Culex pipiens molestus* (Diptera: Culicidae)

Ashraf AKINTOLA (Kyungpook National University, Daegu, South Korea, Ashraf.akintola@gmail.com)

Abstract

Mitochondrial genomes (mitogenomes) are powerful molecular tools for exploring phylogenetic relationships, deciphering adaptation and divergence, as well as disease transmission potential among insects. In this study, we performed a comparative mitogenomic and phylogenetic analysis of two major mosquito vectors – *Aedes albopictus* and *Culex pipiens molestus* – collected from South Korea, together with mitogenome data from 18 additional mosquito species representing three Culicidae genera (*Aedes*, *Anopheles*, and *Culex*) retrieved from GenBank. The assembled mitogenomes, each comprising 13 protein-coding genes, 22 tRNAs, and two rRNAs, revealed conserved gene order and structural features typical of Diptera. Comparative analyses with multiple species representing the three genera uncovered lineage-specific patterns in codon usage, base composition, and control region variability. Phylogenetic relationships inferred using maximum likelihood and Bayesian methods based on concatenated mitochondrial protein-coding genes robustly resolved genus-level relationships and supported the monophyly of the two major Culicidae clades, *Aedes* (tribe Aedini) and *Culex* (tribe Culicini), with *Anopheles sinensis* and *Anopheles gambiae* serving as outgroups. Time-calibrated Bayesian analyses indicated a deep divergence between *Anopheles* and the *Aedes*–*Culex* clade during the Paleogene (~51.8 Mya), followed by the separation of *Aedes* and *Culex* around ~39.7 Mya. Notably, *Ae. albopictus* diverged from its congeners ~11.7 Mya, while *Cx. p. molestus* exhibited a much more recent divergence (~2.35 Mya), suggesting distinct evolutionary pressures and histories. This study demonstrates the utility of mitogenomic data for reconstructing mosquito evolutionary history and provides insights relevant to vector biology, ecology, and public health.

West Nile Virus: results of entomological surveillance in Sardinia (Italy) in 2025

Daniele DEDOLA (Istituto Zooprofilattico Sperimentale della Sardegna, Daniele.dedola@izs-sardegna.it)

Valentina SINI, Cipriano FOXI, Roberto BECHERE, Maria Antonietta DETTORI, Daniela MANUNTA, Angela Maria ROCCHIGIANI, Elisabetta CORADDUZZA, Anna Maria SECHI, Giontonella PUGGIONI, Stefano CAPPAL, Giuseppe SATTA

Abstract

West Nile virus (WNV) is a mosquito-borne arbovirus belonging to the Flaviviridae family. WNV has been isolated from a variety of mosquito species, particularly those belonging to the genera *Aedes* and *Culex*. Of these, the most common vector is *Culex pipiens*. WNV emerged in Sardinia in 2011 and is now considered endemic, given the recurrent reports in birds, mosquitoes and humans. In Italy, the epidemiological surveillance of WNV USUV is currently being conducted in parallel with that of USUV, as part of the "National Plan for the Prevention, Surveillance and Response to Arboviruses (PNA) 2020-2025".

During 2025, a total of 152 locations across Sardinia were monitored. Adult mosquitoes were captured using CO2-CDC Light traps and BG-Sentinel traps. The trapping schedule were as follows: every two months from April to November and monthly during the remaining months. All captured mosquitoes were morphologically identified and grouped into pools containing a maximum of 25 specimens. The pools were analysed for the virus presence using real-time RT-PCR test.

In 2025, a total of 1,803 catches were performed, resulting in the capture of 29,113 adult mosquitoes belonging to six genera and 14 different species. The most prevalent species were *Culex pipiens* and *Aedes caspius*, with 12,930 and 11,190 specimens recorded.

A total of 3,371 pools were analysed and the presence of the virus was detected in 49 mosquitoes pools consisting of *Cx. pipiens* (37 pools), *Ae. caspius* (9), *Ae. albopictus* (1), *Culex* spp. (1), and *Aedes* spp. (1). Subsequent molecular analyses demonstrated that of the 49 pools, 29 were positive for WNV lineage 2 and 19 for WNV lineage 1, while only one pool was positive for both lineages.

Entomological monitoring is indisputably a vital component of the global arbovirus surveillance strategy, providing significant information on potential West Nile virus (WNV) vectors.

Wolbachia endosymbiont detection in wild mosquitoes from Northern Italy

FRANCESCO DEFILIPPO (Istituto Zooprofilattico Sperimentale della Lombardia e Emilia-Romagna, Francesco.defilippo@izsler.it)

Maya CARRERA, VALENTINA CARTA, CRISTINA BERTASIO, DAVIDE LELLI, ANA MORENO

Abstract

Arthropods are commonly infected by maternally transmitted endosymbionts. Although some endosymbionts confer direct benefits to their hosts others, such as Wolbachia, are able to induce a form of conditional sterility, between infected males and uninfected females or females infected by incompatible strains. Such potential manipulations of Wolbachia have led scientists to explore its potential in controlling mosquito-borne diseases. For this reason, our study determines natural Wolbachia infections in different mosquito's specie sampling in Lombardy region (Northern Italy). Mosquitoes were collected across three different ecological sites (urban, rural, and wooded). Samples of *Aedes albopictus*, *Culex pipiens* sl, *Aedes caspius*, *Aedes vexans*, *Anopheles maculipennis* sl, *Coquillettidia richiardii*, and *Anopheles plumbeus* were screened for Wolbachia infection. The sample set was further augmented with *Aedes albopictus* and *Culex pipiens* sl specimens derived from laboratory colonies. Positive samples underwent molecular characterization through Multi-Locus Sequence Typing (MLST) of five genes (coxA, gatB, ftsZ, fbpA, hcpA) and were sequenced using the Oxford Nanopore MinION platform. The relative Wolbachia density was determined via Real Time PCR for three species, *Culex pipiens* sl, *Aedes albopictus* (wild type and laboratory samples) and *Anopheles maculipennis* sl. Wolbachia DNA was detected in *Culex pipiens* sl, *Aedes albopictus*, *Anopheles plumbeus* and *Anopheles maculipennis* sl, whereas *Aedes caspius*, *Aedes vexans*, and *Coquillettidia richiardii* resulted negative. *Culex pipiens* sl were consistently infected with a single wPipB sequence type (ST9), while *Aedes albopictus* harboured two distinct wAlbA and wAlbB sequence types (ST2 and ST464, respectively). No significant differences were observed between specimens collected from different habitats. The study indicated a higher Wolbachia density in wild specimens collected from wooded sites. Conversely, individuals reared under laboratory conditions exhibited a reduced Wolbachia density compared to wild samples. These results provide information on Wolbachia in natural mosquito populations in Northern Italy, which could be used to future control strategies

Italian network for invasive mosquito surveillance and control at points of entry (PoEs)

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Abstract

To face the threat of the global spread of arthropod vectors and the risk of introduction of new or exotic a vector-borne pathogens through Points of Entry (PoEs) i.e. ports, airports, and ground country border crossings, WHO has established a set of standard procedures for member states to be implemented at national and subnational level. Specifically, member states are required to identify major PoEs and carry out surveillance activities through appropriate monitoring programs. A specific entomological surveillance activity carried out with standardized procedures at PoEs would allow the early detection of invasive alien species (IAS), potential vectors of pathogens. Recent reports of autochthonous cases of dengue and chikungunya in Italy demonstrate that this country is vulnerable to exotic diseases favoured also by the widespread distribution of the tiger mosquito (*Aedes albopictus*) other than the occurrence of other invasive alien species, such as *Aedes japonicus*, and *Aedes koreicus*. For these reasons, in 2025, the network of Experimental Zooprophyllactic Institutes (IIZZSS) launched a dedicated research project to support and harmonize surveillance activities in Italian PoEs. A total of 117 sites were monitored including airports, ports, service stations and distribution centres. Ovitrap and BG-sentinel traps were used to collect mosquitoes which were checked biweekly from June to October, (the mosquito activity period). Eggs and adults were identified using morphological and molecular methods. Adult mosquitoes will be also tested for flavivirus and alphavirus screening. A web interface was designed to share the report on sampling activity across the various sites and provide real-time data on trends in species diversity and abundance. This research activity will provide new data and insight about the current spatial and temporal distribution of arthropods vector of medical relevance including IAS as will provide the basis for the development and implementation of the most cost/effective preventive and control measures

Adverse effects between mutualistic and pathogenic bacteria colonising *Aedes aegypti* are stage-specific

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Estelle CHABANOL, Mathilde GENDRIN

Abstract

The bacterial microbiota fundamentally shapes *Aedes aegypti* fitness, development, and insecticide resistance, yet interactions between bacteria and their impacts on the host remain unclear. Employing gnotobiotic models, we investigated the strain-specific effects of three field-derived bacterial isolates—*Asaia bogorensis*, *Serratia marcescens*, and *Acinetobacter radioresistens*—on mosquito life-history traits. Contrary to the common mutualistic role of the *Asaia* genus, our *Asaia* strain failed to support larval development and exhibited significant virulence in adults. *Serratia*, as expected, was highly pathogenic to both immature and adult stages. Notably, *Acinetobacter* acted as a potent larval mutualist, completely rescuing development during lethal co-infections via reducing the virulence of *Serratia* but not its growth. This rescue was mediated through suppression of *Serratia*'s primary toxin, prodigiosin. However, this protective effect was strictly stage-specific; *Acinetobacter* did not mitigate pathogen-induced reductions in adult survival, blood-feeding success, or fecundity. Additionally, both pathogens conferred deltamethrin susceptibility in a genetically resistant field population—an effect unmitigated by *Acinetobacter*. These findings demonstrate that bacterial virulence and microbiota-mediated protection vary along the mosquito life cycle and offer novel perspectives for mosquito rearing, whether in research laboratories or in mass-rearing programs for vector control.

The role of mosquitoes' cognition in the development of behavioral adaptations to chemical control

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Abstract

Chemical control, based on insecticide and repellent compounds, remains one of the most effective strategies for protecting populations from mosquito-borne diseases. It has been shown that mosquitoes detect these chemicals via their chemosensory system, and after interpreting the message conveyed by these molecules, mosquitoes will modify their behaviour accordingly (i.e., excito-repellency, spatial repellency). However, a key question persists: can mosquitoes use this information to adapt their behavior in alternative ways compromising vector control efficacy? For instance, mosquitoes' learning capacity has been proposed to contribute to the development of behavioral adaptations against insecticides and repellents. Various sensory and cognitive mechanisms involved in these behavioral adaptations have been described in some species. These include: i) insensitivity, when olfactory receptors no longer respond to a given molecule. ii) Non-associative learning (e.g. Habituation), decreases individuals' response to the molecule used. iii) Associative learning, individuals modify their behavior as a result of the association of the molecule with a reward or punishment. In this study, the aims were to shed light on these different behavioral adaptation processes in mosquitoes when using chemical control tools such as repellents and insecticides, and to investigate the underlying mechanisms driving these responses. For this, a series of behavioral experiments were conducted to test the effects of pre-exposure and associative learning with a Pavlovian protocol (Biting attempt response) of these tools at different levels of complexity (single molecule vs odor bouquet) and concentration. At the same time, electrophysiology experiments (GC-EAD ; EAG ; SSR) were conducted to understand sensory mechanisms. In this talk, I'll present to which extent these process may influence the efficacy of chemical control against mosquitos.

Vector competence of a field population of mosquito species *Coquillettidia venezuelensis* from French Guiana for Oropouche virus

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Abstract

Coquillettidia venezuelensis (Diptera: Culicidae) is a human-aggressive mosquito species widely distributed in various regions of French Guiana. In this study, field-collected specimens from Matoury city were orally exposed to an Oropouche virus (OROV) strain. Viral infection, dissemination, and transmission were evaluated at 3, 5, 7, 14, and 21 days post-infection by detecting viral RNA in the midgut, carcass, and saliva using reverse transcription real-time polymerase chain reaction (RT-qPCR) and/or Vero cell culture. This is the first study to assess the transmission efficiency of *Cq. venezuelensis* for an OROV strain. These results suggest that *Cq. venezuelensis* is refractory to OROV transmission under the tested conditions. Given previous suggestions of its involvement in the sylvatic transmission cycle of OROV, these findings highlight the need to re-evaluate the vectorial role of this species and continue investigations into its potential epidemiological impact.

Functional characterization of engorgement factor alpha and its regulatory role in the feeding success of *Haemaphysalis longicornis*

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Jaekuk PARK

Abstract

Blood feeding in hard ticks, such as *Haemaphysalis longicornis*, is a physiological prerequisite for successful reproduction. During a 5-to-7-day attachment period, female *H. longicornis* exhibit a dramatic weight increase—up to 100-fold compared to unfed states—primarily driven by a rapid engorgement phase. While this rapid phase accounts for approximately 90% of the total bloodmeal intake, the underlying physiological mechanisms remain poorly understood. In Ixodid ticks, this transition is stimulated by male-derived factors, specifically engorgement factors (voraxin) alpha and beta. In this study, we identified and characterized a candidate gene, Haelo-EFa, from *H. longicornis* through in silico and molecular analyses. Sequence analysis revealed that Haelo-EFa shares 78.18% nucleotide and 75.45% amino acid identity with orthologs in other hard tick species. Quantitative RT-PCR profiling demonstrated that Haelo-EFa expression is specifically induced post-blood feeding, with no detectable expression in unfed females. To further elucidate its physiological necessity, the functional role of Haelo-EFa is being validated via RNA interference (RNAi). Our findings provide critical insights into the male-derived regulatory factors of tick engorgement, offering potential molecular targets for disrupting blood-feeding processes and reducing tick populations.

Linking plant feeding to malaria transmission: An integrative field-to-laboratory study in *Anopheles* mosquitoes

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Abstract

Plant-derived sugars are essential for mosquito survival, yet their role in shaping malaria transmission remains poorly understood. Variation in plant nutritional composition, including sugars and secondary metabolites, may influence both vector fitness and parasite development, with direct consequences for transmission dynamics. Here, we provide an integrative field-to-laboratory assessment linking natural plant feeding to malaria parasite development in *Anopheles* mosquitoes. Using plant DNA barcoding, we identified the natural sugar sources of malaria vectors and characterized the host plant range of both non-infected and *Plasmodium*-infected individuals collected in a malaria-endemic region of western Burkina Faso. Recently plant-fed mosquitoes were identified using the cold anthrone assay, followed by sequencing of plant DNA from abdominal samples to determine host plant identity. *Plasmodium* infection status was assessed through parasite DNA detection from head–thorax tissues. To directly test the effects of plant diets, *Anopheles coluzzii* females were experimentally infected with *Plasmodium falciparum* via membrane feeding and maintained on selected plant-derived diets. Infection success and parasite development to infectious sporozoite stages were quantified at 7 and 14 days post-infection. We demonstrate that *Anopheles* mosquitoes exploit a diverse range of plant species, predominantly cultivated crops, and that plant diets significantly influence both mosquito survival and parasite development. Specifically, plant species had contrasting effects on longevity and exerted stage-specific effects on *P. falciparum*, altering both infection prevalence and progression to transmissible stages. These findings demonstrate that mosquito plant feeding behaviour plays a critical role in shaping both vector fitness and parasite development. By linking ecological interactions with transmission biology, this work identifies plant feeding as a previously underexplored but actionable strategies for malaria control such as vegetation management and attractive targeted sugar baits (ATSBs).

Investigating the bioactivity of insects in open wound care by wild chimpanzees

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Abstract

Open wounds pose a significant risk of infection for wild animals, providing entry points for pathogens that can cause severe complications. Chimpanzees (*Pan troglodytes troglodytes*) in Gabon have been observed applying flying insects to open wounds, a behavior that may help in wound healing. However, the functional significance of this behavior has remained largely untested experimentally.

Here, we first prepared insect extracts for chemical characterization using gas chromatography and liquid chromatography-mass spectrometry, and then used these extracts in downstream bioassays to evaluate their potential medicinal relevance. We collected both taxa reported to be selectively used by chimpanzees during wound care and from sympatric insect species not observed in this context, allowing a non-invasive approach to understand the potential functional basis of this behavior through comparative chemical analyses and bioactivity assays.

To assess potential therapeutic benefits, we conducted antimicrobial assays using extracts prepared from the insect species used by the chimpanzees against *Escherichia coli* (a Gram-negative bacterium) and *Bacillus subtilis* (a Gram-positive bacterium). Our results reveal pronounced inhibitory activity against *B. subtilis*, while showing limited inhibition against *E. coli*.

These findings provide experimental evidence that the insects used by chimpanzees for wound care exhibit antibacterial activity, particularly against Gram-positive bacteria. This supports the hypothesis that this behaviour may confer functional antimicrobial benefits and demonstrates clear promise for follow-up chemical investigations to identify the responsible compounds. More broadly, this study highlights insects as a promising and still underexplored resource for antimicrobial discoveries at the intersection of behavioural ecology, entomology, and disease biology.

Maps of tick's presence and associated tick-borne pathogens in and around Paris, France.

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Abstract

Ticks are strict hematophagous acarids which can transmit a high diversity of pathogens. The distribution of tick species and their hosts is known to be influenced by climate, environmental and socio-economic factors, leading potentially to the emergence of associated tick-borne diseases. For example, urban greening can provide suitable new environments for ticks and their hosts, while outdoor activities increase the risk of encountering ticks and their pathogens for humans. In that context, this study aims to provide evidence-based recommendations and tick risk maps for the general public on the green spaces in urbanized areas in and around Paris, Ile de France region, France.

Based on significant human attendance, urban parks, peri-urban woods, green infrastructures and forests were selected. Tick collections were performed by flagging in 166 sites of 32 different green areas, in both spring and autumn of 2022 and 2023. Tick-borne pathogens (TBPs) were then detected by dedicated PCR, qPCR and Next Generation Sequencing. Human frequentation of green spaces, quantified through social media information, was used to produce risks maps.

In total, 3432 ticks were collected, most of them being *Ixodes ricinus* (92,7%), followed by *Dermacentor reticulatus* (3,7%). Forests showed a higher diversity of TBPs, while peri-urban areas presented a significantly higher prevalence of TBPs. *Borrelia* spp. and *Babesia* spp. were the most common pathogen found. Eyach virus and Jingmen-tick virus were detected in forest and peri-urban areas. We showed that presence of ticks is influenced by the temperature and humidity, presence of wild boars, type of vegetation and the typology.

Even if the typology is a key parameter in the distribution of ticks and their pathogens, frequentation by human population is crucial to modulate the estimation of tick bite risk and pathogen transmission. Despite lower abundance, the higher frequentation of peri-urban woods leads to significant risk in such areas.

A large-cage population study of an engineered gene drive targeting doublesex gene in a malaria vector *Anopheles coluzzii*

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Abstract

Despite long-lasting control efforts, malaria remains a major global health challenge, with an estimated 280 million cases and more than 600,000 deaths, primarily in sub-Saharan Africa. These staggering numbers highlight the urgent need for novel, sustainable vector control strategies. The proposed genetic approaches based on CRISPR/Cas9-based homing gene drives offer the potential for rapid suppression/elimination or modification of vector mosquito populations.

Here, we used age-structured large cage replicate populations of a major malaria vector *An. coluzzii* to study the efficacy of the (QFS)5 gene drive targeting two conserved sequences within the female-specific exon of the doublesex gene. Females homozygous for the gene drive insertion develop as sterile intersex individuals, and an increase in their frequency in the population is expected to lead to population collapse. We introduced (QFS)5 heterozygous males to three stable wild-type *An. coluzzii* populations and, in two cages, observed gene drive frequency increase leading to population collapse after 217-235 days. In contrast, in the third population, after a period of increase to 90%, gene drive frequency steadily decreased, to reach 50% equilibrium after 380 days. Molecular analysis of mosquitoes in that cage revealed high frequency of individuals with internally deleted, non-functional drive that does not restore the dsx function and served as de facto resistance allele. Thus, the observed equilibrium was the product of moderate fitness costs of the functional gene drive and accumulation of non-functional drive allele.

Our long-term evaluation of a (QFS)5 gene drive provided insights into the relative contribution of fitness, construct integrity, and resistance formation to drive dynamics, informing the rational design of robust next-generation gene drive systems for malaria vector control.

Passive copper release from rain chains is harmful to mosquito larvae and deters egg-laying

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Bertrand LE MELLAT

Abstract

Urban mosquitoes use accumulated rainwater in private gardens and public green spaces to reproduce. We observed that decorative copper chains that guide rainwater from gutters to open containers significantly reduced the number of mosquito larvae in the accumulated water, and sometimes eliminated them entirely. While the effect of copper salts or copper objects immersed in water on mosquito larvae has been reported, no detailed analysis has been performed on the effects of dissolved copper in terms of concentration and biological impact. In this study, we present the results of two experimental series, one conducted in the field and the other in the laboratory. These experiments were designed to verify our observations and to describe the sensitivity of mosquito larvae to rainwater containing low quantities of copper. Field experiments were conducted during a season of high abundance of tiger mosquitoes (*Aedes albopictus*), while laboratory experiments used the yellow fever mosquito (*Aedes aegypti*) as a biological model. Our field experiments revealed that copper rain chains, like those widely used in Japan for decorative purposes, release enough metal into the flowing water to inhibit the development of larvae and discourage females from approaching the water surface. In the laboratory, rainwater containing copper released by the chains prevented eggs from hatching and larvae from developing. In both settings, we observed that females of both species actively avoided copper-treated water for egg laying.

This work was undertaken with partial financial support from “Chaînes de Pluie” at their request. The academic author retained full control over the study design, data interpretation, and manuscript preparation, received no personal financial compensation, and declares no conflicts of interest.

Uncovering cyclic respiration in *Aedes aegypti*: metabolic responses to environmental temperature

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Abstract

The invasive mosquito *Aedes aegypti* is a primary vector for the causative agents of yellow fever, dengue, chikungunya, and Zika. Additionally, it is considered a competent transmitter of other viruses and nematodes that pose threats to both human and animal health. Regarded as the most cosmopolitan insect vector, *Ae. aegypti* is now predominantly found in urban environments across 114 countries, with its global spread facilitated by international trade and human mobility. Despite its significant public health impact, the respiratory physiology and energetic demands of hematophagous insects remain understudied, as does the influence of environmental conditions on these processes. Quantifying gas exchange is critical for accurately estimating the metabolic costs of key activities and understanding how factors such as temperature influence these costs. In this study, we employed flow-through and stop-flow respirometry, using oxygen optodes and a respirometric chain, to measure respiratory gas exchange in adult *Ae. aegypti*. We quantified rates of oxygen consumption and carbon dioxide production, characterised the mosquitoes' respiratory pattern, and assessed the thermal sensitivity in both males and females, as well as the impact of blood-feeding in females. For the first time, we observed cyclic respiration in this species, and we were able to calculate energy consumption at rest. Oxygen consumption ranged from 0.017 μmol of O_2 per hour at 15°C to 0.037 μmol of O_2 per hour at 30°C, with Q10 values ranging from 1.46 (15°–25°C) to 2.3 (25°–30°C), highlighting the variable effect of temperature. Our results establish a detailed physiological baseline that links environmental temperature to metabolic performance in this medically important species and provide parameters that are relevant for predictive models of activity, survival, and vector capacity under changing climate conditions.

Acknowledgement. This research was supported by a Travelling Fellowship awarded by The Journal of Experimental Biology to the first author.

Monitoring of chigger mite (Acari: Trombiculidae) populations in Yesan, Chungcheongnam-do, Korea (2017–2024)

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Abstract

Trombiculid larvae (Acari: Trombiculidae) are well known as primary vectors of scrub typhus, and their populations typically increase in autumn. However, variations in their occurrence patterns depending on local environmental conditions indicate the need for long-term monitoring tailored to specific regions, underscoring the importance of region-specific surveillance efforts.

This study investigated seasonal and interannual patterns of trombiculid mite occurrence based on field surveys conducted from September to December, 2017–2024, in Yesan County, Chungcheongnam-do, Korea. Sampling traps were placed at 5-meter intervals across four habitat types—paddy fields, dry fields, waterways, and grasslands—resulting in the collection of 3,386 individuals.

Annual specimen counts exhibited a gradual decline, from 1,104 individuals in 2017 to 110 in 2024. A total of 14 species across six genera were identified through taxonomic analysis, with *Neotrombicula tamiyai* being the most dominant species, accounting for 56.19% (1,892 individuals) of the total.

Notably, *Neotrombicula nagayoi*, a species not previously detected during the 2017–2023 survey period, was newly recorded in 2024. Although represented by a single specimen, this record may reflect microhabitat changes or shifts in local environmental conditions, suggesting the potential for faunal turnover that might not be detected through dominance-based metrics alone.

These findings provide baseline ecological data for the development of localized prevention and management strategies in mite-borne disease risk assessment and highlight the value of sustained, systematic monitoring to support understanding of long-term trends in trombiculid populations and species composition.

The role of hemocytes in the rat flea *Xenopsylla cheopis* and its interaction with the plague bacterium *Yersinia pestis*

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Agustin ROLANDELLI

Abstract

Plague remains a re-emerging zoonotic disease and a persistent global threat. The rat flea *Xenopsylla cheopis* is a major vector of *Yersinia pestis*, the causative agent of plague. Despite its epidemiological importance, flea biology remains largely understudied. Particularly, understanding the flea immunity is essential for clarifying plague dynamics. In this study, we uncovered sizable differences in hemocytes (specialized immune cells) between rat fleas from high plague prevalence (HPP) and low plague prevalence (LPP) regions. We detected that a blood meal triggers hemocytes proliferation in fleas, as their total number increased ~30% after feeding. Notably, we measured higher hemocyte numbers both before and after a blood meal in LPP fleas compared to HPP fleas. Besides, *Y. pestis* infection decreased hemocyte numbers only in LPP fleas, indicating differential response of these cells to a blood meal and *Y. pestis* between flea strains.

We also identified the three main hemocyte morphotypes described in insects: (1) prohemocytes, which are small cells (9 μm in diameter) with minimal cytoplasm; (2) plasmatocytes, larger cells (16.9 μm in diameter) containing clear cytoplasm with pseudopodia; and (3) granulocytes, round cells of 14.5 μm in diameter with darker cytoplasm full of granules. Independently of the strain, prohemocytes proportion decrease after feeding, while granulocyte increased, suggesting that feeding triggers hemocyte differentiation. Strikingly, we found a fourth morphotype represented by colossal cells (42.2 μm in diameter), with a dark cytoplasm and frequently bi-nucleated, that we named coloscyte. Interestingly, coloscyte show pronounced strain-dependent differences: their abundance increases substantially after feeding in HPP fleas but not in LPP fleas. Ongoing RNA-seq analyses aim to clarify the role of hemocytes in flea feeding and infection. Overall, we provide the first description of hemocyte morphotypes in *X. cheopis* and reveal how their abundance varies according to flea strain, nutritional status, and *Y. pestis* infection.

What bridge vectors could favour arboviruses spillover along mangrove-urban continuums in Guadeloupe?

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Abstract

Mangrove ecosystems are biodiversity hotspots that harbour interactions between wildlife, vectors and viruses. The increasing urbanization and mangrove deforestation has increased the contact between these natural environments and urbanized settings. Bridge vectors that move across mangroves and urbanized areas, thus encompassing ecological boundaries, could promote the spillover of vector-borne viruses circulating in the mangroves to humans populations. Hence, the goal of this study is to characterize culicid fauna along a mangrove-urban continuum in Guadeloupe (French West Indies) and to identify potential bridge vectors.

In order to characterize spatial and temporal variations in the composition of the Culicidae community, three sampling sites encompassing mangrove areas and adjacent urban areas were selected. Entomological collections began in 2025 and will continue for three years, with two collection seasons (wet and dry) per year. Mosquitoes were collected using 200-meter transects encompassing mangroves, mangrove edges, and urban areas using BG-Pro light traps (N = 9 per sampling site), spaced fifty meters apart. We identified ten species out of the thirty-six mosquito species present in Guadeloupe. We found five species throughout the mangrove-urban continuum. Interestingly, most of these species are known for their ecological plasticity, opportunistic feeding behaviour, and role as arbovirus vectors, such as *Anopheles aquasalis*. Further studies evaluating the feeding preferences of these potential bridge vector species and the viral communities they harbour are needed to elucidate precisely the risk of viral spread from mangroves to urban areas in Guadeloupe. The future integration of seasonal entomological data into a landscape ecology approach will refine the analysis of the influence of environmental gradients on the risk of viral emergence. Finally, this work will contribute to the development of new surveillance strategies adapted to rapidly urbanizing island contexts, such as the French West Indies.

Pilot trial of the sterile insect technique and the incompatible insect technique for the control of *Ae. albopictus* in Yucatan, Mexico

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Abstract

Aedes albopictus is one of the most important invasive species worldwide and is a known vector for transmitting arboviruses, such as dengue and chikungunya. In recent years, pilot studies using sterile insect technique (SIT) and incompatible insect technique (IIT) have shown promising results, including the combination of both (IIT-SIT). *Ae. albopictus* is naturally infected with two strains of *Wolbachia*, wAlbA and wAlbB, and a new strain with triple *Wolbachia* infection (strain infected with wAlbA, wAlbB, and wPip) has been developed. Males released that carry the triple *Wolbachia* infection inherited from their mothers produce infertile eggs, leading to a reduction in the mosquito population size. We used the combined IIT-SIT approach, conducting a pilot study in the open field by releasing 6,000 *Ae. albopictus* males triple-infected and irradiated weekly, produced in the Biological Control Laboratory in Yucatan. The releases lasted 50 weeks in an 11 Ha site in Yucatan including a non-treated comparison area. During the mass production phase, we evaluated biological cycle traits such as fecundity, fertility, longevity, cytoplasmic incompatibility, male competitiveness, and the presence of *Wolbachia* in *Ae. albopictus* generations by PCR. During the release phase, we evaluated egg hatching and female *Ae. albopictus* density at the release site and compared it with the similar site used as a non-treated, control area. Our study is the first open-field pilot report on mass releases of sterile *Ae. albopictus* males using the combined IIT-SIT technique in Mexico. The results are promising and comparable with other studies that confirm the reduction in abundance due to the flooded releases of incompatible males.

Mosquito Species Checklist and Distribution in Haiti and the Dominican Republic (1905–2025): A Systematic Review

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Abstract

Mosquito-borne diseases represent a major public health threat, particularly in island and resource-limited settings. Hispaniola, shared by Haiti and the Dominican Republic, is highly vulnerable due to recurrent extreme climatic events, endemic diseases such as malaria, filariasis, and dengue, and challenging socio-economic and political conditions that hinder effective vector control. Moreover, knowledge of mosquito (Diptera: Culicidae) biodiversity and distribution on the island remains outdated and fragmented.

We conducted a PRISMA-guided systematic review (1905–2024) of mosquito species diversity and associated vector-borne diseases in both countries, using PubMed and Web of Science databases, complemented by gray literature and entomological collections. Data were synthesized into an updated checklist and historical distribution maps.

We complemented by a field work in Northern Haiti.

Our review identified 13 genera and 63 mosquito species on the island, 12 are exclusive to the Dominican Republic, one exclusive to Haiti and 50 species are shared by both countries. Species richness was higher in the Dominican Republic, with 62 species, than in Haiti, with 51 likely reflecting differences in topography, land use changes and research effort. The most frequently reported species were *Anopheles albimanus*, *Aedes aegypti*, *Culex quinquefasciatus*, *Cx. nigripalpus*, *Ae. albopictus* and *Psorophora jamaicensis*.

We detected in the field the invasive species *Aedes vitittatus* in the north of Haiti, being confirmed by molecular analysis.

This updated checklist and distribution analysis of the last 120 years provides the most comprehensive synthesis of culicid biodiversity in Hispaniola to date. These findings offer a critical foundation for targeted entomological surveillance, risk assessment, and the design of integrated vector management strategies to address future mosquito-borne disease threats in the region.

The rising economic costs and social impacts of mosquito-borne diseases

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Abstract

Aedes-borne diseases, such as dengue, chikungunya and Zika are caused by viruses transmitted by *Aedes aegypti* and *Ae. albopictus* mosquitoes. They are producing an enormous public health burden and a lesser-known economic and social impacts. First, we present a reliable, up-to-date, standardised and easily updatable global-scale synthesis of studies reporting the economic costs caused by these mosquitoes, obtained from 880 records from 118 countries covering the last 45 years. We also identify multi-sectoral effects across multiple domains, combining a systematic review of the literature with the analysis of qualitative data. From 1975 to 2020, the cumulative reported cost of Aedes and Aedes-borne diseases was at least 87.3 billion in 2022 US\$ values, having increased almost 100-fold over this period, while still considerably underreported and underestimated. Costs are mainly due to dengue (80%) and do not consider the medical sequelae of chikungunya and Zika, which would bring this estimate up to US\$ 310.8 billion worldwide. Damage and losses were an order of magnitude higher than investment in management and only a modest portion of the total reported expenditure went to prevention. We explained how the relation among the investment in management and the costs of medical damages and losses are different among tropical and temperate areas. We identify potential effects on politics/governance, economic activity, education, research, the society, and media. We highlight several possible key vulnerabilities such as the saturation of vector control resources, healthcare strain, economic losses (especially in the tourism industry), and social disruption (in case of social movements challenging public policies). Cost-effective control measures are urgently needed to safeguard global health and well-being and to reduce the burden. These researches can inform evidence-based policy and contributes towards a greater awareness of the increasing economic costs and social impacts of mosquito-borne diseases.

Strengthening Tick-Borne Encephalitis Surveillance in Non-Endemic Regions of Kazakhstan

Zhanna SHAPIYEVA (National Centre for Public Health, MoH Kazakhstan, Z.shapiyeva@gmail.com)

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Abstract

Background. Ixodid ticks are widely distributed across the territory of Kazakhstan, and some species act as vectors of tick-borne encephalitis (TBE). Currently, the situation of TBE is unstable, with 30-40 cases reported annually. Despite the low incidence and availability of vaccination, TBE poses a serious public health threat due to the risk of severe clinical outcomes. Traditionally, surveillance and preventive measures are focused on endemic regions, which may lead to an underestimation of infection risk in areas considered non-endemic. In the context of the expanding range of ixodid ticks, investigation of TBE virus (TBEV) circulation in non-endemic regions is of increasing importance.

Objective. To strengthen TBE surveillance and to obtain new data on the distribution of ixodid ticks and their infection with TBEV in non-endemic regions of Kazakhstan.

Materials and Methods. During 2023-2025, ixodid ticks were collected in Zhambyl Region (southern Kazakhstan) and Kostanay Region (northern). Tick collection was carried out using the flagging method in natural biotopes. Species identification was performed using a stereomicroscope. Laboratory testing was conducted using ELISA and PCR methods in accordance with national guidelines; positive TBE virus findings were confirmed by sequencing.

Results. A total of 2,044 ticks were collected in Zhambyl Region, including *D.niveus*, *H.punctata*, *H.asiaticum*, and *H.scupense*. For the first time, circulation of TBEV was detected in *D.niveus* populations in the non-endemic Zhambyl Region (Moiynkum District). The proportion of *D.niveus* in tick collections ranged from 70% to 97%, and the TBEV detection rate was 0.45%. In addition, *A.phagocytophilum* (0.8%) and *E.chaffeensis/E.muris* (0.4%) were identified. In Kostanay Region, 1,575 ticks (*D.reticulatus*, *D.marginatus*, *Ix.persulcatus*) were collected; no TBEV positive samples were detected.

Conclusions. The results demonstrate previously unrecognized circulation of TBEV in ixodid ticks in non-endemic regions of Kazakhstan, supporting the revision of current surveillance strategies and expansion of integrated entomological and laboratory monitoring.

RNA-seq Reveals Cuticular, Detoxification, and Hormonal Mechanisms Underlying Insecticide Responses in *Aedes aegypti* in Jamaica

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Sheena FRANCIS

Abstract

Insecticide resistance threatens the effectiveness of vector control programs targeting *Aedes aegypti*, the primary vector of dengue, chikungunya, and Zika viruses. Understanding transcriptional responses to insecticide exposure is critical for identifying the molecular mechanisms underlying resistance in field populations.

Field-derived *Aedes aegypti* from Kingston and St. Andrew, Jamaica were exposed to malathion and pyriproxyfen using CDC bottle bioassays, and RNA sequencing was performed to characterize transcriptomic responses associated with insecticide exposure.

Field mosquitoes exhibited constitutive overexpression of several detoxification genes relative to the susceptible strain, including carboxylesterases CCEAE1A, CCEAE1B, and CCEAE3B, suggesting an elevated baseline detoxification capacity. Malathion exposure elicited strong induction of both cuticular proteins and detoxification pathways, including additional upregulation of carboxylesterases (CCEAE1A, CCEAE1B, CCEAE3B, CCEAE1O), glutathione S-transferases (GSTD4, GSTS1, GSTX1), and multiple cytochrome P450 genes such as CYP9J17, CYP6BB2, and CYP4J15. In contrast, pyriproxyfen exposure induced a more targeted transcriptional response characterized by differential expression of juvenile hormone-associated genes, including CCEJHE4F, and several cytochrome P450s (CYP325N2, CYP9J24). Pyriproxyfen treatment also strongly regulated genes associated with juvenile hormone signaling, including juvenile hormone-inducible proteins and odorant-binding proteins, (JHA15, OBP4, and OBP13).

These results reveal distinct detoxification and endocrine responses to commonly used vector control insecticides and highlight transcriptomic signatures that may inform molecular resistance surveillance in Jamaica and Caribbean *Aedes aegypti* populations.

Multitrophic interactions around aphids carrying the barley yellow dwarf virus (BYDV)

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Abstract

Rhopalosiphum padi is the main pest affecting cereal crops in Europe. It is a vector of barley yellow dwarf virus (BYDV-PAS), a persistent circulatory virus from the Luteoviridae family, that significantly alters the physiology of infected plants, but not that of its vector. However, it can induce significant behavioral changes in aphids. Persistent viruses tend to reduce vector dispersal, promoting the formation of stable, sedentary colonies - a phenomenon that reinforces virus persistence. Moreover, these immobile colonies (caused by persistent virus), in addition to changes in the volatile organic compounds emitted by infected plants, may reduce the attraction of natural enemies. Yet no studies have demonstrated the impact of BYDV on the dispersal or attractiveness of *R. padi*. We therefore investigated the multitrophic interactions between BYDV and *R. padi*, focusing on the latter's attractiveness for natural enemies and dispersal behavior. We hypothesized that BYDV would reduce both *R. padi*'s dispersal behavior and its attractiveness to natural enemies, as observed with other persistent viruses. The virus's impact on dispersal behavior was studied using barley microplots in a greenhouse, with 12 replicates per treatment (infected or uninfected). We monitored the colony formation and the aphid movements at a given time. Virus spread was assessed using ELISA tests three weeks after the end of the experiment (the time required for the viral load to be detectable within the plant). Attraction of natural enemies was assessed using a Y-tube olfactometer, with infected or uninfected plants in each arm, allowing observation of parasitoid and ladybug preferences (40 replicates each). These findings are essential to improve the accuracy of predictive models on BYDV propagation in agricultural landscapes and contribute to the development of better pest management strategies.

Ectoparasites diversity and distribution of pathogen in Ticks collected from Wild Rabbit and Cape Hare in Algeria

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Faouzi MATALLAH, Francesco DEFILIPPO, Sara RIGAMONTI, Giulia MAIOLI, Patrizia CAVADINI, Antonio LAVAZZA, Tiziana TROGU

Abstract

The Cape hare (*Lepus capensis*) and the wild rabbit (*Oryctolagus cuniculus*) are among the most common game species; however, both have experienced population declines in Algeria in recent years. These wild lagomorphs can act as hosts for various ectoparasites, notably ticks and fleas.

This study was conducted in the High Plateaus of Algeria during the 2023–2024 hunting seasons. A total of 47 wild lagomorphs were collected from 20 different geographic sites and examined for ectoparasites. Among the 44 hares sampled, 25 were infested, whereas none of the examined wild rabbits harbored ectoparasites. A total of 165 ticks were identified, with *Rhipicephalus sanguineus* predominating (89.14%), followed by *Ixodes hexagonus* (5.14%) and 10 fleas with three species were also identified: *Ctenocephalides felis* (4%), *Leptopsylla segnis* (1.14%), and *Xenopsyllacheopsis* (0.57%). Ticks were morphological and molecularly identified, and the presence of bacteria (*Borrelia* spp., *Anaplasma* spp., *Rickettsia* spp., *Coxiella* spp. and *Ehrlichia*) and viruses (TBEV, CCHF, WN, USUTU, Phlebovirus) was determined by quantitative real-time PCR. All 165 ticks were negative in real-time PCR for *Anaplasma* spp., *Coxiella* spp., *Ehrlichia*, TBEV, CCHF, WN, USUTU, and Phlebovirus. Seven zoonotic *Rickettsia* species were detected for the first time in *R. sanguineus* collected from hares. *R. aeschlimannii* was the most prevalent (19.64%), followed by *R. massiliae* (5.35%), *R. sibirica* (3.57%), *R. africae*, *R. japonica*, *R. marmionii*, and *R. raoultii* (each 1.78%). Also, zoonotic *Borrelia* species were identified for the first time in Algeria: *B. afzelii* (3.57%) in *R. sanguineus*, *I. hexagonus*, and *B. burgdorferi sensu stricto* (1.78%) in *R. sanguineus*. The predominance of *R. sanguineus* and the emergence of new zoonotic pathogens in Algeria highlight the need for broader investigations to clarify the role of lagomorphs, particularly hares in the epidemiology of these tick-borne pathogens.

Emergence of Flea-Borne *Rickettsia asembonensis* in the Mediterranean Region: Evidence from Sardinia

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Laura GIUA, Rosanna ZOBBA, Emanuela BAZZONI, Giovana CHESSA, Pierangela CABRAS, Alberto ALBERTI, Giovanna MASALA, Cipriano FOXI

Abstract

Rickettsia asembonensis, a flea-borne member of the *Rickettsia felis*-like organisms, is increasingly reported worldwide, yet its distribution and epidemiological significance in Europe remain poorly understood. In Italy, research has largely focused on tick-borne *Rickettsiae*, while the role of fleas and lice has received limited attention.

Between 2021 and 2024, a total of 456 ectoparasites (96 fleas and 360 lice) were collected from 87 domestic and wild animal hosts across the provinces of Ogliastra, Nuoro, and Medio Campidano (Sardinia, Italy). All specimens were morphologically identified and screened for *Rickettsia* spp. by PCR targeting the *gltA* gene. Positive samples underwent multilocus characterization using additional genetic markers (*ompA*, *ompB*, *sca4*, and *htrA*). Amplicons were sequenced bidirectionally and compared with reference sequences available in GenBank. Six fleas tested positive for *Rickettsia* spp.: one *Pulex irritans* from a dog and five fleas collected from hedgehogs (*Xenopsylla cheopis* and *Archaeopsylla erinacei*). All 360 lice tested negative. Sequencing of *gltA* revealed a single sequence type (*gltA_flea1_Sardinia*) showing 100% identity with *R. asembonensis* strains previously reported from South America, Africa, and Asia. Multilocus characterization confirmed *R. asembonensis* at all additional loci, with one sequence type identified for each gene (*ompA*, *ompB*, *sca4*, *htrA*). These findings represent the first molecular detection of *R. asembonensis* in Italy.

The detection of *R. asembonensis* in multiple flea species associated with domestic and wild mammals expands the known diversity of circulating *Rickettsiae* in the Mediterranean region and demonstrates the epidemiological relevance of non-tick ectoparasites. The involved flea species, characterized by low host specificity and peridomestic habits, may facilitate potential spillover to humans. Given recent reports of *R. asembonensis* in febrile patients, further research is essential to clarify its pathogenicity and zoonotic risk. Incorporating multilocus approaches into regional surveillance programs will enhance early detection of emerging *Rickettsia* species in Europe.

DETECTION OF BLUETONGUE VIRUS IN CULICOIDES SPECIES (DIPTERA: CERATOPOGONIDAE) DURING BTV OUTBREAKS IN SARDINIA, 2025

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Giuseppe SATTA, Valentina SINI, Daniele DEDOLA, Roberto BECHERE, Daniela MANUNTA, Angela Maria ROCCHIGIANI, Elisabetta CORADDUZZA, Stefano CAPPAL, Gantonella PUGGIONI

Abstract

Bluetongue (BTV) is an infectious disease of ruminants that is transmitted by *Culicoides* biting midges. Currently, a number of species including *C. imicola*, *C. pulicaris*, *C. punctatus*, *C. newsteadi* s.l., *C. scoticus* and *C. obsoletus* are considered BTV-competent vectors. During 2025, an outbreak of BTV serotypes 3, 4, 5 and 8 was reported in Sardinia, Italy. An extensive regional research was conducted in order to evaluate the possible species implicated in the transmission of the virus during the course of 2025.

By using Onderstepoort Black-Light Traps, *Culicoides* collections have been performed in 21 sheep farms. *Culicoides* specimens have been morphologically identified to the species level and pooled, according to species, location, date and physiological status (i.e. parous, gravid and engorged females). Each pool (with maximum 50 females) was analyzed for BTV by Real Time RT-PCR.

A total of 330,642 *Culicoides* adults have been collected belonging to 29 species. *Culicoides imicola* has been the most abundant species captured (44%), followed by *C. obsoletus*/*C. scoticus* (39%). The other species have been collected with very low numbers. Overall, 2001 pools (for a total of 27,768 specimens) have been analyzed and 498 were BTV positive.

In addition to the known vector species, including *C. imicola*, *C. pulicaris*, *C. punctatus*, *C. newsteadi* s.l., and *C. obsoletus*/*C. scoticus*, an additional 15 species tested positive and all BTV serotypes circulating in Sardinia (3, 4, 5, 8) were found.

Our results suggest that during an outbreak more *Culicoides* species could be involved in BTV transmission, probably related to the high level of viral circulation, and they could play a role in overwintering, and, even if marginal, in the spread of the disease.

de novo assembly of the genome of *Eretmapodites subsimplicipes*, an overlooked arbovirus vector

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Abstract

Vector borne diseases are a major global issue with increasing number of outbreaks in plant, animal and human populations. Some arthropods including several mosquito species are known to be competent for transmission of arboviruses. Among those, many species have been extensively described but, other species, such as *Eretmapodites spp.* remain poorly studied. *Eretmapodites subsimplicipes*, a highly abundant species in Mayotte island and more generally in Southern Africa, has been recently described to be competent for Rift Fever Valley virus (RVFV). It is crucial to characterize the biology and ecology of this mosquito species and to develop the appropriate tools to assess its epidemiological significance.

No genetic and genomic data are currently available for *Er. subsimplicipes*, therefore we aim to sequence and assemble its genome to perform accurate genomic analyses. We first estimated the genome size using flow cytometry techniques, then we extracted high quality long fragment DNA and performed Long Read Sequencing using SMRT Technology. Additionally, transcriptomic sequence data were also obtained on an Illumina platform on each mosquito development stage. PacBio sequencing provided 2.3 M HiFi Reads with a N50 of 16.53kb and QC30 91.03% that were used for de novo assembly. Despite the high quality of the draft genome assembly, genome size was greater than estimated with flow cytometry. To improve the genome assembly of *Er. subsimplicipes*, we are considering two approaches : the identification of duplicated genes using bioinformatic pipelines ; and the extraction of ultra-long fragments DNA on one individual using an ultra low DNA input extraction kit from PacBio. Stage specific RNA sequences will contribute to identify the gene coding sequences and the stage-specific expression pattern. The resulting data will be an important resource publicly available for population genomics analyses and design of genetic markers to study the biology and ecology of this species.

Relationship between microbiome and genetic diversity in the soft tick *Ornithodoros phacochoerus*, in Central Mozambique

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Mélanie JEANNEAU, David BRU, Maxime DUHAYON, Olivier DURON, Carla GIUPPONI, Thomas POLLET, Florian TARAVEAU

Abstract

Soft ticks of the species *Ornithodoros phacochoerus* infest warthog burrows in Southern Africa. *O. phacochoerus* is a vector of the African swine fever virus, playing a role in maintaining the virus within the sylvatic cycle.

These ticks depend on primary endosymbionts to produce essential nutrients for their development. They also harbour secondary endosymbionts belonging to the *Rickettsia* and *Rickettsiella* genera. The genomes of these bacterial strains have acquired the CI-bacteria gene system, known to induce cytoplasmic incompatibility (CI). Such maternally-transmitted bacteria can drive key evolutionary changes in tick reproduction and impact population genetic structure. Similarly, microbiome diversity can be influenced by the genetic variation among hosts. In this context, our aim is to explore the link between microbiota and genetic diversity in Afrotropical soft ticks.

In Mozambique, we collected tick samples from warthog burrows in two reserves: the Macossa Game Reserve and the Gorongosa National Park. We extracted DNA from more than a thousand ticks sampled in 30 sites. We performed microbiota sequencing targeting the V3-V4 region of the 16S rRNA gene. All individuals were also genotyped using sixteen microsatellite markers designed for this species.

Preliminary results obtained from 600 individuals suggest that the microbiota of *O. phacochoerus* exhibits low bacterial diversity, consisting of one primary endosymbiont (*Francisella*-like) and one secondary endosymbiont (*Rickettsiella*). Genomic analyses revealed that the *Rickettsiella* genome possesses a Cif operon. Surprisingly, very few environmental or pathogenic bacterial species were found. Additionally, a clear spatial structure of the microbiota was observed, with differentiation between sites. This spatial structure is also evident in population genetics, and we demonstrated that the observed genetic variation followed a model of isolation by distance. These preliminary results must be supplemented by further genotyping and microbiota analyses of the remaining samples, and a comparison of microbiota and genetic diversity will be performed.

#10713

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Improving Resilience to the Spread of Plant Diseases via a Regional Pest Common Data Space

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Liis ANDRESEN, Lee PÖLLUMAA, Andres MÄE

Abstract

Climate change is accelerating the spread and impact of plant pests and diseases, causing substantial yield losses across the Baltic Sea Region (BSR). The objective of the PestSpace project is to establish a common data space within the Baltic Sea Region to enable rapid detection and notification of pests and invasive species spreading from south to north. The PestSpace project addresses this challenge by developing a novel, cross-border Pest Common Data Space designed to enhance the detection, monitoring, and management of pathogens and insect pests threatening two regionally important crops: winter wheat and faba bean. The project involves partners from Poland, Lithuania, Estonia, Finland, and Latvia. Field trials were conducted, and standardized methods were implemented across all trial sites. In Estonia, as in the other countries, ten cultivars of faba bean were sown in spring 2025, and ten cultivars of winter wheat were sown in autumn 2025 at four experimental locations. Disease severity was assessed, symptoms were photographed and uploaded to the PlutoF platform, where the images are used to train and improve AI-based diagnostic models, and samples were collected for subsequent molecular analyses. In faba bean, the chocolate spot was the dominant disease in 2025, followed by leaf spot caused by *Alternaria* and *Stemphylium* species, alongside important insect pests: *Sitona lineatus*, *Autographa gamma*, *Bruchus rufimanus*, *Aphis fabae* and *Megoura viciae* (aphids).

Future activities will include the continuation of field observations, species-level identification of pathogens, and the adaptation of molecular methods for characterizing the mycobiome in diseased plant tissues.

Supervised taxonomic classification of bulk insect images using metabarcoding and transfer learning

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John QUINTO, Nicolas CHAZOT, Brendan FURNEAUX, Tomas ROSLIN, Iuliia ZARUBIEVA, Akshita GUPTA, Scott LOWE, Graham TAYLOR

Abstract

Insects are the most diverse organism groups on Earth. To accelerate our understanding of insect diversity, high-throughput approaches are therefore imperative. DNA barcoding and high-resolution imaging show strong potential for automatic taxonomic classification, but most image-based approaches rely on individually curated specimen. This contrasts with the unsorted bulk samples collected in large-scale ecological surveys.

Extracting taxonomic information from images of unsorted samples – i.e., bulk images – poses several challenges. First, individual insects are often represented at low resolution in such images, limiting the effectiveness of image-based classification. Second, unknown taxa are common among insects, especially in species-rich regions. A global application of supervised classification methods is therefore complicated by a lack of taxonomic annotations.

To address the first challenge, we propose combining imaging with molecular data, specifically DNA barcodes, to improve taxonomic resolution. Sample-level metabarcoding data can serve as labels when training image classification models, indicating which taxa are present in the image. By combining the two data sources, we can augment the DNA-based classifications with taxon-level abundance information and trait data extracted from the images.

To address the second challenge, we propose using transfer learning between specimen- and sample-level data. Large databases of publicly available individual specimen images and their associated DNA barcodes provide ready-made training datasets across a broad diversity of taxa. This pre-trained association between molecular and image data can then be transferred to improve taxonomic classification of unsorted samples. To validate this method, we use a smaller set of images where the exact location of each specimen is known, thus establishing a 1:1 correspondence between bulk images and individual specimens. This approach facilitates model generalization while minimizing reliance on exhaustive human annotation.

#11285

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Navigating through the high species diversity of wild bees (Hymenoptera: Anthophila) requires more than modern identification keys

Noé BARBIER CHABOT (Sorbonne Université, Noe.barbierchabot@gmail.com)

Vincent CARLIER, Adrien PERRARD

Abstract

In the context of pollinator decline and species-focused conservation measures, the need for data on wild bees continues to grow, and identifying them at a species level has become a crucial issue. This challenge is linked to a lack of naturalist skills, to the difficulty of the group, but also to a lack of tools to train people in this expertise, such as accessible, comprehensive and up-to-date identification keys. Tools such as online multi-access keys are designed to facilitate identification, better illustrate criteria and enable more fluid updates. These keys require a higher initial investment than dichotomous keys, but they should enable correct identification even when partially filled in, if they contain at least the information found in the corresponding traditional keys. In this study, we tested whether multi-access keys could help identify wild bees in France. We created three multi-access keys for the three most diverse genera of bees in France and tested them against dichotomous keys. These tests were carried out by 102 participants, including 11 specialists, each having 15 minutes per specimen. The resulting 1432 identifications show that the multi-access format is less useful for specialists than their classic keys, with no difference for less-experienced participants. Our results highlight that identifying wild bees of diverse genera to the species level in 15 minutes using only an identification key is difficult, even for specialists. This study suggests that identification keys are not enough for an efficient identification of complex groups such as wild bees.

Insects in Italian Painting through Time: From Symbolism to Naturalism

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Abstract

Insects appear less frequently in Italian painting than in Northern European traditions, yet their presence reveals a wide range of meanings and functions that shift across time, genres, and cultural contexts. This contribution explores how insects have been represented in Italian painting from the Middle Age to the early modern period, highlighting a gradual movement from symbolic and allegorical roles to increasingly naturalistic and observation-based depictions, while highlighting that the boundary between art and science is never rigid. In religious and allegorical works, insects often convey symbolic meanings rooted in ancient mythology or Christian thought. The butterfly, traditionally linked to the soul, is central in Pisanello's *"Portrait of an Este Princess"*, where its function may range from matrimonial symbolism to an allusion to mortality. A damselfly, associated with water and spiritual transformation, appears in Tommaso Aleni's *"Madonna of the Pomegranate"*, whereas grasshoppers signify destructive force in Lorenzo Lotto's *"Saint Jerome"*. Flies and bees provide contrasting associations: flies evoke decay and fragility of life, as in Jacopo Ligozzi's *"Memento Mori"*, while honeybees signify industriousness and civic virtue in Pietro da Cortona's *"Triumph of Divine Providence"*. With the rise of Renaissance naturalism, artists increasingly approached insects with scientific attention. Leonardo da Vinci's studies of dragonflies and beetles (with an almost engineering approach) and Caravaggio's faithful depiction of fruit pests in the *"Basket of Fruit"*, illustrate this convergence between artistic practice and empirical observation. Early modern naturalists—including Ulisse Aldrovandi and Francesco Stelluti—deepened this connection, while still-life painters such as Fede Galizia and Giovanna Garzoni produced highly detailed, taxonomically recognisable insect portrayals. Overall, insect imagery in Italian painting—though not abundant—offers valuable insights into evolving symbolic frameworks and into the progressive integration of naturalistic and scientific observation within visual culture.

#14136

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

EPIC-Bee - Building taxonomic capacity for wild bees to support the EU Pollinator Monitoring Scheme (EUPoMS)

Sarah LESCOT (UMONS, Sarah.lescot@umons.ac.be)

Denis MICHEZ, Sara REVERTÉ SAIZ

Abstract

The European Pollinator Identification Courses – Wild Bees (EPIC-Bee) is a two-year project funded by the European Commission's Directorate-General for Environment. Started in January 2025, its primary objective is to enhance the para-taxonomic expertise in wild bee identification across the 27 EU Member States and contribute to the preparation for the implementation of the EU Pollinator Monitoring Scheme (EU-PoMS). Led by the University of Mons (UMONS) in collaboration with 15 partners, EPIC-Bee has the specific objective of organizing training activities. In total, 35 training courses, each lasting 5 days, with approximately 10-15 participants, are organized. To take account of the different levels of expertise, the project proposes a three-level training program: basic, intermediate and advanced. The training programme is designed to take into account differences in the wild bee faunas between Member States and biogeographical regions ; the 27 Member States are separated in 6 regions. The basic and intermediate trainings are organized at a regional level and the advanced at the European level. The basic training combines field and laboratory work to teach sampling techniques, specimen preparation, and identification of wild bee genera. The intermediate training prepares trainees to identify wild bees at the species level. The advanced training aims to form regional trainers by transferring knowledge from alpha-taxonomists. To support these training efforts, EPIC-Bee develops identification keys, establishes reference collections in all 27 Member States, and provides e-learning tools through the Pollinator Academy.

Ants, cities, and citizens: investigating urbanization effects on biodiversity in French tropical territories

Jérôme ORIVEL (CNRS, CRBE, Toulouse, Jerome.orivel@cnrs.fr)

Abstract

Citizen science has proven highly valuable for exploring and monitoring biodiversity, while also directly engaging people in the scientific process and fostering education and public awareness. In this talk, I will present initiatives establishing citizen science projects focused on urban biodiversity in French tropical overseas territories, with ants as focal organisms. Projects conducted in French Guiana, Guadeloupe, and Martinique involved 78 schools and 153 classes, whose pupils collected 1645 ant samples from their schoolyards and backyards. The compiled dataset enabled the investigation of the effects of urbanization on ant communities. In French Guiana and Guadeloupe, urbanization significantly decreased species richness and increased the proportion of exotic species. In contrast, Martinique showed no significant effect of urbanization on either species richness or the proportion of exotic species. Patterns of beta diversity were driven by both nestedness and spatial turnover across urbanization gradients within territories. Negative co-occurrences were mainly observed among invasive species, especially involving *Pheidole megacephala*, which exhibited exclusionary interactions with both native and other introduced species. These findings underline the complex and context-dependent effects of urbanization on biodiversity, highlighting biotic homogenization as a major consequence. The success of these initiatives encourages the continuation of such efforts, especially in territories where improving biodiversity knowledge is a key priority alongside strong educational needs. Among future perspectives, the development of digital recognition tools to limit specimen collection represents a promising avenue for upcoming projects.

#15356

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

EntoBites: Bringing you insect science, one buzz at a time

Veronika PAVLASOVA (Newcastle University, V.pavlasova2@ncl.ac.uk)

Wendy HARRIS, Madeleine FABUSOVA, Stephanie GLENDINNING, Armando ROSARIO-LEBRON, Matthew SPARKS, Wendy HARRIS

Abstract

Insects are everywhere, and so is the science behind them. EntoBites is a platform run by students and early-career researchers that turns new entomological research into short, easy-to-read summaries. From interesting behaviours to lesser-known ecological roles, we break down studies into bitesized pieces that make insect science more approachable and show why it matters.

EntoBites is also a space for anyone interested to get involved. We are building a community of writers who want to develop their science communication skills, gain experience, and share their interest in entomology. This poster introduces what we do and invites you to join us in making insect science more accessible.

#11296

Poster Session 1 - Ice breaker party
29/06/2026 at 16:00, Exhibition area

Innovating Bedbug Control : Symbiotic Control within a One Health Framework

Charlotte TANNEAU (Laboratoire de Biométrie et de Biologie Evolutive (LBBE) - UMR CNRS 5558, Charlotte.tanneau@univ-lyon1.fr)

Elodie ROSINKI, Guillaume HOFFMANN, Andrés PALENCIA, Fabrice VAVRE, Natacha KREMER

Abstract

Even if bedbugs (*Cimex lectularius*) are currently recognized as non-vector of diseases, their resurgence due to insecticide resistance is a major issue in public health. Indeed, bedbug infestations could lead to mental diseases and have indirect impacts through a management mostly focused on insecticides. Their (mis)use can lead to severe exposition, increases environmental pollution and creates social inequalities. Costs associated leading also to a huge economic burden for public health services. A more sustainable alternative is thus needed to regulate *C. lectularius*. As many strict hematophagous insects, bedbugs depend on a nutritional symbiont (*Wolbachia*, strain *wCle*). Inhibiting its development could thus be an alternative method of control. Recently, Hoffmann et al. developed a molecule named Cmpd9 targeting the inhibition of *Wolbachia* LeuRS in nematodes. This molecule has been tested in vitro and in cellulo, but never in vivo.

The pilot experiment aim was thus to assess the inhibitory potential of Cmpd9 in bedbugs, and to assess the specificity of its action spectrum. We performed an in silico analysis to predict the affinity and efficiency of Cmpd9 against different *Wolbachia* strains. We then selected 3 strains (*wCle*, *wHa*, *wMelCS*) in 3 species (*C. lectularius*, *Drosophila simulans*, *D. melanogaster*, respectively). Insects were fed on diet (human blood or cornmeal) supplemented with Cmpd9. DNA was extracted to measure their relative *Wolbachia* density (qPCR). For the first time, we showed a significant inhibitory effect of Cmpd9 against *wCle* and *wHa*. As predicted, *wMelCS* was not inhibited, showing the specificity of Cmpd9 against particular LeuRS sequences.

Hence, Cmpd9 has the potential to control bedbugs, and associated to mechanical control methods, could represent a potential new pest-management reducing systemic resistance in bedbugs and exposition for human, animal, environmental health.

Vibrational cues in host location process in concealed host

Giorgia CARBONI MARRI (University of Perugia, Giorgia.carbonimarr@dottorandi.unipg.it)

Francesco CASTELLANI, Paolo MASINI, Silvana PIERSANTI, Manuela REBORA, Gianandrea SALERNO

Abstract

Vibrational communication through substrate-borne waves is widespread in insects, particularly in parasitoid species. Among them, species from several families (e.g., Braconidae, Eulophidae, Pteromalidae) use vibrational cues to locate concealed hosts. Here, we report evidence on the role of vibrational cues on the host location of tree Hymenoptera parasitoids, two Bethylidae and one Pteromalidae whose hosts live in concealed environments such as wood galleries and seeds. In particular, we focus on *Sclerodermus domesticus* and *S. cereicollis* (Bethylidae), primarily ectoparasitoids of Cerambycidae larvae and *Theocolax elegans* (Pteromalidae), a parasitoid of stored-product pests. In these parasitoids, visual cues play a limited role in host location, whereas chemical cues play a role in the host habitat location and the role of physical cues, such as vibrations, remains poorly investigated. In this study, the vibrations generated during feeding by larvae of *Hylotrupes bajulus* and *Trichoferus holosericeus* (Coleoptera: Cerambycidae) were used for *S. domesticus* and *S. cereicollis*, while for *T. elegans* we recorded the feeding vibrations generated by larvae of *Sitophilus zeamais* (Coleoptera: Curculionidae). Host vibrations were recorded using a laser vibrometer and delivered to the parasitoid for behavioural bioassays.

The objectives of this study are: i) to develop a tool useful to deliver to hosts such vibrations in order to test parasitoid behaviour ii) to characterize vibrational patterns produced by host species; and iii) to assess parasitoid responses to artificially generated vibrational cues. This work provides the first evidence that *Sclerodermus* spp. and *T. elegans* respond to vibrations generated by their hosts during feeding, highlighting the potential role of physical cues in host location within these parasitoid families.

Cricket stridulation: a biomimetic model for wear-resistant design?

Teddy GAIDDON (Institut de Systématique, Évolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle, Paris, France, Teddy.gaidon1@mnhn.fr)

Claire FRANÇOIS-MARTIN, Yan-Ming CHEN, Dominique GHIGLIONE, Tony ROBILLARD

Abstract

Tribological contacts account for approximately 23% of global energy consumption and generate considerable maintenance costs. While conventional approaches to reducing wear often reach their limits, biomimetics offers promising prospects for innovation. The acoustic communication structures of insects remain largely unexplored in tribology, despite their remarkable durability under strong mechanical constraints.

Male crickets produce their song by repeatedly rubbing specialised cuticular structures together: a rigid plectrum rubbing against a stridulatory file made of micrometric teeth. This system can undergo hundreds of millions of friction cycles during the insect's lifetime, through dry contact, without apparent lubrication and with a limited capacity to regenerate the cuticle. However, preliminary observations suggest limited wear and sustained acoustic function throughout adulthood.

Our objective is to elucidate the multi-scale mechanisms that enable this wear resistance and to transfer the identified principles in order to design more durable bio-inspired components. Our integrated comparative approach in several cricket species combines: (1) morpho-functional characterisation using electron microscopy, 3D profilometry and ultra-fast videography; (2) physico-chemical and mechanical mapping using spectroscopy and nanoindentation; (3) numerical modelling of plectrum-file contact using finite elements; and (4) biomimetic transfer through prototyping and tribological validation.

Preliminary results highlight a sublayered architecture of the cuticle forming the wing and stridulatory structures, which could suggest the existence of gradients in the mechanical properties of the material constituting the functional areas. Data from the scientific literature describe a specific mechanism of interaction between these structures, guiding our characterisation and modelling efforts.

This project bridges functional biology, tribology and biomimetics to explore an untapped category of biological systems. Targeted applications include electrical circuit breakers, lubrication-free valves and miniaturised cams. Beyond the specific results, this work demonstrates how the acoustic structures of insects inspire sustainable solutions to reduce friction and extend the service life of components in all industrial sectors.

#12000

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Insect Neural Mechanisms of Spatial Navigation For and Through Robotics

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Antoine WYSTRACH, Franck RUFFIER, Julien SERRES

Abstract

Desert ants achieve robust route following and homing using low-resolution panoramic memories acquired after minimal exposure. These memories are processed in the Mushroom Bodies (MB), yet classical navigation models assume exhaustive view matching, which is computationally inefficient and inconsistent with observed ant behavior.

Here, we extend recent lateralized opponent-process MB memory models, originally developed for nest-centric homing, to account for route-following. We introduce a dynamic route-segment hypothesis that updates a local goal via odometric feedback, allowing visual memories to be categorized as left- or right-biased relative to the current travel direction. Learning incorporates ant-like visual oscillations, while navigation relies on a simple, continuous control signal derived from opposing MB outputs, eliminating the need for global scanning.

To support bidirectional route use, two additional MB output neurons encode motivational state (foodward versus homeward) and route extremity recognition. Lyapunov stability analysis demonstrates convergence properties of the controller, and embodied experiments on multiple robotic platforms confirm robust route following, homing, and shuttling in indoor and outdoor environments. The model reproduces key ant behaviors, including reduced speed and emergent scanning in unfamiliar scenes.

This work provides a biologically grounded, computationally efficient neural model for insect route navigation, while demonstrating its applicability to autonomous robotics inspired by natural intelligence.

Structural hierarchy in beetle mandibles: a lesson in toughness

Caroline HOURIET (INRAE - BIA, Caroline.houriet@inrae.fr)

Abstract

Insect mandibles are essential for beetle defence and survival. Their internal microstructure—consisting of semi-crystalline fibrous chitin embedded in a protein–mineral matrix—is highly specialised. This architecture enables them to endure significant forces from multiple directions. Despite being used repeatedly throughout a beetle's life and lacking the ability to self-repair, these mandibles offer strong potential as models for bio-inspired shock-absorbing systems. The structure-function-property relationships within the beetle mandibles of *Odontolabis mouhotii* ssp. *elegans* were investigated. Bioinspired shock absorbers, mimicking key microstructural features, were 3D printed using liquid crystal polymers (LCPs).

Wide- and small-angle X-ray scattering (WAXS / SAXS respectively) simultaneously investigated the structure and compressive behaviour of chitin at the atomic and nanometre length scale. Crystalline regions were longitudinally orientated along the length of the mandible. Both SAXS and WAXS showed a reduction in d-spacing from the base to the tip. When compressed (~10% strain along the longitudinal axis), there was substantial densification at the molecular length scale.

Phase-contrast tomography at the ANATOMIX beamline (SOLEIL) was used to image the complex non-planar structure of the chitin fibres. The mandible structure transitioned from a highly dense exterior surface to a fibrous internal architecture. Chitin fibres (~10µm diameter) aligned along the mandible's longitudinal axis. These fibrils were arranged into circumferential layers with a Bouligand stacking sequence between layers.

Following initial tomography scanning, the mandible was fractured using liquid nitrogen. A subsequent re-scanning of the structure, revealed multiple toughening microstructural mechanisms, including crack bridging, twisting, and deflection. Scanning electron microscopy, of both a neat and fractured mandible, showed considerable fibre pull-out of the chitin fibres.

To replicate the hierarchical organisation of the chitin, LCPs were 3D printed using fused filament fabrication. These bioinspired structures enable the production of lightweight shock absorbers capable of resisting repetitive impacts.

Bio-inspired heading detection based on UV skylight polarization measurements

Matthias PACÉ (Aix Marseille Université, Université de Toulon, CNRS, ISM, IM2NP, Matthias.PACE@univ-amu.fr)

Achwak DBIRA, Macel PASQUINELLI, Badre KERZABI, Stéphane VIOLLET, David DUCHÉ, Julien SERRES

Abstract

Although one could consider biological evolution as the result of millions of years of serendipity, the sheer amount of success having passed the trial of environmental pressure should be carefully considered by many fields of human research. Material science is no exception and, in this study, we aim to detect the ultraviolet (UV) polarized light, and use it to guide an autonomous vehicle, taking example on the desert ants *Cataglyphis fortis*.

The ECOPOL project focused on measuring near UV polarized skylight. To achieve this, we selected zinc oxide (ZnO) as the UV reactive component. Beside the electro-optical quality of the material, the chemical elements are extremely abundant, which limits the ecological footprint and the economic cost of the sensor. The UV sensitive material is covered by a grid of interdigitated electrodes, which acts as both the electrical contacts and the polarization structure. While we are still trying to optimize the ZnO layer to shorten its dynamical response, the end goal is to realize an array of UV-sensitive polarized sensors, allowing for a real time observation of the sky polarization through a fast full Stokes polarization measurement.

So far, we built an UV sensor with a good static response but with a dynamic response has to be improved for the intended application. By optimizing the measurement, and deposition condition (temperature and annealing time, layer thickness) or the deposition method itself, we expect to decrease the response time by a factor hundred.

This measurement intend to give the real direction of the sun, even in case of no direct visual contact due to for example natural or artificial obstacles. Comparing this location with the theoretical position of the sun, thanks to a database, will allow a future autonomous vehicle to know its heading, greatly improving available data for real time localization.

Aerodynamic consequences of wing damage in dragonfly flapping flight

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Ramiro GODOY-DIANA, Thomas ENGELS

Abstract

Dragonflies primarily generate flight forces through flapping wings, which are inherently fragile and susceptible to damage. Such damage reduces wing area and alters the original wing planform, leading to diminished flight performance. Furthermore, as the flows around dragonfly forewings and hindwings interact, forewing damage also affects the aerodynamic performance of the ipsilateral hindwing. We generated a series of damaged wing models based on the probability maps reported by Rajabi et al. (2017). Using our open-source code WABBIT (Engels et al., 2021), we performed computational fluid dynamics (CFD) simulations to compare the effects of wing area loss on flapping flight aerodynamic performance and the associated flow fields, thereby analyzing the mechanisms of force alteration. Our comparative analysis reveals how different damage patterns modify vortex structures around the flapping wings, resulting in decreased aerodynamic force production. The causes of diminishing aerodynamic performance are shown to be more complex than simple area loss; they are driven by flow field changes induced by wing damage. Wing-wing interaction becomes especially significant when the forewing is damaged.

1. H. Rajabi, V. Schroeter, S. Eshghi, and S. N. Gorb, “The Probability of the Wing Damage in the Dragonfly *Sympetrum Vulgatum* (Anisoptera: Libellulidae): A Field Study”, *Biology Open*, bio.027078 (2017).
2. T. Engels, K. Schneider, J. Reiss, and M. Farge, “A Wavelet-Adaptive Method for Multiscale Simulation of Turbulent Flows in Flying Insects”, *Communications in Computational Physics* 30, 1118–1149 (2021).

#12251

Poster Session 1 - Ice breaker party
29/06/2026 at 16:00, Exhibition area

Biomimetic Nanofabrication of Photonic Crystals

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Abstract

Biomimetic Nanofabrication of Photonic Crystals

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Structural colors arise from constructive interference of light within periodic nanostructures whose characteristic dimensions are comparable to the wavelength of visible light. By contrast, conventional pigment-based colors result from wavelength-selective absorption of electromagnetic radiation at the molecular scale. These natural architectures combine high brightness with excellent temporal stability due to their purely structural origin. However, the physical and biological mechanisms underlying their formation remain largely unresolved. In particular, the self-organization of soft biological constituents into three-dimensional photonic networks with periodicities of several hundred nanometres is a fundamental question.

In structurally coloured insects, this self-assembly arises from different components: chitin, proteins and lipids. Our work suggests that lipids play a key role in this process by forming lyotropic liquid crystal mesophases. Building on this, we seek to establish a fully biomimetic framework built entirely from biomolecular components. We provide experimental evidence that lyotropic lipid systems can self-assemble into structures with relevant length scales, as demonstrated by X-ray scattering, dynamic light scattering and zeta potential measurements.

Moreover, cholesterol is shown to enhance membrane stability while not directly controlling photonic length scales. Interactions between lipids and cationic biopolymers induce vesicle aggregation and network formation, highlighting the role of electrostatic effects. Upon dehydration, biopolymers preserve their structural organization. However, further research is required to solidify the network more slowly to avoid the formation of structural defects that cause incoherent scattering. These results demonstrate that lipidic liquid crystals and biopolymers play an active role in the formation of natural photonic structures and open the way toward the complete laboratory reconstruction of structural colours.

#10928

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

The structure-function relationships of insect cuticle in scales

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Abstract

How complex traits such as animal coloration and patterning evolve and function is a fundamental question in biology. Animal coloration functions in several different contexts, e.g., intra-specific recognition, mate choice, camouflage, aposematic signal, and thermoregulation. Many lepidopteran species serve as exemplary model systems in biology due to their simplicity and elegance and because of this, they are also increasingly being investigated by physicists and engineers in order to biomimetically inspire new devices and technology. However, these studies are predominantly done on a few charismatic species to date without any comparative evolutionary or ecological contexts. Moreover, we currently do not understand how organisms regulate the composition, deposition and functional properties of biological materials over space and time. Specifically, we do not know the precise materials composition of the insect cuticle that is deposited in scales. Here, we propose to take a comparative, materi-omic approach to understand the structure-function relations of the cuticle during hierarchical butterfly scale development.

#11340

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Fluorescence lights up: insect passion unfurled

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Vasily ANIKIN

Abstract

Insects represent the most diverse and unique group of animals. They have evolved various types of coloration to survive under harsh conditions, such as predation pressure, utilizing it for camouflage and mimicry, as well as in mating behavior. As of today, insects have been investigated meticulously under white light conditions; however, few have observed morphological details of specific species in the blue (Ex: 436 nm / Em: 480 nm), green (Ex: 470 nm / Em: 525 nm), yellow (Ex: 500 nm / Em: 535 nm), and red (Ex: 560 nm / Em: 645 nm) parts of the spectrum. Here, we examined three Hymenoptera families — Eurytomidae, Eupelmidae, and Cynipidae — under these four different light conditions. We found that certain body parts involved in mating rituals, specifically the wings, eyes, and legs, exhibit fluorescence under blue, green, and red light, with the intensity being highest under blue light. Moreover, we documented rare mating behaviors in various species, which differed significantly depending on the group, and correlated these behaviors with the fluorescent body parts. As a result, we found that blue fluorescence of specific body parts may act in species-specific signaling, potentially serving as robust phenotypic markers for differentiating closely related species. Our results suggest that fluorescence microscopy should be integrated into standard taxonomic protocols. These insights underscore the critical importance of investigating entomological models beyond the visible spectrum to uncover hidden mechanisms of evolution, and natural selection.

Control of mealybugs and ant-management: implementation of sugar-providing dispensers in Northern Italy vineyards

Giovanni BURGIO (Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, Giovanni.burgio@unibo.it)

Serena MAGAGNOLI, Antonio MASETTI, Luca CASOLI, Marco PROFETA, Daniele GIANNETTI, Donato Antonio GRASSO

Abstract

Several factors affect mealybug infestations in vineyard, including ants (Daane et al., 2012; Schifani et al., 2024). Many ant species have developed a mutualistic relationship (trophobiosis) with mealybugs, that can be harmful because these social Hymenoptera can facilitate infestations and protect the pests from naturale enemies. A number of management practices have been recently developed to manipulate ant-mealybug associations, including provision of sugar through dispenser-feeders (or artificial nectaries) (Daane et al., 2008; Beltrà et al., 2017; Perez-Rodriguez et al., 2021; Schifani et al., 2024)

An area-wide augmentative biological control program against vineyard mealybugs (Burgio et al., 2025) was conducted in a Lambrusco vineyard cultivation area in the Emilia-Romagna region (Northern Italy), releasing the parasitoid *Anagyrus vladimiri* (Girault) and the predator *Cryptolaemus montrouzieri* (Mulsant) (Burgio et al., 2025). Sugar dispensers were tested at two density (120/ha and 80/ha) in pilot farms involved in the project, as ant-management tools.

Sugar dispenser significantly increased the density of the predator *C.mountrouzieri*; mealybug parasitism was in general high and only partially affected by sugar dispensers (Parrilli et al, 2021; Burgio et al., 2025). The highest sugar dispenser density resulted in greater effectiveness in reducing mealybug infestation, but also the lower density decreased infestations in comparison with the control.

Higher mealybug infestations were recorded in vineyards with the presence of *Lasius paralienus* F., that together *Tetramorium immigrans* Santschi, resulted the dominant ant species.

These validation in commercial vineyards of Emilia-Romagna region demonstrated that an ant management should be implemented for an integrated control of mealybugs. Currently, specific sugar dispensers for ant distraction are not on the market in Italy, but sugar provision could be obtained by slight modification of “trap baits” for ants. Finding a practical solution for field use would improve mealybug control.

#10896

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Evaluation of Adhesive Traps for *Vespa mandarinia* Control: Effects of Presence, Vital Status, and Colony Specificity on Attraction and Non-Target Impact

Moon Bo CHOI (Kyungpook National University, Kosinchoi@hanmail.net)

Kim JAEHEE

Abstract

Vespa mandarinia, the world's largest hornet, poses significant threats to human safety and apiculture due to its aggressive behavior and potent venom. Its collective predation strategy allows for rapid decimation of honeybee colonies, causing severe economic losses. In Korea, adhesive traps are increasingly used in apiaries for control, though their effectiveness remains largely unverified. This study assessed trap efficiency based on hornet presence, vital status, colony origin, and trap location. Live hornets significantly increased capture rates, while dead hornets had minimal effect. Colony-specific attraction was observed, whereas intercolony attraction was negligible. No hornets were captured in forested areas, suggesting reliance on colony pheromones. However, only 9.79% of trapped insects were *V. mandarinia*, indicating high non-target capture. These findings highlight the benefits and limitations of adhesive traps, informing more effective control strategies for *V. mandarinia* management.

Adaptation of native natural enemies to emerging alien pest insects: new associations and assessment for biocontrol.

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Elena GONELLA, Alberto ALMA

Abstract

The widespread use of pesticides is leading to several undesirable effects on human health, environment and agroecosystems sustainability. Therefore, it is ever more necessary to employ sustainable pest control strategies. Biological control is an established method for controlling pest populations through the release of parasitoids and natural enemies into the field. This can permit to maintain invasive species under a certain threshold level. In Italy the invasive planthopper *Ricania speculum* (Walker) has been recently introduced from Asia. For this pest, few natural enemies have been recorded to date. Recently, a possible new association with the parasitoids *Aprostocetus* (*Ootetrastichus*) *crino* (Walker) and *Chaetostricha similis* (Silvestri) was suggested in Italy. This study investigates the associations between *R. speculum* and potential parasitoids in northwestern Italy, aiming to extend knowledge on the newly-established biocoenosis. *Ricania speculum* egg clusters were collected from different plant species and different localities. The samples were maintained under laboratory conditions, in order to obtain potential parasitoids emerging from eggs, and emerged parasitoids were taxonomically identified. Out of 11,075 eggs collected, 18 parasitoids emerged. These parasitoids were reconduted to Trichogrammatidae family. Future studies are needed to further investigate this new association, as well as its potential role in limiting the spread of *R. speculum* in Italy.

Impact of flowering species on performance and parasitism rates of egg parasitoids against *Halyomorpha halys*

Martina FALAGIARDA (Laimburg Research Centre, Martina.falagiarda@laimburg.it)

Sara BORTOLINI, Francesco TORTORICI, Angelika GRUBER, Luciana TAVELLA

Abstract

Flower strips are recognized as important agroecological tools for improving the natural control of harmful arthropods by promoting beneficial insects. This study evaluated the influence of selected floral species on the survival and parasitism rates of three egg parasitoid species against the brown marmorated stink bug, *Halyomorpha halys*. The parasitoid species *Trissolcus japonicus*, *T. mitsukurii*, and *Anastatus bifasciatus* were exposed to 15 floral resources, including eight species commonly found in commercial seed mixtures (buckwheat, mallow, dill, flax, phacelia, calendula, red clover, and serradella) and seven species of regional wildflowers growing in alpine meadows (e.g., bladder campion, brown knapweed, and field violet). The survival of the parasitoids and their ability to parasitize were assessed under controlled laboratory conditions, with honey as positive control and water as negative control. The results demonstrated different responses to floral resources among the three parasitoid species. Kaplan-Meier survival analysis revealed that some treatments, particularly buckwheat, mallow, dill, and brown knapweed, significantly prolonged the longevity of parasitoids compared to both controls. Parasitism rates varied significantly between treatments, with differential outcomes between species. *Trissolcus japonicus* showed significant treatment and temporal effects on parasitism success, while *T. mitsukurii* maintained consistent parasitism regardless of nutritional resources. *Anastatus bifasciatus* showed the highest sensitivity to different floral resources, with brown knapweed significantly increasing parasitism rates compared to the other treatments tested. These results highlight the potential of targeted management of flower strips to optimize the performance of parasitoids in integrated pest management strategies, with brown knapweed emerging as a particularly promising floral resource.

First European record of the Nearctic hyperparasitoid *Cheiloneurus swezeyi* and impacts on *Neodryinus typhlocybae* populations

Marco FALASCO (Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Legnaro, Italy, Marco.falasco@phd.unipd.it)

Fernanda COLOMBARI, Isabel MARTINEZ-SAÑUDO, Emilio GUERRIERI, Laura MARETTO, Alberto POZZEBON, Luca MAZZON

Abstract

The introduction of the Nearctic parasitoid *Neodryinus typhlocybae* (Hymenoptera: Dryinidae) in Europe has been considered a successful example of biological control against the invasive pest *Metcalfa pruinosa* (Hemiptera: Flatidae). Recent reports of increasing *M. pruinosa* populations prompted research to assess biotic factors that may interfere with the activity of the introduced parasitoid. Among these, hyperparasitoids represent a critical yet unexplored component of this system.

In a three-year study, 5,993 cocoons of *N. typhlocybae* were sampled from 28 semi-natural sites in northeastern Italy. Cocoon fate, hyperparasitoid assemblage, emergence patterns, and the influence of vegetation structure on hyperparasitism were examined. Hyperparasitoids were characterized by an integrative approach combining morphological characters and mitochondrial cytochrome c oxidase subunit I (COI) sequencing.

Results showed that adult *N. typhlocybae* emerged from only about 15% of the cocoons, while 31% yielded hyperparasitoids. The Nearctic hyperparasitoid *Cheiloneurus swezeyi* (Hymenoptera: Encyrtidae) was detected for the first time in Europe. This species is known as the primary antagonist of *N. typhlocybae* in its native range. *C. swezeyi* and the native *Pachyneuron muscarum* (Hymenoptera: Pteromalidae) represented the two hyperparasitoids with the greatest impact on the emergence of the primary parasitoid. Multiple individuals of *C. swezeyi* frequently emerged from single cocoons, with an average exceeding five individuals per host. Hyperparasitism by *C. swezeyi* was high in the lower vegetation layer (<0.5 m above ground), a pattern consistent with the high proportion of wingless females and their limited dispersal ability. Molecular analyses revealed six different COI haplotypes of *C. swezeyi*.

These findings indicate that *C. swezeyi* represents an emerging component of the *M. pruinosa*–*N. typhlocybae* system, potentially reducing the efficacy of the biological control program. Continued monitoring of hyperparasitoids is therefore essential to define the distribution of *C. swezeyi* across Europe and to assess the long-term success of biological control programs.

Assessing the potential of methyl salicylate for enhancing parasitoid attraction in Mediterranean vineyards

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María Elena MARTÍNEZ-VILLAR, Luis Rubén ROMÁN-FERNÁNDEZ, Sergio IBÁÑEZ-PASCUAL, Ignacio PÉREZ-MORENO, Ainara CRESPO-SUSPERREGUI, Saioa LEGARREA

Abstract

Herbivore-induced plant volatiles (HIPVs) play a key role in tritrophic interactions among plants, herbivores, and natural enemies. These compounds are mainly released in response to mechanical damage caused by phytophagous insects and can act as attractants for natural enemies. Methyl salicylate (MeSA), a representative HIPV, shows considerable potential as an attractant for these organisms. The aim of this study was to evaluate the effect of MeSA on several parasitoid families in Mediterranean vineyards. Field trials were conducted over four consecutive years (2022–2025) in two vineyards located in Logroño and Ausejo (La Rioja, Spain), using a randomized block design with one factor and two treatments: presence or absence of MeSA dispensers. Eight replicates per treatment were established, and on three sampling dates (May, July, and September), two yellow sticky chromotropic traps per replicate were deployed and removed after 11 days. Captured parasitoids were identified to the family level. The families studied were Aphelinidae, Braconidae, Ceraphronidae, Encyrtidae, Eulophidae, Mymaridae, and Scelionidae. For each family and for total Hymenoptera Parasitica, and for each location and year, data on total captures per replicate were analyzed using Student's t-test for independent samples, after applying Fisher's F-test to assess homoscedasticity. In Logroño across all four years and in Ausejo during 2022 and 2023, a trend toward higher captures in the presence of MeSA was observed, although differences were statistically significant only in a few cases. Conversely, the opposite trend was found in Ausejo in 2024 and 2025, but no significant differences were detected. Further research is needed to clarify the potential role of MeSA as an effective agent for attracting parasitoids.

Experimental evaluation of host specificity of the generalist parasitoid *Pachycrepoideus vindemmiae* (Rondani, 1875)

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Marc F. SCHETELIG, Annette HERZ

Abstract

Two native parasitoid species are currently available for the biological control of *Drosophila suzukii* (Matsumura, 1931) (Diptera: Drosophilidae) in Germany. One of them is the cosmopolitan pupal parasitoid *Pachycrepoideus vindemmiae* (Rondani, 1875) (Hymenoptera: Pteromalidae), which has been recorded from hosts belonging to at least 14 Diptera families, including hoverflies (Syrphidae). If these findings were to represent the realized host range, augmentative releases might bear the risk for unwanted non-target effects and may suffer from low efficacy on the target host.

To improve the understanding of the host range of a population which had been established from *Drosophila* collections, we selected eight species from seven Diptera families. In no-choice parasitism tests with single naïve *P. vindemmiae* females, six species from five Diptera families were parasitized at least once. As the next step, parasitism was determined on pupae of these species in comparison to *D. suzukii* pupae in a choice situation. The first hour was filmed for behavioural analysis, followed by another 23 h of incubation. Under choice conditions, *P. vindemmiae* parasitized *Ophyra aenescens* (Wiedemann, 1830) (Muscidae), *Sphaerophoria rueppellii* (Wiedemann, 1830) (Syrphidae), and *Lucilia sericata* (Meigen, 1826) (Calliphoridae) in 40%, 30%, and 6.7% of observations (each N=30), respectively. No offspring developed from the remaining three non-target species. Both shown in observed behaviour and parasitism, *D. suzukii* pupae were preferred in comparison to all tested non-target species.

This suggests that this strain may have a preference for Drosophilidae, and thus be suitable for the biological control of *D. suzukii*. Since habitat structure and temporal overlap further decrease the number of potentially affected non-target species in the targeted release conditions (mainly net-protected berry crops), non-target effects are expected to be limited and transient.

Optimizing male mating protocols to support half-sib selection in the predatory mirid *Macrolophus pygmaeus*

María del Carmen RECHE GUILLERMO (Universidad Politécnica de Cartagena, Mariadelcarmen.reche@edu.upct.es)

Carolina GRÁVALOS, Amador RODRÍGUEZ GÓMEZ, Virginia BALANZA, Ana Belén ABELAIRA, Pablo BIELZA

Abstract

Augmentative biological control and selective breeding of natural enemies require reliable reproduction under mass-rearing conditions. In mirid predators, limited knowledge of male mating capacity can restrict the use of family-based selection methods such as half-sib selection, which require each male to fertilize multiple females producing enough offspring for line maintenance and evaluation.

We tested a practical mating protocol for the omnivorous predator *Macrolophus pygmaeus* to maximize the number of females functionally fertilized by a single male. Males underwent two consecutive 24-hour mating periods. In the first, they were exposed to either 4 or 7 virgin females. In the second, all males were presented with 7 new virgin females after a resting period of 0, 24, or 48 hours. Mating success was measured by offspring production, considering matings functionally successful when they produced more than 20 first-instar nymphs (N1), a threshold relevant for maintaining selection lines.

During the first period, males exposed to 7 females achieved more total and more functionally successful matings than those exposed to 4 females. While offspring per mating did not differ between treatments, successful matings in the 7-female group produced more offspring on average. In the second period, resting time strongly affected male performance. Males transferred immediately to new females showed the lowest mating activity and fewest successful fertilizations. In contrast, males given 24 or 48 hours of rest achieved significantly more matings and about twice as many functionally successful fertilizations. The number of females encountered in the first period did not influence performance in the second.

Male mating capacity in *M. pygmaeus* depends on female encounter rate and recovery time. For applied programs, exposing males to 7 females for 24 hours, followed by at least 24 hours of rest and a second 24-hour exposure to 7 new females, maximizes productive crosses and supports efficient half-sib selection.

Insecticide resistance in the invasive *Spodoptera frugiperda* and the native *Spodoptera littoralis* in Greece

Emmanouil RODITAKIS (Hellenic Mediterranean University, Department of Agriculture, Crete, Greece, Eroditakis@hmu.gr)

MARIANNA STAVRAKAKI, Nikolaos VAMVOUKLIS, Dimitrios ADAMAKIS, Kiriakos ADAMAKIS

Abstract

The fall armyworm *Spodoptera frugiperda* and the Egyptian cotton leafworm *Spodoptera littoralis* are highly polyphagous pests causing significant agricultural losses. *Spodoptera frugiperda* is a recently introduced invasive pest in Greece (first recorded in 2023), primarily affecting maize, while *S. littoralis* damages crops including alfalfa and potato. Intensive insecticide use has led to resistance, threatening effective control. This study compared field populations of both species to insecticides with different modes of action: spinosyns, avermectins, tebufenozide, diamides, and pyrethroids. Populations were collected in November 2023 from maize (*S. frugiperda*) and vetch (*S. littoralis*) in Crete. Susceptibility was assessed through laboratory bioassays following a modified IRAC Method 020, and resistance ratios (RRs) were estimated relative to laboratory susceptible strains. Resistance levels were generally low for most insecticide classes. In *S. frugiperda*, RRs were mostly <2-fold for diamides and emamectin benzoate, while moderate resistance was detected to abamectin (12-fold). In *S. littoralis*, resistance to the same groups was also low (<10-fold), although a notably higher RR (176-fold) was recorded for cyantraniliprole. In the spinosyn group, both species remained fully susceptible to spinetoram (RR: 1). However, a clear interspecific difference was observed for spinosad: resistance was moderate in *S. littoralis* (RR: 20-fold) but high in *S. frugiperda* (RR: 85-fold). Pyrethroid resistance was extreme in both species. In *S. frugiperda*, RRs ranged from 36- to 490-fold, while in *S. littoralis* they were substantially higher, reaching up to 6,000-fold. Overall, the invasive *S. frugiperda* population in Greece has not yet developed widespread resistance to most insecticide classes, with main concerns being spinosad and pyrethroids. In contrast, *S. littoralis* exhibits broader and much higher resistance levels, particularly to pyrethroids and selected other compounds, making it the more critical species for resistance management. These results provide important baseline data to support effective insecticide resistance management strategies in Greek agroecosystems.

#14101

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Thrips reduction in production systems

Joes TEN THIJ (Leiden University, J.ten.thij@biology.leidenuniv.nl)

Abstract

Pest control is a key ecosystem service provided by insect predators and parasitoids, yet agricultural fields often fail to support these natural enemies due to pesticide use and the limited availability of alternative food sources and shelter present in monocultures. Recently, leek growers in the Netherlands have introduced the flowering plant *Lobularia maritima* as a banker plant, in combination with releasing the predatory bug *Orius majusculus* to suppress *Thrips tabaci*, the main insect pest in leek cultivation. We examined whether this natural-enemy system can provide an alternative for pest control with pesticides. During a two-year field survey we found that crop cultivation with the natural enemy-system is as effective in reducing thrips abundance and feeding damage as chemical pesticides. To study the system in more detail, we conducted a field experiment that compares the introduction of the banker plants with and without the release of *Orius* on thrips suppression to that obtained with the application of pesticides, or no pest control measures. We demonstrate that the introduction of banker plants and natural enemy release in the field is as effective as pesticide application for suppression of *Thrips tabaci*. Moreover, the presence of *Lobularia* enhances natural enemy abundance in the leek, which emphasizes the benefits of using *Lobularia* as a banker plant. Next to that, we showed that *Orius majusculus* disperses over 150 meters and can establish a population in the leek. Together, these findings provide compelling evidence that increasing functional biodiversity in crop fields stimulates ecosystem services like as pest control and therefore provides a sustainable alternative to chemical pest control.

Evaluating Insecticide Seed Treatments for Compatibility with the Earwig Predator *Euborellia annulipes* and Pest Control

Jorge TORRES (Universidade Federal Rural de Pernambuco, Jorge.torres@ufrpe.br)

Maria Vitória Guerra LIMA, Christian Sherley Araújo SILVA-TORRES

Abstract

Beneficial ground-dwelling predators, such as the ring-legged earwig *Euborellia annulipes* (Dermaptera: Anisolabididae), play important roles in agroecosystems, including biological pest control. However, insecticides used in seed treatments (ST) may compromise earwig survival in soil and reduce their biological control services. This study evaluated the survival of *E. annulipes* under two experimental conditions: (i) microcosms containing plants grown from insecticide-treated seeds, and (ii) Petri dish assays in which earwigs were directly exposed to moistened paper enclosing treated seeds. Seed treatments containing cyantraniliprole, chlorantraniliprole, thiamethoxam, abamectin, clothianidin, and fipronil were tested in corn, soybean, and cotton. In addition, we assessed the mortality of fall armyworm (*Spodoptera frugiperda*) neonates confined to corn seedlings grown from ST, both alone and in combination with earwigs. After 8 days in microcosms, insecticide ST supported high earwig survival (approximately 85–100%) across cotton, corn, and soybean, except for deltamethrin-treated corn, where survival decreased to 80%. In contrast, direct exposure to treated seeds resulted in substantially lower survival: 10%, 25%, and 60% for fipronil, thiamethoxam, and cyantraniliprole on cotton seeds; 50%, 45%, 40%, 32%, and 0% for thiamethoxam, deltamethrin, chlorantraniliprole, cyantraniliprole, and clothianidin on corn seeds; and 10% for both thiamethoxam and cyantraniliprole on soybean seeds. Fall armyworm mortality on corn ST plants treated with deltamethrin, clothianidin, chlorantraniliprole, and cyantraniliprole ranged from 32% to 100%. Overall, seed treatment in microcosms reduced insecticide exposure relative to direct contact, though effects varied among seed species and insecticides. Neonicotinoids were highly harmful to earwigs, whereas corn seed treatments containing deltamethrin and the two diamides were effective against fall armyworm while being comparatively less toxic to *E. annulipes*.

#12296

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Biodiversity strips around greenhouses to enhance natural enemies of greenhouse pests

Kyra VERVOORN (Business Unit Greenhouse Horticulture & Flower Bulbs, Wageningen University & Research, PO Box 20, 2665 ZG Bleiswijk, The Netherlands, Kyra.vervoorn@wur.nl)

Marcel HEIJKOOP, Nathan KOEDIJK, Gerben MESSELINK

Abstract

Biodiversity strips around greenhouses to enhance natural enemies of greenhouse pests

Kyra Vervoorn, Marcel Heijkoop, Nathan Koedijk, Gerben Messelink

At the end of 2024, we established flower strips next to the greenhouses of twenty Dutch companies to enhance biodiversity and attract natural enemies of crop pests. The aim is to provide growers with practical guidance on adapting biodiversity strategies specific to their crops and pest pressures, boosting natural enemies while minimizing potential pest risks. We are testing two flower mixtures composed of annual, biennial, and perennial plants across a range of crops, including tomato, pepper, chrysanthemum, gerbera, cymbidium, lily, potted plants, and strawberry. One mixture is optimized to target predators such as lacewings, hoverflies, and ladybeetles to support aphid control, while the other avoids plants attractive to thrips to reduce pest risks. Young trees were also planted to provide nectar in early spring, and to host aphids not found on greenhouse crops, providing alternative prey and further supporting natural enemies with minimal risk. Each strip is compared to a control plot of short-cut grass. Our ongoing research evaluates how flower strip composition influences natural enemy abundance both outside and inside the greenhouse. We also monitor potential risks, including increased pest pressure and virus transmission.

Herbivore-induced plant volatiles influence electroantennogram and behavioural responses of larval parasitoid

Sanjana AKTER (Macquarie University, Sanjana.akter@students.mq.edu.au)

Abstract

The exotic serpentine leafminer (SLM), a highly polyphagous pest that has recently established in Australia poses a significant threat to horticulture industry. Resistance of SLM to various conventional insecticides overseas prompts the urgent need for sustainable management strategies especially in protected cultures. This study explores the potential of herbivore-induced plant volatiles (HIPVs) to enhance natural enemy populations in the field by mediating interactions between host plants and parasitoids. Headspace volatiles were collected from SLM infested, mechanically damaged, and intact celery plants. The chemical profiles of these volatiles were analyzed using gas chromatography-mass spectrometry (GC-MS). Antennal responses of the larval parasitoid, *Neochrysocharis formosa*, to these compounds were assessed by using gas chromatography electro-antennographic detection (GC-EAD). Behavioural responses of the parasitoids were further tested using a Y-tube olfactometer and semi-field trials. Infestation by SLM females and mechanical damaged induced both qualitative and quantitative changes in the volatiles emitted by celery plants. In total, 28 compounds were identified from the celery plants, with five compounds being isolated exclusively from herbivore-induced celery plants. The antennae of *N. formosa* responded to several of these induced volatiles in GC-EAD analyses. In behavioural assays, female parasitoids showed a preference for odours emitted by herbivore-induced plants compared to controls. These findings support the potential use of host plant induced volatiles in enhancing biological control, either by selecting plant varieties that effectively emit attractive volatiles or by manipulating parasitoid foraging behaviour through targeted semiochemical applications.

Comparative characterization of peach fruit deformation induced by *Halyomorpha halys* (Hemiptera: Pentatomidae) and deformative eriophyid mites

Stefanos ANDREADIS (Institute of Plant Breeding and Genetic Resources, Hellenic Agricultural Organization - Dimitra, 57001 Thermi, Greece, Sandreadis@elgo.gr)

Nikoletta STOIKOU, Apostolos KAPRANAS

Abstract

In recent years, peach cultivation in Greece has been facing serious challenges due to severe fruit deformation caused by unknown vectors. The aim of the present study was to investigate both the qualitative and quantitative impacts on peach fruit production caused by infestation of *Halyomorpha halys* (Hemiptera: Pentatomidae), as well as by emerging threats such as deformative mites of the family Eriophyidae. Moreover, we aimed to identify potential differences in deformation characteristics caused by the aforementioned pests. For this purpose, two peach orchards with different levels of fruit deformation (high vs. low incidence) recorded in previous years were selected and controlled infestations by adults *H. halys* were applied during four phenological stages: pink bud, full bloom, petal fall and young developing fruit set. Five shoots per tree, each bearing 10 buds, were selected and four *H. halys* adults were enclosed on each shoot using mesh cages for a period of two weeks. Subsequently, a qualitative assessment of the fruits was conducted to evaluate the degree of deformation caused by *H. halys*, while total fruit drop was also recorded. Furthermore, peach shoot samples were collected from both orchards at the same time points as the placement of *H. halys*, to determine the presence or absence of deformative mites. According to our results infestation by *H. halys* had a marked negative effect on fruit quality, especially at the pink bud stage due to typical cat facing symptoms. Fruit drop was higher at the pink bud and full bloom stages compared to control. On the other hand, eriophyid mites were only detected in shoots from the orchard with previous high incidence, with the highest infestation rate recorded at full bloom. Notably, up to 100% fruit drop was observed at full bloom, highlighting a strong combined effect of *H. halys* and eriophyid mites infestation

Resolving Intra-Guild Interactions in the Parasitoid Community of the Olive Psyllid pest, *Euphyllura olivina*

Marie-Claude BON (European Biological Control Laboratory-USDA-ARS, Mcbon@ars-ebcl.org)

Valentin CHAMBEFORT, Marie ROCHE, Fatiha GUERMACHE, Javid KASHEFI, Gaylord DESURMONT, Chris BORKENT, Viola POPESCU

Abstract

The evolution of facultative hyperparasitism remains poorly understood, yet it may represent a critical transitional step from primary parasitism to obligatory hyperparasitism. Unraveling this process is important both for ecological theory and for improving biological control, as interactions between primary parasitoids and their hyperparasitoids can strongly influence control success. Recent models suggest that extended development times of the primary parasitoids may facilitate the persistence and coexistence of facultative hyperparasitoids, but potentially at the cost of primary parasitoid extinction. Because facultative hyperparasitism is often underestimated when assessed through traditional rearing or host dissections, molecular tools offer a powerful alternative for resolving trophic relationships with greater accuracy. We investigated intra-guild interactions within the parasitoid community associated with the Mediterranean olive psyllid *Euphyllura olivina* (Hemiptera: Liviidae). Across five sites in southern France (2023–2024), we collected alive psyllid mummies of which 201 were analyzed using molecular assays, with congruent rearing. We developed multiplex PCR assays to monitor the detection of four key guild members: the encyrtids *Psyllaephagus euphyllurae* and *P. pulchellus*, the figitid *Apocharips trapezoides*, and the pteromalid *Pachyneuron muscarum*. Both methods revealed similarly low prevalence of *P. pulchellus* and *P. muscarum*, but they differed for the two dominant species. Molecular outcomes showed that the primary parasitoid *P. euphyllurae* was the most prevalent species, whereas rearing results suggested a predominance of *A. trapezoides*. Strikingly, *A. trapezoides*, previously considered a facultative hyperparasitoid, was detected molecularly exclusively in mummies containing *P. euphyllurae*, indicating that it functions as an obligatory hyperparasitoid at our study sites. Compared with rearing-based assessments, molecular analysis provided a complete and more nuanced picture of intra-guild relationships, revealing linkages that were previously uncertain. We discussed the implications of this refined trophic understanding for proactive classical biological control of *E. olivina* in California, particularly in the context of future releases of *P. euphyllurae*.

Host-parasitoid interaction: molecular characterization and biological role of unhatched parasitic wasps in stink bug egg masses

Alessandro BORSOTTI (Faculty of Agricultural, Environmental and Food Sciences, Free University of Bozen-Bolzano, Italy; Institute for Plant Protection, Research Centre Laimburg, Italy, Alessandro.borsotti@student.unibz.it)

Sara BORTOLINI, Martina FALAGIARDA, Manfred WOLF, Hannes SCHULER

Abstract

The brown marmorated stink bug, *Halyomorpha halys* (Hemiptera: Pentatomidae) is a highly polyphagous invasive species causing severe damage to crops and agriculture worldwide. Traditional control strategies have proven largely ineffective, leading in Italy to the implementation of a national campaign for the release of the allochthonous parasitoid wasp *Trissolcus japonicus* (Hymenoptera: Scelionidae), the main egg parasitoid of *H. halys* in its native range. However, the release of this wasp has also created the need for long-term monitoring to assess its impact on native and invasive stink bug species, as well as its competitive interactions with other parasitoid wasps. A phenomenon potentially affecting the establishment of *T. japonicus* is the frequent observation of unhatched stink bug egg masses in the field, from which neither the host nor the parasitoid successfully emerge. This phenomenon, previously described as “egg abortion” or an “evolutionary trap”, may be associated with unsuccessful parasitisation attempts or multiparasitism involving parasitoid species that are unable to complete their development due to a lack of shared evolutionary history with this new host. To elucidate the trophic network between stink bug hosts and their parasitoids, here we present the development of a highly sensitive ddPCR assay, with the design of species-specific primers and probes for eight native and invasive parasitoid wasp species. This approach allows the detection of single or multiple parasitoids presence in unhatched eggs belonging to two invasive and one native Pentatomidae species. The results are expected to reveal previously unknown trophic relationships and shifting ecological dynamics, providing valuable data for agroecosystem management and optimisation of a biological control strategy.

The role of aphid protective symbionts in mediating interactions between rhizobacteria, plants, aphids and parasitoids in the field

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Sharon ZYTYNSKA, Daniel LEYBOURNE, Greg HURST, Julia FERRARI, Helen HESKETH

Abstract

Aphid pests are increasingly managed via top-down biological control, such as parasitoid wasps. Yet, aphids host facultative bacterial endosymbionts that protect against natural enemies, potentially reducing biocontrol success. A complementary strategy involves rhizobacteria inoculation of plant roots, offering bottom-up plant protection by enhancing chemical defences that reduce aphid population growth. The interplay between aphid facultative symbionts, parasitoids and rhizobacteria inoculation remains poorly understood. In a field trial, we examined symbiont and parasitoid prevalence for aphids collected from three barley (*Hordeum vulgare*) cultivars inoculated with rhizobacteria species, *Acidovorax radialis* or *Bacillus subtilis* versus controls. Aphid symbiont *Fukatsuia symbiotica* varied with rhizobacteria–cultivar combinations, suggesting a role in aphid adaptation. Parasitoids species shifted seasonally, with *Aphidius avenae* prevalence varying across rhizobacteria treatments, possibly reflecting changes in plant and/or aphid quality. Our work highlights how aphid symbionts mediate community-wide multitrophic interactions, and must be considered in biocontrol strategies.

Mechanisms and consequences of Microbial-Induced Resistance on trophic interactions and biocontrol efficacy

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Martin ARVID NIHLMAR, Nicolai VITT MEYLING, Paul BECHER

Abstract

Root-colonizing beneficial fungi can establish mutualistic interactions with plants, promoting their growth and triggering microbial-induced resistance (MIR). This mechanism enhances plant defence against various stress agent, including insect herbivores, offering a promising strategy for sustainable pest management in agricultural and horticultural systems. However, while the short-term effectiveness of MIR against insect pests is well documented, the longer-term effects are not elucidated. Repeated exposures across insect generations may induce broader ecological consequences on insect population dynamics. Similarly, the potential consequences of MIR on higher trophic levels, such as populations of natural enemies of pests, including predators and parasitoids, have received little attention. Together, these mechanisms may shape multitrophic interactions and ultimately affect the success of biological control strategies. To address these knowledge gaps, sweet pepper plants (*Capsicum annuum*) will be inoculated with *Metarhizium robertsii* KVL12-35 or *Trichoderma harzianum* T22 and subsequently infested with the potato aphid, *Macrosiphum euphorbiae*, or the green peach aphid, *Myzus persicae*. First, aphid lines will be monitored across generations of exposure to MIR to assess effects on reproduction and thus population dynamics. Further, volatile organic compounds (VOCs) profiles and behavioural assays will evaluate the attraction and the trans-generational exposures effects to MIR for aphid natural enemy efficacy. For this, the parasitoid *Aphidius ervi* and the hoverfly *Eupeodes corollae* will be investigated. The expected findings will provide key knowledge of the underlying mechanisms of this intricate plant-microbe-insect interaction and establish a foundation for predicting how beneficial microorganisms can be implemented in future sustainable crop production systems and in integrated pest management strategies.

Impacts of artificial light at night on predatory invertebrate community composition and nutritional networks

Mia CROFT (Newcastle University, M.croft2@newcastle.ac.uk)

Katherine BALDOCK, Darren EVANS, Jordan CUFF

Abstract

Artificial light at night is an increasingly pervasive global pressure, rapidly expanding in extent, brightness and spectral range, and has been suggested as a significant and overlooked driver of recent dramatic declines in insect biomass and diversity. There is mounting evidence for the effects of artificial light at night on plant nutrient content and animal foraging behaviour, with cascading impacts across trophic levels. However, few studies have investigated the role of light pollution in driving changes in ecological network structure via altered nutritional dynamics.

This study explores how invertebrate communities respond to a novel source of artificial light through a replicated field experiment at a research farm. Solar-powered floodlights were installed in arable field margins and hedgerows, with invertebrate sampling using pitfall and vane traps ongoing. We present preliminary data on the response of predatory arthropods (spiders and carabid beetles) to the introduction of novel lighting. We anticipate that predatory invertebrate species will respond asynchronously to light pollution, driven by differences in nutritional requirements and resource availability.

To investigate impacts at the ecosystem level, we will analyse ecological networks informed by two key methods: dietary DNA metabarcoding and nutritional analysis. Gut DNA of spiders, carabid and staphylinid beetles will be analysed using high-throughput sequencing to construct highly resolved ecological networks. In addition, the macronutrient composition of predators and prey will be determined using colorimetric assays to assess the flow of carbohydrates, lipids and proteins through these networks. Together, these novel methodologies will provide mechanistic insights into how artificial light at night rewires ecological networks via optimal foraging.

#10919

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Disentangling trophic interactions in stored-product ecosystems using high-throughput sequencing

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Nuria AGUSTI, Jordi RIUDAVETS

Abstract

Stored-product arthropods represent a major threat to global food security, causing substantial economic losses. The current reliance on chemical control is becoming increasingly unsustainable due to pest resistance, environmental impacts, and food safety concerns. Therefore, advancing sustainable pest management requires a detailed, evidence-based understanding of trophic networks within storage ecosystems. Uncovering these complex interactions is essential for defining the ecological role of natural enemies and optimising their deployment in biological control strategies.

This study aims to disentangle the predation ecology within commercial grain warehouses by analysing the trophic interactions of two key predatory mite species: *Blattisocius tarsalis* and *Cheyletus malaccensis*. Initial feeding trials were conducted using eggs of the pest *Rhyzopertha dominica* to define the temporal window for reliable prey DNA detection in the predator's gut. Subsequently, a year-long field survey was carried out across multiple commercial warehouses to collect naturally occurring predatory mites. Gut content analysis of these individuals was performed using high-throughput sequencing with universal arthropod primers. This methodological approach is intended to map the food web, and other trophic interactions occurring within this ecosystem.

The results will be presented and discussed in the context of existing literature, with the aim of providing critical data to inform the development of improved, sustainable biological control strategies for storage ecosystems.

Effect of soil orchard management on apple blossom weevil and its predators and parasitoids

Aya EL MEZIANE (National Institute of Horticultural Research (InHort), Ayaelmeziane.ae@gmail.com)

Eligio MALUSÀ, Małgorzata TARTANUS

Abstract

The influence of multifunctional living mulches including herbal species, cover crops and cash crops on the dynamics of the apple blossom weevil (*Anthonomus pomorum*) and the associated predators and parasitoids community was investigated in an apple orchard managed according to organic farming practices.

The presence of living mulches was on average reducing the abundance of the weevil in comparison to the natural cover. Consequently, also the percentage of damaged blossoms was reduced, showing a significant positive correlation between the two observations that confirmed the role of pest pressure in determining damage levels. Living mulch of white clover and, to a lower extent, mint and wild strawberry induced a reduction of the abundance of the weevils on the apple trees compared to the natural cover. This was paralleled by a lower abundance of the weevil also on the living mulch plants.

Parasitoids belonging to several families were recorded, yet no significant correlations were detected between their abundance and either weevil occurrence or damage level. However, a modification of the presence of the weevils was noted in relation to the biological cycle, which could have been either prolonged or reduced by some living mulches or as an effect of the presence of different beneficials. The results are discussed also in relation to the other ecosystem services that the studied living mulches have, e.g. as providers of feed and shelter for pollinators or limiting weeds or providing additional economic benefits to the farmer as cash crops.

Trichoderma–plant–arthropod interactions: a field study on cascading effects across trophic levels

PIERLUIGI FORLANO (UNIVERSITY OF SALERNO, Pforlano@unisa.it)

DANIELE CURCIO, ANTONINO MODAFFERI, RAFFAELE CAVALIERE, STEFANIA MIRELA MANG, ENRICA DE FALCO, GIULIA GIUNTI

Abstract

Trichoderma (Ascomycota, teleomorph: Hypocrea) can colonize many plant species and establish complex physiological interactions. *Trichoderma*-induced alterations in plant palatability can influence populations of phytophagous arthropods and their biological control agents. It may also trigger inducible defence mechanisms against phytophagous insects and pathogens.

This field study evaluated the effects of *Trichoderma afroharzianum* strain T22 on the growth and yield of common bean (*Phaseolus vulgaris* L., var. Fagiolo di Controne) and on key phytophagous and entomophagous arthropods. Experiments were conducted at two sites (Fisciano and Postiglione, Italy), using a randomized block design. The fungus was applied as spores via irrigation, and root colonization was confirmed by plating inoculated roots on PDA. No pesticides were used, and weed control was mechanical. Plant physiological traits, plant growth parameters, and arthropod populations were monitored.

Leaf chlorophyll content (SPAD index) did not differ between treatments but varied between sites. *Trichoderma* promoted plant growth and increased seed yield (+7.55% and +11.22%), with site-related soil effects. Yellow sticky traps and leaf sampling indicated a higher attractiveness of *Trichoderma*-treated plants to aphids and hymenopteran parasitoids, although no significant aphid infestations occurred. Thrips, leafhoppers, stink bugs, and predatory insects showed no significant differences between treatments. Leaf sampling revealed increased populations of the two-spotted spider mite (*Tetranychus urticae* Koch) on treated plants, and at one site an increase in acarophagous communities (e.g., *Feltiella acarisuga*, *Phytoseiulus persimilis*, *Stethorus* spp.) was observed. Conversely, non-treated plants showed a higher incidence of agromyzid leaf miners.

Seed damage by stink bugs, lepidopterans, and coleopterans was recorded. Higher stink bug damage was observed on *Trichoderma*-treated plants (12.8% vs 7.8% and 5.7% vs 3%). Despite this, the enhanced overall yield and marketable production of treated plants offset the damage (+5.3% and +4.6%). No differences were observed in rust or virus symptoms.

Comparative characterization of two related viruses in different parasitoid species

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Jesica PÉREZ-RODRÍGUEZ, Salvador HERRERO SENDRA, Laila GASMI

Abstract

Parasitoids are key players in biological control strategies and essential components of terrestrial ecosystems. Despite their importance, little is known about how parasitoids and viruses interact, except for domesticated endogenized DNA viruses (DEVs) that have developed an obligatory, mutualistic interaction with their parasitoid hosts. Within this interaction, DEVs benefit from the host machinery for their replication and propagation, meanwhile the successful development of the parasitoid progeny within the parasitoid's host depends on the DEV immunosuppressive genes. In contrast, RNA viruses associated with parasitoids are often overlooked. Herein, we aim to characterize the association between RNA viruses, parasitoids and their respective mealybug hosts. In a previous study, we identified the RNA virome of two mealybug–parasitoid systems relevant to Mediterranean Basin citriculture: the native *Planococcus citri*–*Anagyrus vladimiri* system and the invasive *Delotococcus aberiae*–*Anagyrus aberiae* system, native to South Africa and employed in a classical biological control strategy. Despite their original geographical distribution, the two parasitoid species are each infected with a distinct phasmavirus sharing around 70% sequence homology. Each phasmavirus is injected by its respective parasitoid through oviposition suggesting a potential role in parasitism success. Herein, we aim to obtain insights into the interaction Phasmavirus-parasitoid-host by assessing: viral prevalence within populations, tropism, transmission and implication in the parasitism success. Adding to this, we explored whether the phasmaviruses dynamics and effects are conserved between both parasitoid species.

#14210

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

The progress of 3MP field trials on greenhouse and open-field tomato in Asia and Europe

Peng HAN (Yunnan University, Penghan1394@163.com)

Benjamin GARD, Antonio BIONDI, Antonio GUGLIUZZO, Judit ARNO, Patcharin KRUTMUANG, Van Chung NGUYEN, Hang DAO THI, Nhat LE MAI, Abid ALI, Khasan ISMOILOV, Anne-violette LAVOIR, Paula MOLINA, Ming-hui WANG, Jon KNIGHT, Adrian LEACH, Gina NICHOLS, Nicolas DESNEUX

Abstract

In IPM practices, the adoption of “green” tactics by growers is limited by their high costs resulting from the insufficient integration of various components. In 2024, we proposed a novel theoretical framework - Multidimensional Management of Multiple Pests (3MP). The 3MP approach integrates complementary agroecological measures to deliver effective and sustainable pest control while reducing dependence on chemical inputs via: a) optimising fertiliser use to naturally strengthen crop resilience, b) releasing and conserving beneficial insects, and c) introducing insect-friendly companion plants to enhance biodiversity. We are now conducting the field trials to compare the outcomes of the 3 groups: 3MP approach, local farmer practices and untreated control on open-field and/or greenhouse tomato in China, Vietnam, Thailand, Pakistan, Tajikistan, Italy, France and Spain. Our first field data has shown that the 3MP strategy has high potential in conferring pest management, maintaining fruit yields and enhancing fruit quality, while reducing substantially the insecticides input and bringing various environmental benefits including conserved soil health and reduced greenhouse-gas emissions, compared to local farmer practices. Furthermore, the 3MP strategy is easy to implement for growers following appropriate training. Questionnaire feedback is going to be obtained from the local growers and extension specialists to get what they think of the 3MP approach and their willingness of adoption in future. Elicitation interviews are performed with all the partners to understand the advantages of 3MP in practice. Granted by Yunnan FVF-IPM International Joint Lab and ADOPT-IPM project, the work is still ongoing across all the countries to get a clear conclusion.

Arthropod biodiversity in Danish apple orchards: Influence of semi-natural habitats and management practices

Stine Kramer JACOBSEN (University of Copenhagen, Stikra@plen.ku.dk)

Dennis Günther RIED, Troels Vogelius BANG, Helle MATHIASSEN, Lene SIGSGAARD

Abstract

Sustainable fruit production is balancing requirements of high yield, quality, and ecological integrity. Approaching this balance depends on the interplay between orchard management practices and the surrounding semi-natural habitats. This study investigates how semi-natural habitats and orchard management (organic/conventional) affect arthropod natural enemy abundance and functional biodiversity, and their potential impact on major apple pests; the Apple sawfly (*Hoplocampa testudinae*), the Rosy apple aphid (*Dysaphis plantaginea*), and the Codling moth (*Cydia pomonella*). We conducted visual observations, and beating samples, from flowering to shortly before harvest in Danish apple orchards. Furthermore, we compared effects of semi-natural habitats in the centre versus edges of the orchard to assess arthropod biodiversity. This study focuses on local biodiversity effects, while future steps will compare local biodiversity indices to surrounding landscape on a landscape diversity gradient. This study is part of the European SusCrop ERA-NET project AgroBioConnect (Connections in the landscape. Role of landscape complexity in agroecosystem sustainability) that aims to investigate the effect of landscape complexity over time and land cover/productivity dynamics on the above and belowground ecosystem services in European agricultural landscapes.

The life cycle of the phytophagous nematode *Schistonchus caprifici*, specialist of male *Ficus carica* figs and phoretic in its pollinator *Blastophaga psenes*

Frederic LANDMANN (CRBM, CNRS, Université de Montpellier, France, Frederic.landmann@crbm.cnrs.fr)

Kevin TERRETAZ, Magali PROFFIT, Finn KJELLBERG, Yannis BERLE

Abstract

The 800 plus species of *Ficus* (Moraceae) are characterised by their enclosed inflorescences called figs. They are pollinated by species-specific mutualistic wasps (Agaonidae, Chalcidoidea). The wasps enter receptive figs to oviposit. Some weeks (months) later, offspring wasps born in the fig mate, and female offspring leave the fig, in search of a new receptive fig to enter. Diverse organisms, most notably nematodes, have specialised on feeding within figs, moving from fig to fig in the Agaonid wasps. The nematodes include entomophilous and phytophagous lineages that have specialised on figs. However, their biology, especially that of the phytophagous species is poorly known.

Schistonchus caprifici (Nematoda: Aphelenchoididae) develops and reproduces in the figs of male *Ficus carica*, and is detected in its specific pollinator, *Blastophaga psenes*. We followed *S. caprifici*'s life cycle, concomitantly with the development of *B. psenes* from larva to adult in natura, in figs collected from wild fig trees in the Montpellier area. We used a series of new observation techniques such as FISH in transparentized insects. We establish that *S. caprifici* reproduces only in the fig tissues and does not feed on *B. psenes*. We demonstrate that a specific development stage of the nematode shows a tropism for the female insect nymph suggesting the nematode uses a specific signal produced by these nymphs. It enters the nymph but remains confined in specific tissues, without entering the coelom or hemolymph during the phoretic phase. It only leaves these tissues once the adult wasp has entered a new fig to oviposit. Our observations contradict previous descriptions of the biology of *S. caprifici*, but are compatible, though more precise, with observations on another species of *Schistonchus* and on two species of *Ficophagus*, suggesting homogeneous biology in phytophagous fig nematodes.

Molecular detection of *Hypera postica* predation by *Coccinella septempunctata* in response to aphid availability

Alexandre LEVI-MOURAO (University of Lleida, Agrotecnio Centre, Lleida, Spain; Santarém Polytechnic University, Santarém, Portugal, Alexandrelevi.garcia@udl.cat)

Roberto MESEGUER, Xavier PONS

Abstract

This study investigates, through molecular trophic analysis, the consumption of *Hypera postica* Gyllenhal by *Coccinella septempunctata* L. under both controlled and natural field conditions. Species-specific primers targeting the COI region of *H. postica* were designed and validated, demonstrating high sensitivity and specificity. To determine how long prey DNA remains detectable, adult and fourth-instar *C. septempunctata* were fed with alfalfa weevil larvae in the laboratory, and gut content samples were collected over a 24-hour period. Prey DNA was detectable for an average of 15.37 hours in larvae and 19.05 hours in adults. Field-collected larvae and adults from eight alfalfa fields, located in the Ebro Basin region, also tested positive for *H. postica* DNA, confirming natural predation. Because *C. septempunctata* is primarily aphidophagous and may shift to alternative prey when aphids are scarce, we evaluated how varying aphid densities in the field shaped its predation on *H. postica*. Samples of *C. septempunctata* were obtained from fields infested with *H. postica* that varied in aphid density. High detection rates of *H. postica* DNA were recorded in low-aphid fields (82–100% in adults; 86–100% in larvae), whereas medium aphid pressure resulted in lower detection, especially in larvae (13–45%). In fields with the highest aphid abundance (>80%), only 33% of adults and 13% of larvae were positive. Overall, the results reveal prey-switching behaviour driven by aphid availability and support the role of *C. septempunctata* as a facultative predator of the alfalfa weevil.

Selective feeding and niche differentiation in adult boreal Odonata revealed by DNA metabarcoding

Hana MERCHANT (Uppsala University, Hana.merchant@ebc.uu.se)

Abstract

Meso-predators such as odonates occupy a crucial niche within freshwater food webs, where their dietary choices can cascade through ecosystem dynamics. Despite the importance of meso-predators, detailed insights into their prey selection and niche differentiation remain scarce. Here, we explore the dietary habits of three sympatric Odonata species, the dragonfly *Libellula quadrimaculata* and the damselflies *Erythromma najas* and *Coenagrion hastulatum*, inhabiting boreal floodplain wetlands in central Sweden. Using COI metabarcoding of faecal pellets alongside arthropod sampling from Malaise and emergence traps, this study provides new insights into fine-scale trophic interactions in these freshwater communities. We found considerable/significant overlap in prey choice between the three species, but also differences in diet variance. Despite this, there were no significant differences in Shannon diversity or Evenness. The largest species, *L. quadrimaculata*, exhibited lower taxonomic richness than the smallest species, *C. hastulatum*. Diptera was a dominant prey source across all three species, with Chironomidae as the most abundant prey, while mosquitoes (Culicidae) formed only a minor component. Diet composition differed significantly between *L. quadrimaculata* and the two damselflies, which did not differ from each other. The larger *L. quadrimaculata* also consumed larger prey likely inaccessible to the smaller damselflies, suggesting a size-based constraint on prey use. Comparisons with prey availability from traps revealed significant deviations from random feeding. Jacobs' D values indicated consistent prey selectivity in all three species, with preference for Ephemeroptera and avoidance of Diptera. This study provides the first molecular evidence of selective feeding in Odonata and highlights the role of species-specific traits in shaping trophic interactions and dietary niches in boreal wetlands.

Behavioural responses of an egg parasitoid to substrate-borne semiochemicals in a multi-herbivore patch: effect of non-host traces on foraging behaviour

Ezio PERI (Department of Agricultural, Food and Forest Sciences - University of Palermo, Ezio.peri@unipa.it)

Tuğcan ALINÇ, Simona CONTI, Derya DEVECI, Antonino CUSUMANO, Stefano COLAZZA

Abstract

Insect parasitoids commonly rely on substrate-borne semiochemicals to locate hosts, yet little is known about how these cues are exploited in multi-herbivore patches where hosts are present alongside non-hosts. In open arena behavioral assays, we studied the response of the egg parasitoid *Trissolcus basalis* to walking traces left by the host *Nezara viridula* either alone or in combination with larval traces left by the non-host *Spodoptera littoralis*. We tested whether the interference effects are dependent on the host sex and physiological state (male, virgin female, or gravid female) as well as on non-hosts' density and developmental stage. We found that the presence of non-host larval traces significantly reduced the egg parasitoid response to walking traces left in the arena by *N. viridula* hosts, reducing residence time and increasing walking speed. According to our prediction, parasitoid responses were dependent on host sex and physiological state, and we observed stronger interference due to *S. littoralis* in arenas contaminated with traces left by gravid *N. viridula* females. Furthermore, the disruptive effects increased with non-host density and developmental stage, such that the strongest interference with parasitoid responses was found in the presence of fifth-instar *S. littoralis* larvae. Our results show that non-host herbivores can disrupt egg parasitoid exploitation of substrate-borne host cues with potential consequences for foraging efficiency of biological control agents in multi-herbivore environments.

Assessing the multitrophic compatibility of *Bacillus* surfactins as biopesticide in a sugar beet–aphid–parasitoid system

Adeline ROHART (Ecologie et Dynamique des Systèmes Anthropisés - UMR CNRS 7058 UPJV – Université de Picardie Jules Verne, Centre National de la Recherche Scientifique – France, Adeline.rohart@u-picardie.fr)

Arnaud AMELINE, Clément BARRACHINI, François COUTTE, Aude COUTY

Abstract

Bacterial lipopeptides (LPs) produced by the *Bacillus* genus are lipophilic compounds that display a broad range of biocide activities. Among these LPs, surfactins have exhibited lethal and sublethal effects on various orders of insects, including aphids, and thus represent a promising option as biopesticide. However, their impact on beneficial insects, such as natural enemies, remains largely unknown. The purpose of the current work was to investigate the lethal and sublethal effects of different modes of exposure to surfactins, obtained from *B. subtilis*, on the following tritrophic chain : the sugar beet *Beta vulgaris*, the black bean aphid *Aphis fabae*, and the parasitoid wasp *Aphidius colemani*. To do so, treatments were applied to the host plant, the aphid and parasitoid mummies to assess respectively bottom-up effects on aphids and parasitoids. Life-history traits were measured as physiological endpoints to assess the fitness of both aphids (survival) and parasitoids (emergence rate, development time, sex ratio, longevity, size). Also, surfactin neurotoxicity was assessed for topically exposed aphids using a measurement of acetylcholinesterase (AChE) activity. Results confirmed the insecticidal efficacy of surfactins when applied topically to both adult and nymph aphids and revealed a bottom-up effect on aphids when applied to beet leaves. AChE assay did not highlight any neurotoxic activity of surfactins. No negative bottom-up effect on parasitoids was found regardless of the treatment level. This study, highlighting that exposure of aphid hosts to surfactins from *B. subtilis* did not impact life-history traits of parasitoids, suggests that surfactins could be safely used as biopesticides without interfering with parasitoid top down regulation of aphid pests.

#11746

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Climatic factors drive community and predator responses to *Osmia* bees (Hymenoptera: Megachilidae) in temperate South Korea

Minwoong SON (Division of Apiculture, Department of Agricultural Biology, National Institute of Agricultural Science, Republic of Korea, Sonmiou807@naver.com)

Heeji KIM, Dong Hee LEE, Kyu-Won KWAK, Su Jin LEE, Su-bae KIM, Sung-Kuk KIM, Bo-Sun PARK

Abstract

In temperate mosaic landscapes, *Osmia* bee communities are expected to respond sensitively to shifts in climate and floral resources. We quantified the joint effects of post-winter climate and local floral diversity on the abundance and community structure of cavity-nesting *Osmia* bees and on nest-emerging predators. In 2025, bamboo tube traps were deployed at 23 sites across South Korea. We recorded four native *Osmia* species and nest-emerging predators. Monthly climatic variables (November-April) were summarized by PCA (PC1 representing cooler-drier-lower sunshine conditions). Floral diversity was indexed by the number of flowering plant species within 50 m. We fitted negative binomial GLMs/LMs and performed RDA on Hellinger-transformed species data. We recorded 5,398 *Osmia* individuals. Floral richness had a strong positive effect on total bee abundance, and PC1 (cool-dry conditions) also increased abundance. Predator abundance was positively related to floral richness rather than climate. Species-specific models showed consistent positive responses of *O. pedicornis*, *O. cornifrons*, and *O. taurus* to PC1 and floral richness, whereas *O. satoi* exhibited a distinct pattern. The RDA model was not statistically significant, yet ordination suggested partial segregation among species along climatic and floral gradients.

The microbial ecology of honeydew under a changing climate

Francine VAN NEERBOS (University of Bremen, Vanneerb@uni-bremen.de)

Abstract

Honeydew, produced by phloem-feeding Hemipteran insects, is a sugar-rich and ephemeral resource that plays a central role in sustaining insect communities. Together with floral nectar, honeydew represents one of the main sugar resources in many ecosystems. Beyond its nutritional value, honeydew also contains volatile compounds and diverse microbial communities, both of which can mediate interactions among insects across trophic levels. Despite its ecological importance, the factors shaping honeydew chemistry and microbiome composition remain far less understood than those governing floral nectar.

Anthropogenic climate change (ACC) is expected to profoundly alter plant–insect–microbe interactions by modifying temperature and humidity regimes, with cascading consequences for ecosystem stability. Recent studies indicate that climate-driven changes can affect honeydew sugar composition and microbial diversity, yet it remains largely unknown how these changes influence honeydew-associated microbiomes, volatile profiles, and insect-mediated interactions.

Here, I present an experimental framework to investigate how ACC influences the qualitative characteristics of aphid honeydew, including its nutritional composition, volatile emissions, and microbial community structure. Using multiple plant–aphid systems reared under controlled climate scenarios, this work examines how changes in environmental conditions shape honeydew quality and aphid feeding behavior. I further explore the ecological role of honeydew-associated microbes by testing whether insects from different functional groups can acquire and disperse these microbes, and whether such dispersal leads to homogenization of honeydew microbiomes across plants.

#10977

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Insect-based circular bioeconomy: Converting agrifood side-streams into animal feeds and organic fertilizers using black soldier fly *Hermetia illucens* in Greece

AMALIA ANTHOUSI (Research & Development Department, MAGMA Agro S.A., Kathiana, Akrotiri, 73100, Chania, Greece, Amalia.anthousi@magma-agro.gr)

Emmanouil PAISIOS, Ayse YARALI PAISIOS

Abstract

Insects, together with their gut microflora are excellent nutrient recyclers, an ecosystem service that can be harnessed: Larvae of black soldier fly (BSF) *Hermetia illucens* can be “farmed” on agrifood side-streams to be post-processed into a protein-rich meal which can be incorporated into animal feeds. The leftover material “frass” on the other hand is an organic fertilizer with soil-improving, plant bio-stimulating effects. If adopted at meaningful scale, this technology can significantly contribute to the sustainability and resiliency of our food system by reducing the dependence on and environmental damage due to extensive use of fish- and soymeal in animal feeds as well as mineral fertilizers in crop cultivation.

In much of Europe, BSF farming takes place in heavily climatized facilities with costly agrifood side-streams due to competition with other bioindustries. Greece combines a naturally favorable climate with abundant un-valorized side-streams, enabling low-cost, low-energy BSF farming with significant socioeconomic and environmental benefits. We present our results on adapting the technology to Greek climatic conditions and side-streams. We show that year-round BSF farming in a minimally climate-controlled greenhouse using brewer's grains, olive pomace, cheese whey, bakery discards and greenhouse crop residues is feasible. We outline the relevant parametric dependencies, technical obstacles and boundary conditions, to guide subsequent commercial implementation. As an outlook we present a pilot-scale BSF farm made of natural building materials and designed based on bioclimatic architecture for viable, sustainable BSF farming in Greece, with direct relevance to the wider Mediterranean region.

#11325

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Bioconversion of fat-rich raw ham residues by *Hermetia illucens*

Luana BATAGLIA (Università Cattolica del Sacro Cuore , Luana.bataglia@unicatt.it)

Gabriella RAVERA, Maria Cristina REGUZZI, Antonio CONVERSANO, Daniele DI BONA, Davide SOGNI, Diego VOCCIA, Emanuele MAZZONI, Lucrezia LAMASTRA

Abstract

The meat industry is of main economic importance in the Emilia-Romagna region (Italy). Raw ham production waste varies from 15 to 40% of the entire processed product, with high management and disposal costs associated with it, addressing the need for sustained alternatives for treating these residues. In this context, the use of insects, such as *Hermetia illucens* (Black Soldier Fly - BSF) for bioconversion emerges as a promising solution, especially for their capacity to transform organic waste into valuable insect biomass, rich in protein and lipids. This study aims to test the ability of BSF larvae to digest fat-rich meat residues, produced by the ham industry. For that, 3-day-old BSF larvae were fed with raw ham residues (alone or mixed with other organic substrates) for 10 days, using ventilated plastic boxes with a density of 1 larva per cm² and 0.1 g of food per larva per day. At the end of 10 days, the weight of the larvae, the weight of the remaining substrate, and the survival rates were compared with the control condition (larvae fed with the standard diet of chicken food). Feeding raw ham alone resulted in total larval mortality due to the high fat and salt content of the meat. The ham was then pretreated in water for 24 hours at 35°C and mixed with other organic substrates to ensure adequate larval nutrition. The best result was achieved with a diet mixture of pretreated ham and macerated wheat residues (1:2 ratio), a condition in which larval weight was statistically equal to the control. These larvae and digested residues will next be added in a bioreactor, in a process to generate biomethane and biochar as part of the MEAT-ICO project, which aims to valorize the waste from the meat processing line with the recovery of materials and energy.

Monitoring individual larval development in black soldier fly evidences differences between sexes growth and sexual maturation

Christophe BRESSAC (IRBI University of Tours, Christophe.bressac@univ-tours.fr)

Harmony PITEROIS, Pauline BELLOIR

Abstract

Monitoring precisely larval growth in insects is necessary to test nutritional values of diet or impacts of abiotic factors such as temperature and toxic or favourable substances. Moreover, it can be a way to infer traits measured in adults to their larval development. However, when larvae are inside their substrate, and cannot be individually marked, inferring adult performance to larval development can be tricky. Moreover, most insect larvae cannot be sexed, preventing any monitoring of traits differing between males and females. In Black Soldier Fly (BSF), optimising larval growth while limiting resource use is a challenge for mass production. In lab conditions, we reared larvae individually in small cups from neonates (less than 10mg) to prepupae (250-350mg). This system allows to record the weight and food consumption of the identified larvae, to follow their individual development until adulthood, and to record the differences of growth between males and females sexed after emergence. Surprisingly, growth of isolated larvae is faster than larvae grouped in collective vials. In BSF, males emerge before females -i.e. protandry -, but the question of their different development in the larval and pupal stages remains. Analysis of growth curves evidenced that male larvae reached their maximum weight before females, confirming that the developmental program is sex specific. We dissected successive stages of larvae and pupae to find gonads. In late larval stages we found only testes, with visible condensed chromosomes and some elongating spermatids. Ovaries could not be seen before pupal stage. It results in an early maturation of males in comparison of females. These observations will allow to investigate more precisely the sexual maturation in BSF from larvae to the reproductive adult, and test the effects of diets, toxics and abiotic factors on the reproductive performances in lab and mass production.

#12097

Poster Session 1 - Ice breaker party
29/06/2026 at 16:00, Exhibition area

Valorisation of olive by-products within a circular economy framework: the OLIWA approach

Reyhane SORAYANI BAFQI (University of Turin, Department of Agricultural, Forest, and Food Sciences (DISAFA), Italy, Laura.gasco@unito.it)

Athanassia ATHANASSIOU, Paolo BARATTINI, Simona Lucia BAVARO, Eva Maria LOPEZ HERNANDEZ, Zakia CHERIFI, Titouh KHAYREDDINE, Hocine MEZIANI, Carlos GARCES NARRO1, Jesus DE LA OSADA GARCÍA, Emilija Ivanova STOJCHEVA, Christos G. ATHANASSIOU, Fernando ALEGRE SASIAN, Alicia NADERPOUR PEÑALVER, Adamantini PARASKEVOPOULOU, Fatma TRABELSI, Emna BEN BOUBAKER, El Akram HAYOUNI, Begum YURDAKOK-DIKMEN, Mehmet Sedat CEYLAN

Abstract

The olive oil sector is a cornerstone of Mediterranean agriculture but it generates large quantities of by-products that are often underutilized. The OLIWA project addresses this challenge by developing circular strategies to convert olive by-products (OPs) into sustainable resources. OLIWA brings together a multidisciplinary partnership of academic institutions and industrial partners from several Mediterranean countries, with the objective of demonstrating innovative and sustainable valorization pathways. The project adopts a circular economy framework in which OPs are repurposed into animal feed ingredients, functional additives, bio-based materials, and renewable energy, contributing to waste reduction and improved resource efficiency across agro-food value chains.

A key component of the project is the bio-conversion of OPs through insect rearing systems, particularly using black soldier fly larvae. Olive residues are investigated as alternative substrates for insect production and generating high-quality insect meals for animal nutrition, including aquaculture applications. This approach offers a promising opportunity to reduce reliance on conventional feed ingredients while supporting circular and environmentally sustainable production systems.

OLIWA explores the extraction of bioactive compounds from OPs for potential use as functional feed additives, as well as the development of innovative biodegradable packaging materials derived from olive residues and insect-based components. Additionally, the feasibility of biogas production from olive by-products and organic residues is assessed to enhance energy recovery and close material loops within the system.

Overall, OLIWA aims to demonstrate how OPs can be converted from waste into strategic resources through interconnected circular pathways. By integrating feed, food, material, and energy applications, the project contributes to more resilient and sustainable agro-food systems and provides transferable models for circular bioeconomy implementation.

This OLIWA project is supported by PRIMA, a program supported by the European Union, under the GA 2432 (Call 2024 Section 1 Food Value Chain in Nexus).

Growth performance of juvenile rainbow trout (*Oncorhynchus mykiss*) fed *Hermetia illucens* meal with different levels of chitinase

Alessandro Antonio MELIS (University of Turin, Department of Agricultural, Forest, and Food Sciences (DISAFA), Italy, Laura.gasco@unito.it)

Sara BELLEZZA ODDON, Michel VAN SPANKEREN, David DERUYTTER, Laura DE JONG

Abstract

Insect meal is a valuable alternative protein source and functional ingredient due to its, amongst others, high protein content and favorable amino acid profile; however, a high inclusion level of chitin could reduce the feed digestibility and affect fish growth and health. This study evaluated the growth performance of juvenile rainbow trout fed diets containing different levels of dietary chitinase. 480 juvenile rainbow trout were allocated in 24 tanks (20 fish/tank; 4 replicates/treatment) and fed six experimental diets containing 10% *Hermetia illucens* (HI) meal. Four diets differed in chitinase inclusion levels (0%, 0.25%, 0.5%, and 0.75%; CTRL, CH1, CH2, and CH3) derived from *Aspergillus niger*. Two additional diets included 10% pretreated HI meal: one thermally treated without chitinase (PRO1) and one with 0.75% chitinase (PRO2). Individual weight gain (iWG), specific growth rate (SGR), feed intake (FI), protein efficiency ratio (PER), survival rate (SR), feed conversion ratio (FCR), and final body weight (FBW) were evaluated on a tank basis when fish triple their weight. Data were analyzed using one-way ANOVA for parametric data (PER, SGR, FCR, SR, IWG, FBW, $P > 0.05$) and the Kruskal–Wallis test for non-parametric data (FI, $P < 0.05$). Fish fed the CH1 diet showed higher FCR and lower FBW compared with CH3 ($P < 0.05$). Regarding PER, CH3 and PRO1 did not differ from each other ($P > 0.05$) but differed significantly from CH1 ($P < 0.01$), which showed higher values. No significant differences were observed for iWG, SGR, FI, or SR ($P > 0.05$). In conclusion, dietary chitinase inclusion and HI meal pre-treatment with chitinase did not result in clear improvements in growth performance compared with the control diet, while showing differences between the level of chitinase included and the type of treatments.

The HiGa project is supported within the Green Era Hub call by the Green Development and Demonstration Programme, GUDP, under the Italian Ministry of Agriculture, Food Sovereignty and Forests (MASAF). CUP: D23C23000570005

Genotype by Diet Interactions Drive life-history traits in Black Soldier Fly (*Hermetia illucens*)

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Marie MERLE, Kondé MHANT, Meroua FOUGHAR, Chloé GENEVEY, Agus D. PERMANA, Pierre-Olivier MAQUART, Jonathan FILÉE

Abstract

The black soldier fly (*Hermetia illucens*), belonging to the order Diptera is increasingly valued in applied entomology due to its remarkable capacity to bioconvert organic waste and its high nutritional value. As a result of global expansion and domestication, the species now displays substantial genetic diversity, yet performance differences between strains remain poorly documented. This study aimed to better understand the relationship between genotype and phenotype, as well as their interaction, to support the improvement of Black Soldier Fly domestication.

Five distinct strains (Cameroon, China, Europe, Indonesia and Myanmar), collected from artisanal and industrial farms, were genetically characterized using mitochondrial and whole genome sequencing. These analyses revealed high genetic divergence based on mitochondrial genome phylogeny and principal component analysis of nuclear SNP data. To assess phenotypic performance, the strains were reared on three diets differing in nutritional value: a poor diet (Alfalfa Meal, AM), an intermediate diet (Wheat Bran, WB), and a rich diet (Chicken Feed, CF). At harvest, we evaluated different life history traits such as survival rate, average larval mass, feed conversion ratio etc.

Statistical analyses revealed strong effects of both diet and strain, but the key result was the pronounced strain $\times$ diet interaction. Performance varied drastically depending on substrate quality and strains did not respond uniformly. Indonesia showed high versatility across all diets, China performed mainly on nutrient-rich substrates, and Cameroon excelled in substrate degradation. In contrast, Europe and Myanmar displayed more specialized profiles, with marked sensitivity to fibrous diets. These contrasted reaction norms highlight that diet performance cannot be interpreted independently of the strain genetics..

Overall, this work highlights the combined influence of diet quality and genetic origin on the biological performance of *H. illucens*. The findings underscore the value of preserving diverse local genetic resources and the need for improved molecular tools to guide strain selection .

Biodegradation of Plastic/Bioplastic Food Packaging by *Tenebrio molitor* and *Zophobas atratus* Larvae

Lara MAISTRELLO (Università di Modena e Reggio Emilia, Dipartimento di Scienze della Vita, Centro BIOGEST-SITEIA, Reggio Emilia, Italy, Lara.maistrello@unimore.it)

Sara D'ARCO, Andrea FEROCCE, Matteo PROFETI, Fabio LICCIARDELLO, Patrizia FAVA, Augusta CALIGIANI

Abstract

The accumulation of plastic waste represents a pressing environmental challenge. Conventional recycling often faces limitations due to the complex and heterogeneous nature of plastic materials, prompting the exploration of biological alternatives. Insect larvae, particularly *Tenebrio molitor* and *Zophobas atratus*, have attracted attention for their ability to degrade and metabolize plastics, especially polystyrene (PS). This study aimed at verifying the performance of these insect larvae to biodegrade PS and bioplastic (BP) food packaging materials. We used 900 *T. molitor* and 120 *Z. atratus* larvae per treatment, reared under standardized conditions (27°C, 70% RH, darkness). After a 48-hour starvation period, larvae were exposed to wheat bran (WB) alone (control), or WB mixed with either clean, water-contaminated, or meat-exudate contaminated PS or BP. Key parameters, including plastic mass loss, larval weight and survival were monitored for at least 60 days. Additionally, nutritional analyses assessed larval protein and lipid content following consumption. Frass collected during a 48-hour purging period after larval isolation underwent chemical characterization and scanning electron microscopy (SEM) to evaluate residual PS/BP content, structural changes, and potential environmental impacts. By studying the feeding behaviour, degradation efficiency, and biochemical and structural properties of larvae and frass, this research provides insights into the feasibility of entomoremediation as a sustainable waste management strategy for plastic and bioplastic food packaging materials.

Funding: The project “Bioconversion of Packaging, Residues, and Waste from Food Supply Chains (BIO-R&R)” (ID 37970 - PG/2023/312510 - CUP E87G22000640003) is part of the PR ERDF 2021–2027 program, supported by European Funds from the Emilia-Romagna Region.

Optimizing Black Soldier Fly Larval Performance Through Controlled Fermentation of Agri-Food By-Products

Lara MAISTRELLO (Università di Modena e Reggio Emilia, Dipartimento di Scienze della Vita, Centro BIOGEST-SITEIA, Reggio Emilia, Italy, Lara.maistrello@unimore.it)

Sara D'ARCO, Enrico MAURIZZI, Matteo PROFETI, Augusta CALIGIANI, Andrea PULVIRENTI, Patrizia FAVA

Abstract

Hermetia illucens (Black Soldier Fly, BSF) larvae are increasingly valued in the feed and other industrial sectors for their ability to bioconvert organic waste into high-quality biomass. However, substrate variability and spoilage remain challenges. This study investigates the effects of controlled fermentation on substrate stabilization, larval growth performance, and final nutrient composition.

We formulated substrates using fruit and vegetable by-products (summer and winter mixes) combined with either water or whey. These mixtures were inoculated with starter cultures of *Lactobacillus curvatus*, *Lactobacillus sakei*, and *Saccharomyces cerevisiae* (4.8×10^7 CFU/mL) and incubated for 48 hours prior to introducing third-instar larvae. Rearing was conducted under standardized conditions (27°C, 70% RH) until the emergence of the first prepupae.

We monitored larval growth parameters, waste reduction efficiency, and substrate hygiene, specifically assessing the potential of fermentation to limit mold growth and reduce Enterobacteriaceae loads. Comprehensive nutritional profiles (protein, lipids, amino acids, ash) were determined for substrates, larvae, and frass. Additionally, substrate fiber fractions (cellulose, hemicellulose, lignin) and frass chitin content were quantified. Preliminary observations suggest that microbial starter cultures enhance substrate stability and could positively affect larval performance. While further analyses are ongoing to confirm these trends and precisely quantify bioconversion efficiency, these findings indicate that controlled fermentation could be a pivotal tool for the industry, offering a scalable method to standardize heterogeneous waste streams and ensure safer production.

How *Hermetia illucens* reacts towards substrate infesting fungi?

Emanuele MAZZONI (Università Cattolica del Sacro Cuore, Emanuele.mazzoni@unicatt.it)

Matteo CROSTA, Maria Cristina REGUZZI, Filippo COMINELLI, Ilaria CHILLIN, Rim HAMZE, Paola BATTILANI

Abstract

In recent years, *Hermetia illucens* (Diptera: Stratiomyidae) has gained worldwide importance as one of the most widely reared insect species for industrial-scale feed production. This development has led to its classification as a new and emerging agricultural sector. Within the framework of the circular economy, the ability of *H. illucens* larvae to feed on a broad range of organic materials can play a significant role in waste, by-product, and crop residue valorisation. In particular, it offers opportunities for reducing the volume of organic waste and converting it into valuable products, with additional environmental and social benefits, including improved food and feed security in developing countries. The products derived from *H. illucens* are exploited in various economic sectors, including energy, bioplastics, cosmetics, and fertilisers, as well as other sectors that are still in the experimental stage.

The natural presence of microorganisms in waste substrates and the rearing conditions used for *H. illucens* larvae can promote the bacterial and fungal proliferation during the production process and potentially affect larval performance. In particular, it was observed that high levels of fungal development by *Aspergillus flavus* and *Fusarium graminearum* present on the substrate at the start of larval rearing were found to reduce larval growth. However, when larvae and fungi developed simultaneously on the substrate, without prior fungal colonisation, no negative effects were observed on larvae. This tolerance may be related to the larval ability, as a saprophagous species, to respond to microbial presence by producing antimicrobial peptides (AMPs), which may facilitate larval competitiveness against the early stages of fungal growth. The mechanisms involved are currently poorly understood, yet they may have significant implications for larval rearing management and for the discovery and isolation of potential new antifungal compounds in the medical and veterinary fields.

Evaluation of the bioconversion efficiency of *Hermetia illucens* (black soldier fly) larvae in a controlled environment

Arkeita MENDY (PhD student, Mendymariereinearketa@gmail.com)

MAURICE CORREA, FULGENCE DIEDHIOU, WALY NDIANCO NDIAYE, PATRICE BREHMER, TOFFENE DIOME

Abstract

Black soldier fly larvae are generally produced from organic waste of any origin, usually obtained free of charge. The nutritional profile of black soldier fly larvae is similar to, and sometimes better than, that of conventional feed ingredients (e.g. fishmeal) for use in livestock feed. The aim of our study is to recover organic macro-waste by bioconverting black soldier fly larvae for use in animal feed.

This thesis examines the impact of different diets on the growth and bioconversion of black soldier fly (BSF) larvae. DSP larvae are a promising source of protein and can be used in the sustainable management of organic waste. The study compares four diets: poultry feed (PF), broiler droppings (BD), fruit and vegetables (FV) and household food waste (HW). The results show significant differences in larval growth, substrate pH and bioconversion between the diets. Larvae fed RD showed the fastest growth and an efficient bioconversion rate (at 6.10 ± 1.01), while those fed FP showed less growth and bioconversion. The RDs also had a more acidic pH, while the FPs had a more alkaline pH. Overall, the results suggest that domestic food scraps are the best substrate for rearing MSN larvae because of their nutritional balance and their positive effect on larval growth and the bioconversion of organic waste. Larvae reared on this substrate can be transformed into meal to partially or totally replace fish meal in farm animal feed, hence the term entotechnology.

Determining the gut microbiota composition of the yellow mealworm *Tenebrio molitor* in its industrial rearing environment

Emilie MOLLARD (LMGE UCA, Emilie.mollard@doctorant.uca.fr)

Frederic DELBAC, Hicham EL ALAOUI, Ivan WAWRZYNIAK, Valentin AGEORGES

Abstract

Over the past decade, insects have received increasing interest as an innovative and sustainable source of alternative protein for both human food and animal feed. The yellow mealworm (*Tenebrio molitor*) is one of the most promising candidates due to its high protein content and ease of breeding and feeding. As in all livestock sectors, understanding and managing the microbiological aspects of mealworm production is crucial to ensuring quality and profitability. To date, the scientific literature is limited regarding mealworm gut microbiota under large-scale rearing conditions, as most studies have been conducted under controlled laboratory conditions. Thus, this study aimed to characterise the microbial communities present in the gut microbiota of *T. molitor* under industrial rearing conditions.

Regular sampling of insects and substrates was performed throughout the life cycle of the insect under large-scale production conditions, including young larvae, fattened larvae, pupae, and beetles. In parallel, welfare indicators and zootechnical performance were rigorously monitored over the insect full cycle. To analyse the gut microbiota of the collected samples, DNA extractions followed by high-throughput sequencing were performed. Two complementary strategies were used: an exploratory shotgun metagenomic approach and a targeted 16S rRNA metabarcoding.

The sequencing data are currently under analysis, but the preliminary results provide initial insights into the microbial composition of *T. molitor*. Among all microorganisms detected in *T. molitor* larvae, bacteria represent 94 %, while eukaryotes, viruses, and archaea account for 3 %, 2 %, and 1 % respectively. Focusing on the bacterial population, the predominant phyla are Bacillota, Pseudomonadota, and Bacteroidota. The data generated in this study may offer new perspectives on the interactions between the insect's gut microbiota, its zootechnical performance and the environmental conditions of industrial rearing.

Mating behaviour and sensory cues involved in partner recognition of *Hermetia illucens* (Diptera: Stratiomyidae)

Giulia PETRONI (University of Perugia, Giulia.petroni@dottorandi.unipg.it)

Silvana PIERSANTI, Gianandrea SALERNO, Florian MENZEL, Manuela REBORA

Abstract

Hermetia illucens (BSF), is a key species in the circular economy due to the larval capacity for waste bioconversion. While extensive research focuses on larval biomass production, basic research concerning adults remains scanty. This study provides further details in the ethogram of mating behaviour, adds further information on BSF sexual dimorphism, and highlights sensory cues potentially involved in partner interactions and recognition.

Morphological studies reveal marked sexual dimorphism in tarsal adhesive structures, with special discoidal setae, exclusively in males, suggesting their importance during mating. Behavioural observations, conducted through slow-motion video recordings, confirmed that the mating sequence is initiated by the female's flight, which immediately triggers the male's pursuit. A peculiar behaviour, "male hindlegs crossing," was identified for the first time: the male firmly grasps the female mid-air by crossing his hindlegs across the abdomen. After landing, the receptive female remains still while only the male performs vigorous wing fanning. The male simultaneously performs over the female: "tapping" behaviour, a rhythmic touch on the female's abdomen with the middle and hind legs, and "rubbing," where the male's forelegs are used over specific areas of the female's body. Likewise in *Drosophila*, these actions may serve as a form of communication between partners, involving 1) tactile stimulation of the female, 2) chemical perception through tarsal gustatory sensilla of cuticular hydrocarbons to assess sex recognition. Wing fanning may represent a signal of mating motivation for females or intraspecific competition with other males. Behavioural observations indicate that agonistic encounters between males exhibit interaction patterns that mirror these courtship attempts, suggesting a possible role in competition.

This research enhances BSF reproductive biology knowledge and improves mass rearing optimisation.

#11940

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Adult Morphology of Wild and Mass-reared Black Solider Flies, *Hermetia illucens* (Diptera: Stratiomyidae)

Lisa ROLLINSON (University of Cambridge, Dragonflies4321@gmail.com)

Chris JIGGINS

Abstract

The black soldier fly, *Hermetia illucens* (Diptera: Stratiomyidae), is mass-reared industrially because its larvae bio-convert organic waste into insect biomass. After two decades of captive rearing, populations now show genomic signals of domestication. However, while larval traits such as size and nutrition have been recorded and even used in artificial selection schemes, the morphology of adult flies has not been extensively studied. This study provides an analysis of how the morphology of adult black soldier flies varies across populations. The morphology of historical, wild populations of black soldier flies from museum collections is compared to modern, mass-reared populations. The size and scaling of structures, including the head, thorax, and wings, are analyzed. The results inform how mass-reared black soldier fly adults may differ from wild black soldier fly adults.

From Pomace to Performance: Evaluating Growth and Bioconversion Efficiency of *Hermetia illucens* Larvae on Two-Phase Olive Pomace-Based Diets

Panagiota SOULIOTI (Laboratory of Entomology and Agricultural Zoology, Department of Acriculture Crop Production and Rural Environment, University of Thessaly, Pasoulioti@uth.gr)

Georgia BALIOTA, Christos I. RUMBOS, Maria Teresa CAPUCCHIO, Christos G. ATHANASSIOU

Abstract

Two-phase olive pomace (TPOP) is a major byproduct of olive cultivation in Mediterranean countries, however, its high moisture content (>60%) poses challenges for valorization. Black soldier fly larvae (BSFL), recognized as an efficient insect bio-converter, have been extensively studied for the bioconversion of organic wastes. Given their moisture requirements and high conversion capacity, BSFL offer a promising pathway for TPOP utilization. This study evaluated the impact of partially replacing chicken feed with this byproduct. TPOP was tested in two forms - wet and dry (74°C for 5 h) - at inclusion levels of 10, 15, 25, 50, and 75% for dry TPOP, and 5, 10, 15, 25, 50 and 75% level for the wet TPOP. Chicken feed served as the control and all diets were adjusted to 70% moisture content. Larval survival and weight were recorded every three days, and the experiment was terminated when 10% of larvae reached the prepupal stage. Nutritional composition analyses of diets and larvae were performed, alongside the calculation of six performance indicators: survival rate (SR), feed conversion ratio (FCR), bioconversion rate (BCR), corrected bioconversion efficiency (BE_{corr}), waste reduction index (WRI), and specific growth rate (SGR). Results revealed significant differences in individual larval weight and nutritional composition across treatments. Survival rates remained consistently high (>90%) with no significant variation. Performance outcomes were closely linked to diet composition, with substrates exceeding crude fat (3-6% DM) or protein (16-20% DM) thresholds yielding reduced larval growth. These findings demonstrate the potential of incorporating TPOP into BSFL diets and underscore the critical role of substrate nutritional balance in optimizing larval growth and bioconversion efficiency.

This research is supported by the EU-PRIMA program - project OLIWA- Repurposing OLIVE WASTE in circular economy solutions for feeds, additives, packaging, and biogas - GA 2432, Call 2024 Section 1 Food Value Chain in Nexus.

Engineering gut antimicrobial peptide expression in black soldier fly to enhance antimicrobial function for sustainable feed applications

Conall STANFORTH (University of Cambridge, Cs2089@cam.ac.uk)

Abstract

Global food demands are rapidly rising, while simultaneously, over one-third of all food produced is currently wasted, highlighting the pressing need for efficient and sustainable bioconversion systems. The black soldier fly (*Hermetia illucens*, BSF) converts organic waste into protein- and lipid-rich biomass for animal feed, yet current production remains insufficient to meet rising demand. The addition of exogenous antimicrobial peptides to BSF-derived feed offers to increase the value of BSF within animal feed, fostering greater uptake within industry while reducing the reliance on conventional antimicrobials within animal agriculture.

PiggyBac-mediated transgenesis was used to insert exogenous antimicrobial peptide (AMP) constructs into BSF. Although piggyBac has previously been established in this species, it is applied here to drive AMP expression in larvae intended for animal feed. Expression was restricted to the gut using candidate gut promoters, as constitutive expression of AMPs is likely to impose fitness costs, and the gut represents a major site of microbial interaction and peptide excretion. Candidate AMPs were selected based on the literature and screened using minimum inhibitory concentration (MIC) assays against poultry-associated bacterial pathogens.

Transgenic gut-AMP lines will be evaluated for population-level fitness traits, including survival, development and fecundity, alongside antimicrobial activity, enabling assessment of trade-offs associated with AMP expression. This work seeks to establish transgenic BSF as a method for adding exogenous products within established insect-derived feed whilst maintaining productivity, with relevance to improved feed biosecurity and animal health in a more circular economy.

#10987

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Impact of a newly discovered virus on the mating choice and behaviour of the black soldier fly (*Hermetia illucens*).

Matthis GOUIN (IRBI (UMR 7261), CNRS/Université de Tours, Matthis.gouin@univ-tours.fr)

Frédéric MANAS, Christophe BRESSAC, Elisabeth A. HERNIOU

Abstract

In a changing society aiming for more ecological productions, insect rearing seems to have a rosy future. The black soldier fly (BSF, *Hermetia illucens*) is nowadays one of the most reared insect species because of its exceptional ability to rapidly convert a wide variety of organic waste into high-quality protein and fat, of use ranging from animal feed to biofuel production. However, as for every rearing, pathogens can cause important damage to the livestock. Until recently, BSF was considered immune from any viruses, yet sporadic mortality was reported, and several viruses have since been identified in BSF rearing. Among them, the solinvivirus was found to cause mortality and is suspected to reduce fecundity. In this study we explore the impact of this virus on the sexual partner choices, on the fecundity and on the mating behaviour of the black soldier fly. Different groups of flies were given the choice of mating with healthy or infected individuals to see if there are any mating rate differences. We expect healthy individuals to have a higher and longer mating rate than for the infected ones and thus increased their reproductive output. This study advances knowledge on the impact of the solinvivirus on the reproduction and behaviour of the black soldier fly.

#12450

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Cold vs. CO₂: anaesthetic effects on insect antennal functionality

Eric DARROUZET (Université de Tours, Eric.darrouzet@univ-tours.fr)

Benoit LAPEYRE, Claire MARCOUT

Abstract

Anaesthesia methods play a crucial role in ensuring the integrity of the animal during experimental studies. This study investigates the impact of two anaesthesia methods, CO₂ and cold treatment, on an insect antennal response to synthetic alarm pheromone compounds.

Adult worker hornets were anesthetised, and their antennae excised and tested using an electroantennography set-up with controlled stimulation of alarm pheromone components. Results showed that CO₂-anesthetised hornets exhibited robust antennal responses, while coldanesthetised individuals displayed none. This result suggests that freezing may impair the functionality of olfactory receptors. In contrast, CO₂ anaesthesia preserves receptor integrity, offering reliable and interpretable results. This study highlights the importance of selecting appropriate anaesthesia techniques to avoid artefacts in insect sensory physiology research and underscores the ecological relevance of studying *Vespa velutina nigrithorax* alarm signalling.

Diel rhythm shapes sensory tuning in hawkmoth visual systems

Zibo LI (University of Liège, Ziboli95@gmail.com)

Natalie ROBERTS, Minglei MA, Wendy VALENCIA-MONTOYA, Olle LIND, Naomi PIERCE, Jean-Marc LASSANCE, Marjorie LIÉNARD

Abstract

Hawkmoths (Lepidoptera: Sphingidae) are active pollinators and remarkable flyers relying on color vision and a suite of neural specializations to accomplish precise navigation and foraging. Multiple transitions from nocturnal to diurnal ecologies have occurred across the lineage, providing a powerful system to study how their trichromatic visual systems adapt to contrasting light environments. However, it remains unclear whether independent hawkmoth diel reversals are associated with convergence in phototransduction pathways or light-sensing opsin receptors, and how these sensory adaptations may inform visually guided flower perception under different light regimes.

We performed a comparative analysis of eye transcriptomes from 24 hawkmoth species, including nocturnal and diurnal representatives, to test whether the independent evolution towards a diurnal diel state involves similar molecular mechanisms. We found strong signature of diel rhythm in gene expression profiles, with transcriptomes from hawkmoths sharing the same diel state being more similar to each other than to those from the opposite state. This shows that the independent evolution of diurnal diel states involves shared molecular mechanisms.

Examining the ommatidial retinal mosaics of photoreceptors tuned to ultraviolet (UV), blue (SW) and green (LW) sensitivity, we show that they are broadly conserved. Visual modeling informed by opsin-based sensitivity supports robust color and achromatic discrimination under varied light conditions irrespective of diel ecology. In contrast, we identify several instances of opsin spectral tuning associated with activity period, where amino acids under selection generate substantial shifts in spectral sensitivity in opsins. Functional mutagenesis coupled with visual modelling show that discrete opsin tuning can modulate the balance between chromatic and achromatic visual information across light levels, without compromising overall visual performance.

Together, our results support that fine-scale proximal changes in visual pigment expression and biochemical properties can optimize photon capture under different illumination regimes, illustrating how distinct diel rhythms contribute to visual sensory tuning.

An Opioid Mechanism for Nociceptive Suppression in Wasp-Stung Cockroaches

Frederic LIBERSAT (Ben Gurion University, Libersat@bgu.ac.il)

Abstract

The wasp *Ampulex compressa* injects venom into the brain of its host, the American cockroach (*Periplaneta americana*), which turns the cockroach into a fresh food for the wasp's offspring. The venom targets the central complex (CX), a sensory-motor hub. Stung cockroaches are not paralyzed; however, they respond poorly, if at all, to noxious stimuli.

Previous study showed that although nociceptive signals are carried forward to the brain, they fail to trigger robust nocifensive behavior in stung cockroaches. Electrophysiological recordings from the CX of stung cockroaches showed reduced evoked activity in response to nociceptive stimuli. Another study suggested that the venom of the wasp might contribute to the manipulation of cockroach behavior by affecting the opioid system.

Here, we used morphological electrophysiological and behavioral methods to investigate if nociception in cockroaches can be affected by modulation of the opioid system in the CX. Behavioral studies show that injection of Loperamide (Opiate receptor agonist) into the CX elevates the threshold for nocifensive behavior. Electrophysiological recordings of the CX combined with injection of loperamide show a reduced evoked activity of CX neurons to nociceptive stimuli. To uncover the existence of opiate receptors in insects, we used hybridization chain reaction with probes specifically designed to target the cockroach's opioid-binding-like protein to map opioid neurons. This method revealed a high concentration of these neurons near the central complex.

In conclusion, our study shows the involvement of the opioid system in the CX in controlling nociception in the American cockroach.

Diel rhythm shapes sensory tuning in hawkmoth visual systems

Marjorie LIENARD (GIGA-R, Laboratoire des Systèmes Sensoriels, University of Liège, Marjorie.lienard@uliege.be)

Natalie S ROBERTS, Zibo LI, Minglei MA, Wendy A VALENCIA-MONTOYA, Olle LIND, Naomi E PIERCE, Jean-Marc LASSANCE

Abstract

Hawkmoths (Lepidoptera: Sphingidae) are active pollinators and remarkable flyers relying on color vision and a suite of neural specializations to accomplish precise navigation and foraging. Multiple transitions from nocturnal to diurnal ecologies have occurred across the lineage, providing a powerful system to study how their trichromatic visual systems adapt to contrasting light environments. However, it remains unclear whether independent hawkmoth diel reversals are associated with convergence in phototransduction pathways or light-sensing opsin receptors, and how these sensory adaptations may inform visually guided flower perception under different light regimes.

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Together, our results support that fine-scale proximal changes in visual pigment expression and biochemical properties can optimize photon capture under different illumination regimes, illustrating how distinct diel rhythms contribute to visual sensory tuning.

Toxicity of novel neurotoxic insecticides on *Tetranychus urticae* and various phytophagous and predatory mite species

Omar MASOUD (Department of Zoology and Agricultural Nematology, Faculty of Agriculture, Cairo University, Giza 12613, Egypt, Omar.masoud@agr.cu.edu.eg)

Berke DEMIRCI, Emre İNAK

Abstract

Tetranychus urticae Koch (Acari: Tetranychidae) is a widespread pest that causes significant

crop losses. Although acaricides are commonly used for its control, the development

of resistance often leads to control failures under field conditions. Therefore, there is a

constant need for new compounds with novel modes of action. Novel neurotoxic insecticides

targeting γ -aminobutyric acid (GABA) receptors, such as isoxazolines and metadiazines,

represent one of the most recent classes of insecticides. However, their toxicity

to *T. urticae*, other tetranychid mites, and predatory mites remains poorly understood.

The isoxazoline insecticides fluralaner and isocycloseram showed very high toxicity to

all *T. urticae* populations, with LC₅₀ values ranging from 0.53 to 2.64 mg a.i./L and 0.04

to 0.26 mg a.i./L, respectively. Isocycloseram also caused 100% mortality in two other

phytophagous mite species, *Eutetranychus orientalis* and *Bryobia kissophila*, at field application

rates (30 mg a.i./L). In contrast, the meta-diazine broflanilide exhibited no toxicity

against any of the tested phytophagous mites at the recommended field rate (20 mg

a.i./L) and even at very high concentrations (5000 mg a.i./L), the mortality rate remained

below 65% in all *T. urticae* populations except one. On the other hand, both isocycloseram and broflanilide, at their field rates, exhibited strong side effects –causing 100% mortality– on three predatory mite species: *Phytoseiulus persimilis*, *Neoseiulus californicus*, and *Amblyseius swirskii*. These findings highlight the potential of novel insecticides for mite control, while also emphasizing the importance of evaluating their non-target effects to support the development of sustainable pest management strategies.

BumbleDate: Identification of key pheromones and neural mechanisms involved in bumblebee reproduction

Jorn OPPERSMA (Evolution, Genomes, Behavior and Ecology, CNRS, IRD, Université Paris-Saclay, Gif-sur-Yvette, France, Jorn.oppersma@universite-paris-saclay.fr)

Zsolt KARPATI, Thomas SCHMITT, Julie CARCAUD, Jean-Christophe SANDOZ

Abstract

Sex pheromone communication is crucial in insects for attracting mating partners. Despite its fundamental role in insect ecology and its implications for conservation, it remains poorly understood. Current research on the detection and neural processing of species-specific sex pheromones, and how they initiate copulation, has primarily focused on a few species of Lepidoptera and Diptera. In contrast, the mating systems of social insects have been strongly overlooked, despite their complex mating behaviours. This is particularly true for the buff-tailed bumblebee (*Bombus terrestris*), a widespread pollinator and influential model for studying perception, learning and memory. Even if we know that *B. terrestris* males establish flight paths along which they deposit pheromones from the cephalic labial glands (CLG), attracting both virgin queens and other males, the compounds involved are utterly unknown. Although extracts of male CLG are behaviourally attractive for queens, and some CLG compounds elicit electrophysiological responses in the queen antenna, it is still unclear which are sexually attractive to males and queens and how they are processed in the neural systems of both castes. In our project, we aim to obtain a complete picture of *B. terrestris* sex pheromone communication by i) investigating which pheromonal CLG compounds attract males and queens; ii) describing possible adaptations in their olfactory systems; and iii) recording neural activity by means of in vivo calcium imaging to reveal how sex pheromones are processed in the brain. Ultimately, we hope to assist conservation efforts, as well as inspire research into the evolution of sex communication in bumblebees.

#12405

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

The role of electrical fields in the sensory ecology of arthropods – a survey of recent studies

Ryan PALMER (University of Bristol, Ryan.palmer@bristol.ac.uk)

Abstract

Arthropods possess a variety of novel senses to acquire environmental and biotic cues. In this talk, I will present a suite experiments and models that show the role electrical fields play in sensory life and ecology of terrestrial arthropods. The discovery that many arthropods (e.g. bees, spiders, caterpillars, hoverflies) can sense and respond to weak electrical fields has motivated investigations into (i) the mechanics and dynamics of mechanosensory hairs that enable this sense, (ii) the typical electrical signals experienced in nature such as those generated by other arthropods and by plants, and (iii) the possible effect of electrical fields on other sensory processes. Here, I will touch on several of these aspects, giving an overview of our research to date, and some of the problems that remain.

#11281

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Bacterial taste regulates immunity and feeding

Léo SILLON (CSGA - GustaBrain Lab, Leo.sillon@ube.fr)

G rard MANIERE, Pierre-Yves MUSSO, Naziha BOUICH, Isabelle CHAUVEL

Abstract

How sensory systems encode microbial information to coordinate physiology and behavior remains largely unknown. Here, we show that *Drosophila melanogaster* larvae use defined gustatory circuits to detect bacterial cues and regulate both immune state and feeding. Activation of specific taste pathways is sufficient to modulate macrophage homeostasis in the absence of infection, revealing that sensory neurons can directly prime immune function.

Bacterial detection by the gustatory system also shapes feeding behavior. Larvae alter their feeding decisions in response to bacteria-associated sensory cues, indicating that microbial information is processed within taste circuits to guide foraging. Importantly, distinct sensory pathways differentially contribute to immune and behavioral outputs, highlighting a functional segregation of microbial information within the gustatory system.

Together, these findings uncover a neurobiological framework in which taste neurons act as microbial sensors that couple environmental detection to immune preparedness and behavior. This work positions sensory circuits as central regulators of host-microbe interactions during development.

#16109

Poster Session 1 - Ice breaker party

29/06/2026 at 16:00, Exhibition area

Acoustic ecology of Neuropterans in South Africa

Anza SIMON (University of Bristol, Om24913@bristol.ac.uk)

Abstract

Echolocating bats exert strong predation pressure on nocturnal insects, driving the repeated evolution of ultrasound-sensitive hearing. These sensory adaptations allow prey to detect bat calls and initiate evasive behaviors. Here, we report previously undocumented ultrasonic hearing and phonotactic behavioural responses in the Neuropteran family, Nemopteridae (spoonwings and threadwings). Using a tethered flight setup, individuals were exposed to ultrasonic pulses from a speaker positioned 10 cm away. Threadwings responded with flight cessation or briefly pausing before resuming but spoonwings only responded with complete flight cessations. Behavioural responses in threadwings were initiated at 20 kHz, these responses were most frequent and pronounced in the 60–90 kHz range for threadwings. As for spoonwing, responses were initiated at 10 kHz, with sensitivity reaching to a minimum threshold of 67 dB pe SPL at a frequency of 60 kHz. Their hearing frequencies align with bat echolocation frequencies and sensitivity seen in related neuropterans, adding to evidence that many nocturnal insects have ultrasonic hearing for predator avoidance. So far, only the green lacewing hearing organ has been described, but evidence now shows that other neuropterans, such as antlions and nemopterids, also hear. Because their auditory organs have not yet been characterized, we are investigating wing-base morphology using scanning electron microscopy (SEM) and preliminary histology to determine whether these structures resemble those of the green lacewing. Our work focuses on the Myrmeleontidae, Nemopteridae, and Ascalaphidae families. We find substantial variation, even within species, with swellings occurring not only on the forewings but in some cases on the hindwings for some species. Our ongoing morphological work suggests that auditory structures in neuropterans are more diverse than previously recognized, indicating multiple evolutionary modifications of wing-base hearing organs.

Involvement of nicotinic acetylcholine receptor subtypes in learning and memory performance in the honeybee *Apis mellifera*.

Emiliane TAILLEBOIS (P2E laboratory, University of Orleans, France, Emiliane.taillebois@univ-orleans.fr)

Alison CARTEREAU, Steeve THANY

Abstract

The type of memory formed during learning in the honeybee depends upon the number of learning trials during the training phase. Multiple-trial of olfactory conditioning of the proboscis extension response (PER) leads to long-term memory (LTM) which can be retrieved more than 24h after learning. We studied the involvement of nicotinic acetylcholine receptors (nAChRs) in learning performance by injecting nAChR agonists/antagonists and insecticides into the brain.

In previous study, we demonstrated that post-training injection of nicotine improved retention of olfactory memory, suggesting that nAChR subtypes could be involved in learning retention in the honeybee. Moreover, we have identified several nAChR subunits which are expressed in different brain regions such as antennal lobes and mushroom bodies.

Here, we demonstrated that sulfoxaflor (SFX), a new neurotoxic insecticide proposed as an alternative to neonicotinoids in crop protection, affected honeybee learning performance. SFX is known to act on nAChRs in a similar way to neonicotinoids. Interestingly, we found that intoxicated bees with learning defects showed a strong expression of the *Amelβ1* subunit. They displayed overexpression of *Amelα9* and *Amelβ2*, and down-regulation of *Amelα1*, *Amelα3* and *Amelα7* subunits. These results demonstrated for the first time that a sublethal dose of SFX could affect honeybee learning and memory performance through the modulation of nAChRs in the brain.

Characterization of seminal fluid proteins affecting the female post mating switch in *Drosophila melanogaster*

Vladimir TRAJANOVIKJ (Faculty of Science and Medicine, University of Fribourg, Fribourg, Switzerland, Vladimir.trajanovikj@unifr.ch)

Anne VON PHILIPSBORN

Abstract

Species that depend on internal fertilisation transport sperm along with seminal fluid containing a variety of biomolecules, such as hormones, metabolites, and seminal fluid proteins (SFPs), to ensure successful reproduction. Enhancing female fertility involves the stimulation of post-mating reactions, prevention of remating, boosting egg production, and aiding in sperm storage and utilisation of sperm in sperm storage organs. Male accessory glands are the primary source of SFPs. By mass spectrometry, we identified new candidate SFPs that exhibit transfer dynamics like established SFPs.

Among these candidates, we find tyrosylprotein sulfotransferase, Tpst, to be required in the male accessory gland for a sustained female post-mating switch. When Tpst is knocked down by RNAi in male main and secondary cells of the accessory gland, females mated to knockdown males remate after 4 days, show reduced fertility and absence of sex peptide on the sperm in the seminal receptacle of mated females. We identified potential Tpst substrates among SFPs involved in the female post-mating response, suggesting a regulatory role for post-translational modification in SFP activity. Further candidates are currently under investigation.

These results show how SFPs and their post-translational changes influence female reproductive behavior. Since signaling peptides and enzymes are conserved across organisms, these mechanisms have broader implications for understanding SFPs' role in mammalian fertility, particularly reproductive signaling and female tract responses. Defining how SFPs influence female remating behavior and fertility gives targets for regulating reproductive success of disease vector and agricultural pest, leading to novel vector control and population management tactics.

First Records of Predatory Coccinellids in Urban Green Spaces of Northern Jordan: Ecological and Conservation Implications

Asem ABU ALLOUSH (NARC, Asemhabes2020@gmail.com)

Amani AL_AWAMLEH, Jafar AL-WIDYAN, Wafa ABU HAMOUR, Nawar ALOMARI

Abstract

This work reports the first recorded occurrences of three predatory coccinellid beetles—*Parexochomus nigromaculatus*, *Chilocorus bipustulatus*, and *Hyperaspis polita*—in urban green spaces of northern Jordan during the summer of 2025. These species were observed preying on aphids, mealybugs, and scale insects infesting ornamental plants such as *Nerium oleander*, *Hibiscus rosa-sinensis*, and *Ceratonia siliqua*. Field surveys and spatial analysis confirmed tri-trophic interactions among host plants, herbivorous pests, and natural enemies. Remarkably, all three predators remained active during a regional heatwave, with temperatures reaching 48 °C, indicating significant thermal tolerance. Predator diversity and host-plant associations were assessed using Simpson's Diversity Index (SDI) and the Dominance Specialization Index (DSI). SDI indicated moderate to high diversity (0.65), while the DSI for *P. nigromaculatus* revealed a strong association with oleander (DSI = 0.80). These findings expand the known geographic and ecological ranges of these species and emphasize the role of urban vegetation as Ecological Compensation Areas (ECAs) that enhance biodiversity, promote natural pest regulation, and improve the aesthetic value of green corridors. This work supports conservation biological control strategies in arid and semi-arid urban ecosystems and aligns with global biodiversity goals under the Post-2020 Global Biodiversity Framework and SDGs 11 and 15.

New records of shore flies (Diptera, Ephydriidae) from Morocco

Rachida AKHRIF (LESCB URL-CNRST N°18, FS, Abdelmalek Essaadi University, Tétouan, Morocco., Racha.akh rif@gmail.com)

BOUTAÏNA BELQAT

Abstract

Among the families of acalyptate Diptera, the Ephydriidae (commonly known as shore flies or brine flies) are among the most abundant and diverse, with approximately 2,000 species currently recognized worldwide (Mathis & Zatwarnicki, 1995, with updates). Shore flies are small to medium-sized insects (1–8 mm in length), generally dull and dark coloured. Species of Ephydriidae typically develop in aquatic or semi-aquatic habitats, where larvae feed on bacteria, algae, yeasts, decaying excrement or animal matter, or mine leaves and stems (Zatwarnicki, 1992). The family exhibits considerable structural diversity, reflected in its classification into four subfamilies and 20 tribes worldwide (Zatwarnicki, 2023).

In this study, a total of 650 Ephydriidae specimens (282 males and 368 females) were collected between 2011 and 2022 using sweep net and Malaise traps. Sampling was conducted at 30 sites distributed across the Rif, Middle Atlas, High Atlas and Anti-Atlas Mountains, as well as the Central Plateau of Morocco.

Among the 25 species collected and identified, seven species of shore flies (Diptera: Ephydriidae) are recorded for the first time in Morocco, four of which are new records for North Africa: *Gymnoclasiopa aulisioi* (Canzoneri, 1976), *Gymnoclasiopa flavoantennata* (Strobl, 1900), *Hydrellia fascitibia* (von Roser, 1840), and *Scatophila signata* (Loew, 1860).

These findings increase the number of Ephydriidae species known from Morocco and contribute significantly to the understanding of the biodiversity and biogeographical distribution of the family Ephydriidae in Morocco and North Africa.

Effects of landscape fragmentation and warming on the recovery of invertebrate communities following soil disturbance

Ana BURÓN-UGARTE (BC3 (Basque Centre For Climate Change-Klima Aldaketa Ikergai), Ana.buron@bc3research.org)

Abstract

The wide diversity of arthropods makes them fundamental contributors to trophic interactions and, consequently, to key ecosystem functions. Yet global change (including land-use modification, habitat fragmentation, and warming) constitutes major threats to arthropod communities and the ecological processes they sustain. Predicting how food webs will respond remains challenging because different components of the community and different properties of the network can react in distinct ways when multiple disturbances occur simultaneously.

In this study, we investigate how combined global-change drivers alter the structure, composition, and functional roles of terrestrial arthropod communities. By integrating data across trophic levels (from primary consumers to predators) we assess how these drivers interact to reshape community organization and the interactions that underly ecosystem stability. Our approach examines also changes in the strength and configuration of trophic links that influence top-down and bottom-up processes. We aim to identify the mechanisms through which global-change stressors disrupt community dynamics, alter the balance among herbivores, and predators, and ultimately affect the resilience of ecosystems to further environmental perturbations.

The factors we study are threefold: tilling, warming, and dispersal limitation, which we apply in twelve connected pairs of enclosures. The enclosures are located in a grassland that we studied from 2023 through 2025. Plants were monitored ten times each year, and invertebrates were trapped four times per year.

Occurrence and strength of herbivory decreased within three months following tilling, although warming and fragmentation mitigated this effect. Also, perturbed cages appeared to recover interactions faster than Global Change cages. Further analysis of the data will assess changes in communities of plants and insects, identify and quantify shifts in trophic networks, and evaluate their capacity to resist and recover under multifactorial disturbance. Results will provide background information necessary to anticipate global change-driven repercussions on plant-insect communities and herbivory and better target adaptation measures.

Landscape configuration filters dispersal-related traits in phytophagous scarab beetles (Coleoptera: Scarabaeidae) of the Serranía del Perijá

Sandy GARCIA-ATENCIA (Professor, Sandygarcia@mail.uniatlantico.edu.co)

Valentina TOVAR REDONDO, María A BONILLA GÓMEZ, Yamileth DOMÍNGUEZ-HAYDAR, Claudia E MORENO

Abstract

Agricultural expansion transforms the structure and connectivity of tropical landscapes, altering the environmental filters that determine the functional composition of insect communities. We evaluated the variation in the functional composition of phytophagous scarab beetles (Coleoptera: Scarabaeidae) in response to landscape composition metrics (percentage of area) and configuration metrics (patch shape and inter-patch distance), together with local variables (canopy cover and elevation), in the Serranía del Perijá, northern Colombia. Four landscape windows were surveyed, each including three land-cover types (forest, regeneration, and crop). Six functional traits related to dispersal and resource use were measured. Functional composition was analyzed using community-weighted means (CWM), principal component analysis, and generalized additive mixed models. A total of 3,661 individuals representing 30 species were recorded. At the regional scale, no significant differences among cover types were detected; however, specific associations emerged within the landscapes. Spatial configuration, particularly patch distance and shape, explained most of the functional variation. Traits linked to dispersal (wing aspect ratio and relative hind-leg length) responded consistently to spatial gradients, whereas biomass and diet showed weak effects. These findings highlight that landscape configuration, rather than habitat amount, acts as a functional filter on dispersal-related traits, emphasizing the need to integrate patch geometry and connectivity into restoration and agroforestry management strategies to sustain functional diversity in fragmented tropical landscapes.

The effects of treed crop borders and roadside floral abundance on bee abundance and flight direction next to highways

Lesia Shea GIESBRECHT (University of Alberta, Lgiesbre@ualberta.ca)

Tyler COBB, Carol FROST

Abstract

Agricultural expansion contributes to native bee habitat loss by altering nesting habitats and limiting naturally occurring nectar and pollen resources. Highways are also a common feature in these settings which poses a mortality risk from high-speed traffic. Habitat management near roads could be used to improve outcomes for native bees. Treed (as opposed to herbaceous) crop borders may provide a variety of undisturbed nesting sites. Additionally, previous studies have demonstrated that other taxa like butterflies are less likely to cross roads when there are sufficient flowers on their side of the road. I hypothesized that: 1) treed crop borders and high roadside floral abundance would increase bee abundance; 2) the degree to which treed crop borders increase bee abundance would depend on floral abundance because high floral abundance would attract more bees to the nesting sites provided by treed borders; and 3) proportionally more bees would be found traveling along versus to and from highways when floral abundance was high. To test these hypotheses, I installed blue vane traps to collect activity-density data (interpreted as abundance), and Malaise traps to compare numbers of bees flying along, to, and from highways at 22 sites next to highways in Alberta, Canada throughout the 2025 summer. Treed crop borders were present at half of the sites and floral surveys were conducted throughout the summer. Significantly more bees were caught entering the roadside from the crop when bordered by trees; however, fewer bees were caught in blue vane traps in roadsides adjacent to trees than adjacent to herbaceous crop borders. Floral abundance did not independently or interactively affect bee abundance or movement direction. Further analysis will be conducted to explore how floral abundance and border type may influence species composition in this environment.

Epigeal insect diversity in *Nothofagus pumilio* forests in Chilean Patagonia

Mauricio GONZALEZ-CHANG (Instituto de Producción y Sanidad Vegetal, Facultad de Ciencias Agrarias y Alimentarias, Universidad Austral de Chile, Mauricio.gonzalez.chang@uach.cl)

Rodrigo BARAHONA-SEGOVIA, Khatrina MENESES, Rodrigo OJEDA, Daniel SOTO

Abstract

Insect decline worldwide is a global concern. Human activities that ultimately degrade the natural environmental conditions where these inhabit such as agrochemicals and land use change are among the main drivers of such a decline. Native forest ecosystems can contribute to insect diversity and conservation while these provide several ecosystem functions that regulate organic matter turnover, pest/prey predation or pollination. Therefore, insect community composition is a key indicator of forest condition. Identifying forest ecosystem functions by taxonomically grouping insects based on their respective behavior as a proxy of these can help in the understanding of forest conservation strategies or sustainable silvicultural outcomes in terms of forest health. Here, we use a total of 216 pitfall traps to sample 3 native-undisturbed Lenga forests (*Nothofagus pumilio*) alongside a precipitation gradient (Mesic, Humid, Dry), in Aysén region, Southern Chile. The sampling was carried out the first week of January 2020, as local weather conditions did not allow the melting of snow in the sampled forests up to November 2019. Species accumulation curves and NMDS shown differences in richness and community composition along sites, respectively, in which the Humid site had the highest number of species, then Mesic, then Dry. Predation and organic matter decomposition were the dominant ecosystem functions, represented by Carabidae, Staphilinidae and Phoridae. Across sites, although different species composition was observed, the same ecosystem functions dominated at each site. Lenga forests suffer from increasing human pressure for timber extraction used for heating houses and buildings in Aysén region. Therefore, unveiling the insect community composition in undisturbed Lenga forest areas could contribute to understand conservation efforts across the region, as well as to understand the extent of degradation in ecosystem functions associated to timber extraction and its related silvicultural practices elsewhere within Aysén region.

Post-disturbance deadwood retention increases moth diversity in Central European mixed mountain forests

Laura HARMS (Forest Research Institute (FVA) of Baden-Württemberg, Laura.harms@gmx.net)

Abstract

Climate change is severely impacting Central European forests, causing widespread die-off of Norway spruce (*Picea abies*) in a short amount of time due to drought and bark beetle infestations. While causing economic loss for forest owners, disturbances can positively affect biodiversity, as they enhance structural diversity, in particular if sites are not salvage-logged. Especially open structures and deadwood are beneficial for many insect taxa but mostly deficient in commercial forests. We investigated the effects of drought- and bark-beetle-induced disturbance sites on moths, an insect group with highly diverse habitat requirements, ranging from strict forest specialists to open-land species. Moth data was collected using light traps from May to August of 2023 on 10 recently disturbed (2018-2020) mixed mountain forest sites where deadwood had been retained, and 10 undisturbed, regularly managed control sites in the Black Forest, Southwestern Germany. We tested for differences in moth abundance, species richness, diversity and community composition, and related them to plot type, forest structure, vegetation composition and microclimate. While moth abundance was similar, diversity was significantly higher in disturbed forest sites along with a strong phenological turnover in the community composition between months. Deadwood volume and quality emerged as the primary drivers of both overall and open-land moth diversity, while the number of Red-Listed species increased with soil moisture, suggesting humid microclimates as limiting factor. As moths are indicators of structural complexity in forest ecosystems, our results support that retention of disturbance sites can contribute to biodiversity conservation in temperate mountain forest ecosystems.

Linking Landscape Complexity to Wild Bee Diversity: Evidence from Estonian Agroecosystems

Riina KAASIK (Estonian University of Life Sciences, Riina.kaasik@emu.ee)

Silva VILUMETS, Villu SOON, Eve VEROMANN

Abstract

Wild bee communities in farmland are strongly shaped by habitat structure and resource availability, yet species-level data remain scarce in intensively managed systems. Across Europe, agricultural intensification and habitat loss have driven sharp declines, making semi-natural habitats essential for sustaining pollinator communities and ecosystem functioning. Despite biodiversity-friendly policies, wild bee populations continue to decline, and in 2025, an additional 100 species were classified as threatened. Understanding how landscape composition and field-boundary structures influence wild bee diversity is essential for effective conservation within farming systems.

These findings from research conducted under the Horizon 2020 projects Quessa (2013–2017) and FrameWork (2020–2025), examined wild bee diversity in Estonian agricultural landscapes. Our objective was to quantify species-level responses to habitat structure at both local and landscape scales. To capture variation in boundary vegetation, we selected 18 sites featuring common field-edge types—herbaceous strips and woody linear elements—within one-kilometre-radius sampling circles. For broader landscape context, we implemented a stratified design across 18 one-square-kilometer areas dominated by arable land. Each landscape unit included a one-kilometre transect spanning major land-use classes, from intensively managed crop fields to semi-natural habitats. Bees were sampled using standardized pan traps deployed along transects, and all specimens were identified to species level using morphological keys.

During the studies we collected ~75% of *Bombus* and ~17% of other wild bee species recorded at national level. Most solitary species were rare, often singletons. Bee diversity declined with increasing average field size but rose with higher edge density, highlighting the role of microhabitat complexity. Our findings underscore the importance of structurally diverse field boundaries for sustaining pollinator communities and ecosystem services in agricultural landscapes.

Study on spatial and temporal changes in butterfly communities in Mt. Hallasan, Korea

Yeongdom LEE (World Heritage Office, Jeju Special Self-Governing Province, Jeju, Republic of Korea, Ajsl1980@korea.kr)

Honglim KIM, Misuk KO, Taewan HAN

Abstract

Butterflies are effective indicators of climate change. Changes in their population dynamics and occurrence patterns serve as early-warning signals for environmental shifts. In this study, a monthly survey was conducted using the linear survey method in nine sections from Yeongsil to Baeknokdam to identify the distribution of butterfly populations in the subalpine region of Hallasan Mountain. The survey was conducted for a period of five years (2018 to 2022). Thirty-five species belonging to 5 families of Lepidoptera insects were identified from a total number of 15,943 individuals. The highest number of species and number of individuals were recovered in 2018. Based on sections, section (D) from Seonjakjiwat to Witseoreum Control Office had 29 species, and section (H) from Nambyeok Control Office to Baeknokdam had the highest number of species and individuals, with a total of 4,590 individuals. The dominance index and the richness index were highest during the month of June and July in section A and section D, respectively. The species evenness was highest during the month of July in section G. The highest species diversity index was recorded in July. Species diversity index was relatively high in most sections, with the lowest being recorded in section A. As a result of analyzing eight bioclimatic factors based on meteorological data, the distribution of major occurring species was possibly influenced by the effect of the previous year's precipitation and the number of precipitation days on the population fluctuations.

Warming and insecticide contamination interact to disrupt molecular pathways, physiology, and survival in flies and bees

Felipe MARTELLI (University of Melbourne, Felipe.martelli@unimelb.edu.au)

Abstract

Insect population declines are accelerating worldwide, and increasing evidence points to sublethal insecticide exposure as a major, yet underappreciated, driver. Using *Drosophila melanogaster*, we demonstrated that chronic, contaminating doses of the neonicotinoid imidacloprid and the organic insecticide spinosad impair mitochondrial function and trigger oxidative stress in the brain. This initiates systemic metabolic disruption, including altered lipid storage, reduced ATP, and progressive neurodegeneration—phenotypes suppressed by antioxidant treatment, highlighting oxidative stress as a causal mechanism. These responses differ markedly from the acute toxicity seen at label-recommended doses, suggesting a conserved mode of action shared across agrochemicals and relevant to field-realistic exposures. Rising temperatures represent an additional and unavoidable threat to insect survival, yet their interaction with low-dose insecticides remains poorly understood. To address this gap, we examined how chronic imidacloprid exposure (0.1 µg/mL in diet) interacts with warming in both *D. melanogaster* and the native Australian reed bee *Exoneura robusta*. Individuals were maintained under two ecologically realistic thermal cycles averaging 18 °C or 28 °C. In both species, the combination of warming and imidacloprid produced the strongest reduction in survival. Mechanistic analyses revealed temperature-dependent effects. In flies, transcriptomic profiles were minimally affected by insecticide exposure at 18 °C, yet at 28 °C showed pronounced changes in genes linked to immunity, reproduction, mitochondrial function, and xenobiotic metabolism. In reed bees, metabolomic analyses (LC-MS) indicated that warmer, insecticide-exposed individuals exhibited metabolic signatures consistent with impaired energy production, alongside the highest levels of oxidative damage. Together, these results dissect the individual and combined impacts of warming and insecticides on insect physiology. Our findings highlight the selective pressure imposed by sublethal conditions: even without causing immediate mortality, the combination of warming and low-dose insecticides stresses pathways involved in immunity, fecundity, and development, ultimately threatening insect populations and ecosystem health.

Priority Areas for the Conservation of Natura 2000 Lepidoptera Species in Zagreb County (Croatia) Based on a Five-Year Survey

Tatjana MASTEN MILEK (Zeleni prsten Public institution for nature protection of Zagreb County, Tatjana.masten.milek@zeleni-prsten.hr)

Stanislav GOMBOC, Tomica RUBINIĆ

Abstract

Comprehensive and repeated field surveys of Lepidoptera were conducted in Zagreb County (northwestern Croatia) over five seasons (2020, 2022–2025) to assess the distribution, habitat requirements, and conservation status of Natura 2000 species. Daytime and nocturnal surveys confirmed the presence of over 1,200 Lepidoptera species, including five listed under the Natura 2000 network: *Lycaena dispar*, *Euphydryas aurinia*, *Eriogaster catax*, *Euplagia quadripunctaria*, and *Arytrura musculus*. Most records represent new or updated data for the county. Three species were recorded consistently, whereas *E. aurinia* and *A. musculus* were not detected annually, likely due to variable phenology, seasonal fluctuations in adult activity, and the impact of extreme weather years.

The majority of records originate from wet and moderately wet meadows, marshy grasslands, shrub-encroached habitats, and ecotonal zones along forest edges, predominantly within Natura 2000 sites originally designated for other species or habitats. These areas support small and often fragmented populations, particularly of *L. dispar* and *E. aurinia*, whose long-term persistence depends on traditional management, such as regular mowing and shrub control. In contrast, *E. quadripunctaria* exhibits broader ecological tolerance, occurring more widely in thermophilus and humid forest habitats, especially on warm, moisture-rich hillsides.

Wet meadows and associated habitats in Lazina, Pisarovina, Crna Mlaka, Odransko polje, Turopoljski lug, and Žutica, alongside shrub-rich wetland margins and structurally diverse forest edges, are identified as priority areas for conservation. Ongoing habitat degradation driven by agricultural abandonment, invasive plant species, and land-use change represents a significant threat. This study emphasizes the importance of targeted habitat management and long-term monitoring to safeguard Lepidoptera diversity and ensure the favourable conservation status of Natura 2000 species at the regional scale.

#12559

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

20 years of *Lycaena helle* and *Phengaris teleius* protection in Kampinoski National Park

Michał MIAZGA (Regional Environmental Center, REC Poland, Mmiazga@recpolska.org)

Abstract

In Kampinos National Park in central Poland, active conservation efforts have been underway for 20 years for *Lycaena helle* and *Phengaris teleius* – butterflies protected under the Natura 2000 network.

Kampinos National Park covers 38,000 hectares of forests and meadows approximately half of which form natural and semi-natural wetlands. It is a Natura 2000 site and a UNESCO Biosphere Reserve. Relatively strong populations of *Lycaena helle* and *Phengaris teleius* still exist here, but they are under pressure from environmental changes, primarily related to the abandonment of semi-natural meadows and the decline in groundwater levels.

Since 2006, mainly thanks to the LIFE projects and Common Agricultural Policy tools, conservation measures have been carried out in this area, including restoring abandoned meadows to extensive agricultural use, mowing, planting trees and shrubs, and regulating water conditions in semi-natural meadows used extensively.

The lecture will discuss the conservation measures in place and their short- and long-term impacts in the context of butterflies population trends for these species in Europe.

#16466

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Conservation value of secondary and plantation forests for fruit-feeding butterflies in northern Vietnam.

Thi Minh Thi NGUYEN (Paris Cité University, Thi-minh-thi.nguyen@etu.u-paris.fr)

Freerk MOLLEMAN, Tan PHAM

Abstract

Assessing the conservation value of secondary forests and reforestation is important for conservation planning. Butterflies indicate environmental change, but the effects of habitat and season on their communities remain poorly understood in tropical landscapes. We examined temporal variation in fruit-feeding butterfly diversity, abundance, and community composition across a primary forest, a secondary forest, and a plantation forest in northern Vietnam. We sampled butterflies nearly monthly during one year using baited traps. Butterfly abundance and community composition varied across months, without showing a clear seasonal pattern. Primary and secondary forest supported higher species richness than plantation forest. Moreover, while secondary forest had mainly a subset of species found in primary forest, the plantation forest had a distinct butterfly fauna. This suggests that secondary and plantation forests do not fully replace primary forests, but they contribute meaningfully to butterfly conservation in human-modified tropical landscapes.

Biodiversity of Scale Insects (Hemiptera: Coccoomorpha) in the Brazilian Cerrado, Including a New Genus and Two New Species

Vitor PACHECO DA SILVA (Universidad de la República, Uruguay, Vitorcezar@gmail.com)

Peronti ANA, Takumasa KONDO

Abstract

The Cerrado is the second largest biome in Brazil, covering more than 2 million km² and representing about 23% of Brazilian territory. This tropical savanna harbors exceptional biodiversity and a wide range of plant species, making it one of the most species-rich savanna ecosystems worldwide; however, it has undergone intense land-use change in recent decades, with more than half of its original area converted to agriculture. Despite its ecological relevance, insect diversity in the Cerrado remains poorly documented. In this context, this study reviews current knowledge of scale insect (Hemiptera: Coccoomorpha) biodiversity in the Cerrado and reports the discovery of two new species of soft scale insects (Coccidae). The new species were collected during less than one hour of sampling in Cerrado areas of São Paulo State, Brazil. Considering only Brazilian states predominantly covered by Cerrado vegetation, at least 38 species belonging to six families have been recorded: Aclerdidae (1 sp.), Asterolecaniidae (1 sp.), Coccidae (6 spp.), Diaspididae (27 spp.), Monophlebidae (2 spp.), and Rhizoecidae (1 sp.). This number is likely underestimated, as several Brazilian states that are not predominantly covered by Cerrado vegetation were excluded from this assessment. Notably, São Paulo State, currently the richest in terms of known scale insect diversity in Brazil, with approximately 33% of its territory covered by the Cerrado, was not considered, nor were six other states with significant Cerrado areas. One of the newly discovered species required the erection of a new genus, while the second was assigned to the genus *Philephedra* Cockerell. The discovery of two undescribed species, including a new genus, reinforces the underestimated diversity of scale insects in the Cerrado and highlights the urgent need for continued taxonomic surveys in tropical savanna ecosystems. These findings demonstrate that even limited sampling effort can reveal substantial taxonomic novelty in this underexplored biome.

Genomics of *Bombus veteranus*, an endangered bumblebee in restored floodplains in the Netherlands

Bart PANNEBAKKER (Wageningen University & Research - Laboratory of Genetics, Bart.pannebakker@wur.nl)

Dominic DIJKSHOORN, Joost VAN DEN HEUVEL, Frank BECKER

Abstract

The critically endangered bumble bee *Bombus veteranus*—once widespread across western Europe—has since the 1980s seen its populations in the Netherlands collapse to just two isolated areas: the Haringvliet former tidal inlet system and the Biesbosch floodplains. Following large-scale nature restoration on the island of Tiengemeten and in the Biesbosch, *B. veteranus* populations have rebounded, earning it the nickname “the Panda of the Dutch Delta.” However, despite its establishment in the Biesbosch since 2004, the species has yet to expand further, raising questions about the long-term viability of these populations.

To assess their resilience and connectivity, we employed a genomics-based approach. We collected tarsi samples for whole-genome resequencing, mapping reads to a de novo assembled *B. veteranus* genome generated using Oxford Nanopore long-read sequencing. Our analysis focused on key genomic indicators for conservation: population structure, genomic diversity, and inbreeding. Given the vulnerability of bumble bees to inbreeding due to complementary sex determination—which can result in sterile diploid males under inbreeding—we also screened for their presence.

Our findings provide the first insights into the genetic health of these populations and lay the foundation for a long-term genomic monitoring program. This work will inform conservation strategies aimed at restoring and protecting *B. veteranus* and other endangered pollinators in the Netherlands.

#12601

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Taxonomic and functional responses of wild bees to semi-natural habitats embedded in agricultural landscapes

Anna SOBIERAJ-BETLIŃSKA (Kazimierz Wielki University, Anna.sobieraj.betlinska@wp.pl)

Abstract

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Ground beetle assemblage structures in solar parks: What drivers shape them?

Márton Zoltán SZABÓ (Lendület Landscape and Conservation Ecology, Institute of Ecology and Botany, MTA–HUN–REN Centre for Ecological Research, Alkotmány utca 2–4, Vácrátót, 2163, Hungary Doctoral School of Biological Sciences, Hungarian University of Agriculture and Lif, Bsmarci14@gmail.com)

Nikolett GALLÉ-SZPISJAK, Tomáš HAMŘÍK, Róbert GALLÉ

Abstract

In the last two decades numerous solar parks have been established across Europe. In Hungary, these facilities now account for a significant proportion of land use, making them relevant in conservation as well. Depending on their characteristics, solar parks can either contribute to habitat fragmentation or serve as refuges for biodiversity. While vegetation can be shaped through sowing or management, little is known about the arthropod communities colonizing these habitats. Ground beetles (Carabidae) are dominant in grassland ecosystems and serve as excellent indicators due to their specific habitat requirements and well-documented functional traits. Furthermore, as predators and consumers of weed seeds, they may provide ecosystem services in agricultural areas.

We aimed to explore ground beetle assemblages and their functional diversity by addressing two main questions:

1. Do species richness, abundance, and functional composition differ between microhabitats within solar parks (under panels vs. between rows) and adjacent reference grasslands?
2. How do park area, management, former land use, vegetation structure, and landscape context influence these assemblages?

We sampled 32 solar parks across the Great Hungarian Plain. In each park, we surveyed under-panel and between-row areas alongside adjacent control grasslands. We recorded data on previous land use, management intensity, area, landscape context, and vegetation structure. Linear mixed models were used to identify the main drivers of assemblage structure, while ordination methods to visualize community differences. The studied functional traits included body size, feeding type, and preferences for humidity, light, and habitat.

Results showed that habitat type, park area, and vegetation cover significantly affected species richness, while abundance was primarily determined by management strategy. Functional diversity patterns closely followed species richness. Ground beetles exhibited fine-scale responses to different microhabitats within the parks. Notably, solar parks host several grassland specialist species, suggesting they play a role in the conservation of open habitat specialist species.

Diversity and Temporal Distribution of Carrion-Associated Ants (Hymenoptera: Formicidae) on Decomposing Rabbit Carcasses in Two Mountainous Sites of Southwestern Saudi Arabia

Reem ALAJMI (Professor of Entomology, Zoology Department, Faculty of Science, King Saud University, Riyadh, Saudi Arabia, Ralajmi@ksu.edu.sa)

Asma ASIRI, Fares ALZHRANI, Mohammed WADAAN, Fahd AL-MEKHLAFI

Abstract

Ants (Hymenoptera: Formicidae) are frequently associated with decomposing carcasses and may influence the structure of carrion insect communities, yet their role in forensic entomology remains relatively understudied in many regions. The present study investigated the diversity, abundance, and temporal distribution of ant species associated with decomposing rabbit carcasses in two mountainous locations in the Asir region of southwestern Saudi Arabia: Abha and Al-Sodah. A total of ten rabbit carcasses were exposed during the autumn season from 18 October to 20 December, with five carcasses placed at each site. Ant specimens were collected daily throughout the decomposition process and identified morphologically to species level. Decomposition was categorized into four stages: fresh, bloated, decay, and dry. Twelve ant species belonging to the family Formicidae were recorded during the study. Ant abundance varied significantly among species and decomposition stages. The decay stage showed the highest ant activity at both locations. At Abha, *Monomorium sarawatsensis* was the dominant species, reaching the highest abundance during the decay stage, whereas *Cataglyphis asiriensis* was the most abundant species at Al-Sodah. Overall, ant abundance was higher in Abha than in Al-Sodah. Statistical analysis using a generalized linear model indicated significant effects of species and decomposition stage on ant abundance, with significant species $\times$ stage interactions. The results highlight the ecological importance of ants in carrion decomposition and provide baseline data on carrion-associated ant fauna in southwestern Saudi Arabia, which may contribute to the development of regional forensic entomology databases.

Investigations on Root Colonies of the Woolly Apple Aphid (WAA) *Eriosoma lanigerum* on Apple Plants

Manfred WOLF (Laimburg Research Centre (Autonomous province Bozen; Italy), Manfred.wolf@laimburg.it)

Abstract

Several authors report that first-instar crawlers (N1) of the Woolly Apple Aphid (WAA) (*Eriosoma lanigerum*; Hausmann) migrate annually to the apple tree's root system for overwintering. However, because WAA has been introduced far beyond its native range into major apple-growing regions (e.g., South Africa, New Zealand, Europe), some elements of its original behavior appear to have been lost, including probably root-based overwintering.

Preliminary field observations in 2020 produced contradictory results. Surveys in two orchards (both cv. Fuji on the WAA susceptible rootstock T337) in the Lower Adige region (South Tirol; Italy) assessed a variable WAA colonization on lower root sections in a representative number of heavily infested trees in one orchard and a prevalent absence on trees from the second orchard. These findings raised new questions about the frequency of root colonization on apple trees inside apple orchards in our region and the impact on the pest activity.

Building on these results, we monitored WAA migration behavior on a fixed set of observational trees during 2021 and 2022. The plants were removed in 2023, providing an opportunity to examine their root systems for permanent colonization. We hypothesized that downward migration of N1 individuals would be more intense in trees possessing well-established root colonies, on the WAA-susceptible rootstock T337.

Most upward and downward annual migration occurred during the spring migration period, over 116 days in 2021 and 102 days in 2022. Therefore, we focused on mean and maximum downward migration data during these periods of the two years on different groups of trees with different characteristics. Trees were grouped according to root characteristics (presence or absence of permanent root colonies). The results of this comparative study on migration intensity and root colonization patterns are presented and discussed.

Changes in Female Genital Morphology Following Copulation in *Schizocosa tristani*

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Rowan MCGINLEY

Abstract

Like in other Entelegynes, wolf spider reproduction follows species-specific courtship behavior, with sexual selection often times following female choice based on male performance. That process morphologically involves complex female genitalia and differentiated palps in males. For the neotropical *Schizocosa tristani*, this premise continues to be true. However, after the examination of several unmated females, we noticed the presence of an epigynal structure, that has not been document for this species' anatomy, which after copulation, gets removed. To test the prevalence of the structure and the mechanism for said morphological change, we conducted two experiments. First, we photographed unmated female (n=27) genitalia each day after reaching maturity, over a series of 26 days, to document the development. We performed mating trails on days 21 and 24 to detect the presence or absence of the structure. An additional experiment involved conducting mating trials with three groups (n=20, per treatment). Treatments comprised of a series of mating trials with females at different days of maturity, starting at days 3, 6, and 9 for each treatment respectively. This ensured if the presence of the structure was required for copulation and revealed other characteristics of sexual importance for the species. Preliminary results show female *S. tristani* produce this structure 5 days post-reaching maturity and it gets removed by physical contact via natural detachment or palp insertion post-copulation. Additionally, *S. tristani* demonstrates tendencies of early copulation after female maturation (≥ 3 days), with extremely rare instances of re-copulation. Although the structure is not required for successful copulation, its consistent development and removal suggest an unrecognized role in reproduction. Together, these results crucially expand our knowledge of genital morphology and sexual behavior in neotropical wolf spiders.

Not all Aphytis are idiobionts: host reproduction allowed but molting prevented in a new species targeting San Jose scale

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Álvaro GARCÍA, Marianela LARRAMENDY, Irene PANDULLI

Abstract

Aphytis sp. nov. (Hymenoptera: Aphelinidae) is the main parasitoid of the San Jose scale, *Comstockaspis perniciosa* (Hemiptera: Diaspididae), in deciduous fruit orchards of southern Uruguay. In a previous study aimed at optimizing rearing for inundative releases, a low emergence rate was obtained on the alternative host, the oleander scale (*Aspidiotus nerii*), and reproduction by parasitized adult oleander scales was observed—contrary to reports for congeners characterized as idiobiont ectoparasitoids. The present study determined whether the poor performance on oleander scale and the allowance of host development are linked to host- or parasitoid-associated traits. To this end, the immature developmental stage(s) on oleander scale at which parasitoid mortality occurs were assessed; parasitoid oviposition and emergence were compared between San Jose scale and oleander scale; the capacity to reproduce while parasitized was evaluated for both hosts, and the ability of nymphs to molt to adults was evaluated for San Jose scale. Parasitoid mortality on oleander scale was found to occur mainly at early stages (egg and/or early larva). Emergence was higher on San Jose scale than on oleander scale (51% vs. 11%), although values were far from high. Adult scales of both hosts parasitized by *Aphytis* sp. nov. were able to reproduce, whereas San Jose scale nymphs did not molt to adults. Taken together, the results indicate that *Aphytis* sp. nov. behaves as a koinobiont ectoparasitoid, with host reproduction being permitted but molting being blocked—possibly the first report of this strategy for the genus and for Aphelinidae. The reduced emergence on oleander scale is most consistent with host-associated constraints, although additional factors appear to reduce emergence on the natural host as well. Future studies will examine how allowing host development and host mobility affect the ability of the parasitoid to complete immature development.

Immune anticipation in *Drosophila melanogaster*

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Fleur PONTON, Soo Jean PARK

Abstract

Social interactions are increasingly recognised as important factors shaping immune function in animals. In insects, socially mediated immunity refers to immune responses that are influenced by the social environment and indirect cues from conspecifics. While this phenomenon is well established in eusocial insects such as ants and bees, emerging evidence suggests that non-eusocial species may also regulate immunity through social cues. However, experimental evidence for such mechanisms in solitary or gregarious insects remains limited.

To address this gap, we examined whether exposure to infected conspecifics can induce anticipatory immune activation in *Drosophila melanogaster*. Using *Serratia marcescens* as a bacterial pathogen, we generated populations containing different proportions of infected individuals (0%, 20%, 40%, 60%, 80%, and 100%) and exposed healthy flies to these groups for 48 hours without direct contact. We then assessed bacterial resistance, reproductive output, immune gene expression, and cuticular hydrocarbon (CHC) profiles in the exposed individuals.

We predicted that olfactory cues from infected conspecifics would trigger immune activation in healthy flies, leading to reduced reproduction, with response intensity increasing alongside infection prevalence. Consistent with these predictions, flies exposed to infected individuals showed enhanced bacterial resistance before direct infection, demonstrating anticipatory immune activation. This effect scaled with the proportion of infected flies, indicating a dose-dependent social influence. Moreover, exposed flies displayed reduced reproductive output, suggesting a trade-off between immunity and reproduction.

These findings indicate that olfactory cues from infected individuals act as early warning signals, prompting immune and physiological adjustments in healthy conspecifics. Ongoing analyses of CHC composition and immune gene expression will clarify whether chemical communication underlies these responses. This study broadens the concept of socially mediated immunity beyond eusocial systems, revealing that even non-eusocial insects can mount collective defences through social and chemical interactions.

Z-chromosomal and autosomal influence on diapause termination in *Cydia pomonella*

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Christian OEHLMANN, Peter NEULICHEDL, Katrin JANIK, David G. HECKEL, Johannes A. JEHLE, Jörg T. WENNMANN

Abstract

The codling moth (CM, *Cydia pomonella* L.) is one of the main pests in pome fruit cultivation. From early spring on the larvae penetrate the fruits leaving them unmarketable. The codling moth hibernates in a state of low metabolism as diapausing larva. The point at which diapause ends and pupation begins, varies significantly both between and within CM populations. Through inbreeding over several years, two CM strains were isolated from an original population in South Tyrol. One strain terminates diapause in early spring, around March/April (early strain, ES), while the other strain terminates distinctly later, around May/June (late strain, LS). Both strains demonstrate stable inheritance of diapause termination over several generations, suggesting a genetic basis for their phenotypes (<https://doi.org/10.1016/j.jinsphys.2025.104904>).

Reciprocal single-pair crosses between ES and LS revealed the involvement of the Z chromosome and autosomal factors in diapause termination. So far, chromosome 4 (chr4) was identified as a promising candidate via quantitative trait locus (QTL) analysis.

Using whole genome sequence data from both strains, we are developing genetic markers for linkage analysis to contribute to fine mapping of the two potentially involved chromosomes (Z and chr4). This will enable us to further narrow down the chromosomal regions and genes, that contribute to diapause termination. Furthermore, analysing the interactions between Z and chr4, provides important insights into the genetic and physiological mechanisms behind diapause termination of CM.

#11152

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Parental care in burying beetles as a behavioural link between climate change and soil nutrient dynamics

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Abstract

The decomposition of organic matter is central to nutrient and energy cycling and is fundamental for ecosystem functioning. Carrion represents a pervasive but under-studied source of organic matter in ecosystems, providing intense and ephemeral pulses of nutrients. *Nicrophorus* burying beetles are known as nature's undertakers, as they breed on animal carrion, and have elaborate parental care that can promote nutrient cycling and improve soil fertility. Climate change is driving increases in global mean temperature and the frequency and severity of heatwaves, which has been shown to reduce the amount of parental care provided by burying beetles. This reduction in parental care under climate change could, in turn, have consequences for carcass decomposition and nutrient cycling. To this end, we will investigate the effect of temperature stress on parental care in the burying beetle *Nicrophorus vespilloides*, and the downstream consequences for soil characteristics. We expect that heat stress will reduce the duration and likelihood of beetles providing care, leading to a reduction in the effect of beetle presence on soil characteristics. This could have consequences for ecosystem functioning, such as a reduction in soil fertility limiting plant growth, or increased microbial decomposition leading to larger amounts of gases released into the atmosphere. Considering that global temperatures are expected to rise between 1 and 4°C by 2100, there is increasing necessity to understand behavioural responses to climate change and to link these effects with wider ecosystem processes.

Physiological and behavioral responses of the parasitoid *Ganaspis kimorum* to volatile compounds from fruits infested by *Drosophila suzukii*

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Francesco TORTORICI, Pasquale CASCONE, Gianluca MELONE, Domenico ELIA, Stefano PARISI, Maria DEL CARMEN RECHE GUILLERMO, Gianfranco ANFORA, Marco Valerio ROSSI STACCONI, Massimo GIORGINI, Luciana TAVELLA

Abstract

Chemical cues are key drivers of host-searching efficiency in larval parasitoids of *Drosophila suzukii*, yet the olfactory ecology of *Ganaspis kimorum*, one of the most effective biocontrol agents of the fly, remains poorly characterized. Previous olfactometer bioassays have shown that parasitoid females are attracted to early-stage infested fruits (1–3 days after fly oviposition), whereas they avoid fruits degraded by older larvae (4–6 days after fly oviposition). This behavioral shift corresponds to marked temporal changes in the volatile profile: tetradecanal, hexadecanal, heneicosane and (Z)-9-tricosene dominate early infestation and differentiate infested from healthy blueberry fruits, while 2-phenylethanol increases only when fruits are deteriorated by larval feeding. Building on this framework, we investigated whether *Ganaspis kimorum* detects these key volatiles and whether physiological antennal sensitivity aligns with its behavioral responses. We quantified antennal responses to the five candidate compounds using electroantennography (EAG) across six concentrations. Tetradecanal and 2-phenylethanol produced clear, dose-dependent depolarizations starting at 0.1 mg/mL and increasing through 1, 10 and 100 mg/mL, indicating high antennal sensitivity across a broad concentration range. Hexadecanal displayed a higher activation threshold, with significant responses only at 1, 10 and 100 mg/mL. In contrast, (Z)-9-tricosene and heneicosane produced no detectable antennal response at any dose. To determine whether physiological detection translates into attraction or repellency, behavioral assays using a Y-tube olfactometer were conducted by exposing females to the same compounds and concentrations tested in EAG. Bioassays revealed distinct behavioral valences consistent with the host quality hypothesis: 2-phenylethanol elicited significant repellency at 0.1, and 1 mg/mL. Conversely, hexadecanal triggered significant attraction at 0.1, and 1 mg/mL. Taken together, these data integrate physiological and behavioral evidence, providing a comprehensive view of how *Ganaspis kimorum* perceives and responds to host-associated volatiles across ecologically relevant concentration ranges.

Effects of symbiont acquisition timing on performance of host insects, *Riptortus pedestris* (Hemiptera: Alydidae), under laboratory conditions

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Kho JUNG-WOOK, Lee DOO-HYUNG

Abstract

Most insects vertically transmit their beneficial symbionts to their offspring, ensuring reliable symbiont acquisition and associated benefits. In contrast, several hemipteran species in the families Alydidae and Coreidae have been reported to acquire symbionts environmentally from soil in every generation. Therefore, in these hemipteran species, symbiont acquisition timing is likely to vary among individuals depending on their surrounding environments. In this study, we characterized the symbiont acquisition window and evaluated the effects of acquisition timing on the performance of host insects, *Riptortus pedestris* (Hemiptera: Alydidae). First, when symbionts were provided to the insects of all developmental stages including adults, >90% of nymphs from 2nd to 5th instar stages successfully acquired the bacteria. Second, when the effects of symbiont acquisition timing on the performance of *R. pedestris* were evaluated, developmental rate and body size of nymphs significantly decreased at all instar stages as symbiont acquisition timing was delayed. In contrast, its effect on reproduction of adults exhibited a different pattern. Pre-oviposition period gradually increased with delayed acquisition. However, the overall reproductive performance, including both pre-oviposition period and fecundity, was significantly enhanced compared to aposymbiotic insects, regardless of symbiont acquisition timing. Overall, our study demonstrates different effects of delayed symbiont acquisition for nymphs and adults; while symbiotic benefit on nymphal development was reduced, it was maintained for reproduction of adults. These findings help us better understand the ecological significance and adaptive potential of symbiont acquisition timing in the environmental acquisition system.

Symbiotic effects on predator-prey interactions of host insect *Riptortus pedestris* (Hemiptera: Alydidae)

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Jung-Wook KHO, Doo-Hyung LEE

Abstract

Symbiotic bacteria are known to affect various physiological and behavioral traits of herbivorous host *Riptortus pedestris* (Hemiptera: Alydidae). For instance, the host insect has been reported to benefit from gut symbiont *Caballeronia insecticola* enhancing the host performance including growth and development. Moreover, our recent study showed that the symbionts induced an altered foraging pattern of sustained feeding on food sources followed by reduced locomotor activity in *R. pedestris*. However, this dichotomic behavior in symbiotic insects has not yet been explored to address its implications for predator-prey interactions. Therefore, in this study, we evaluated the effects of symbionts on behavioral responses of *R. pedestris* to predators and resulting predation mortality under laboratory conditions. We employed a generalist predator *Tenodera sinensis* (Mantodea: Mantidae) to characterize and compare behavioral responses of aposymbiotic and symbiotic *R. pedestris* nymphs to predation risk while foraging food resources. In addition, we recorded predation mortality of *R. pedestris* by *T. sinensis* over 7 days in an arena designed to mimic field conditions. This study provides fundamental information to better understand ecological implications of symbiotic effects on the host insects in the context of tri-trophic interactions.

Natural Enemies of *Halyomorpha halys*: Parasitism and Host-Tracking in an Urban Area in Serbia

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Milana COVIC, Vojin PUZIC, Francesco TORTORICI, Luciana TAVELLA

Abstract

The Brown Marmorated Stink Bug (*Halyomorpha halys*) is an invasive pest that presents challenges in agricultural and urban areas in Serbia. This multi-year research, primarily conducted in the urban parks of Novi Sad, aimed to investigate pest's population dynamics, focusing on oviposition preferences and natural enemies. The study involved the systematic sampling of *H. halys* egg masses across four consecutive seasons in urban parks. Collected egg masses were reared in the laboratory to determine larval survival (vital) or parasitism (wasp eclosion). Parasitoid species (Hymenoptera) were identified morphologically to species level in order to assess their impact and distribution.

A study on parasitic wasps in Serbia identified a total of 12 species in stink bugs eggs. Notably, the two most effective alien egg parasitoids for *H. halys*, *Trissolcus japonicus* and *T. mitskurii* (Scelionidae), were recorded for the first time in Serbia in 2022. Further monitoring confirmed the active dispersal of *T. japonicus* to seven additional locations, while *T. mitskurii* has remained limited to its initial discovery site.

Research in 2024 showed that 221 out of 319 collected egg masses of *H. halys* were parasitized (69.3%). These parasitized egg masses were found on plants across 10 plant families, with the Fabaceae family being the most significant (38.87% of parasitized masses). The highest concentration of parasitized eggs was observed on *Styphnolobium japonicum*.

The results revealed a clear ecological pattern: plant families with a high number of egg masses (e.g., Fabaceae) also had a proportionally higher share of parasitized egg masses. This indicates that while *H. halys* shows clear oviposition preferences, the parasitoids effectively track the abundance and concentration of the host's eggs, rather than being strictly limited by the plant species. This pattern emphasizes the significant potential of parasitoids for effective biological control of *H. halys* in Serbia.

Insights into the Oviposition Behaviour of *Ceutorhynchus picipitarsis*

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Meike BRANDES

Abstract

The rape winter stem weevil (*Ceutorhynchus picipitarsis*) is an insect pest of oilseed rape (*Brassica napus*) that oviposits on young oilseed rape plants in autumn. Larval feeding in the terminal bud can cause significant damage during winter, leading to plant death or loss of the main shoot, resulting in yield loss and quality reduction. In Germany, this insect pest, which inhabits most of Central Europe, can be found mostly in the south and south-west, but further spread is expected. So far, control with pyrethroids is still largely effective, but *kdr*-mutations are already prevalent in France and more populations are expected to become resistant due to the limited number of available modes of action. Only very few research articles deal with *C. picipitarsis*, leaving important aspects of its biology and damage potential unknown.

To provide information on its oviposition behaviour, experiments were performed under laboratory conditions. In one of these experiments, 30 mated *C. picipitarsis* females were kept at 20 °C and supplied with new oilseed rape plants every week to ensure continuous oviposition. The plants of the previous week were then dissected. The results show that females are capable of laying more than 300 eggs in extreme cases, with a median of 119.5 eggs per female.

Furthermore, an experiment on host plant preferences showed that, contrary to oilseed rape and oil radish (*Raphanus sativus*), white mustard (*Sinapis alba*) is an unfavourable host for oviposition of *C. picipitarsis*. White mustard plants were observed to form calluses pushing eggs out of the plant tissue to dry out in the open.

Further research is needed to elucidate the species' damage potential and the ideal time of control.

Effect of mowing on assemblages of epigaeic ants, beetles and spiders in green spaces at Walter Sisulu University, Mthatha Campus

THABISA MKUZO (Walter Sisulu University, Thabisamkuzo@gmail.com)

Abstract

Biomes, such as grassland and savanna are important habitats for arthropods. Some arthropods are vital for their roles in decomposition of organic matter, pollination and nutrient cycling. However, environmental factors and anthropogenic activities, such as habitat fragmentation and management practices of vegetation cause significant declines in arthropod diversity. This study investigated the impact of mowing on the species abundance, richness and composition of epigaeic arthropods in green spaces at Walter Sisulu University, Mthatha campus. Sampling was carried out in two site categories, mowed green spaces and un-mowed open savanna. Each site category had five sampling units, and each unit was a 4 m x 4 m quadrat. The sampling units in mowed green spaces were paired with those in un-mowed open savanna, and the distance between pairs was approximately 20 m. Arthropods were sampled using the pitfall trapping method. Results showed significant differences in the species composition of ants and spiders between mowed green spaces and un-mowed open savanna, while beetle assemblages did not differ. The mowed green spaces had significantly greater species abundance and richness of all taxa than un-mowed open savanna. These significant differences in mowed green spaces may be due to this habitat being less dense in terms of vegetation and having greater exposure to sunlight, which facilitates easy foraging and support species that can tolerate heat. Similarities in beetle composition suggests that some species tolerate disturbance and are generalists. Although mowing did not reduce species richness nor abundance of ants, beetles and spiders it altered arthropod assemblages, highlighting the sensitivity of arthropods to habitat change.

The Hidden Half of the Woolly Apple Aphid and Its Parasitoid: Subterranean Populations and Overwintering Behaviour.

Elena MONARI (University of Modena and Reggio Emilia, 226670@studenti.unimore.it)

Elena COSTI, Ainara PEÑALVER-CRUZ, Aleksandra KONJEVIC, Kartik KHERA, Lara MAISTRELLO

Abstract

The woolly apple aphid *Eriosoma lanigerum* (Hausmann, 1802) is a major pest in apple orchards, capable of establishing populations in the roots and above-ground parts of trees. Despite its ecological relevance, knowledge of its overwintering strategies and the seasonal dynamics of its primary parasitoid, *Aphelinus mali* (Haldeman, 1843), remains limited, particularly below ground. A multi-site study was conducted to investigate the overwintering patterns of *E. lanigerum* and *A. mali* as well as their response to climate along the heterogeneous European north–south axis. Improving our understanding of these ecological interactions and survival strategies is essential for developing effective biocontrol.

During the overwintering season, *E. lanigerum* and *A. mali* were monitored in organic apple orchards in Italy, Serbia, Germany and Spain using a comprehensive approach that combined several methods: monthly soil-core sampling to quantify subterranean aphids and parasitoid mummies; assessment of overwintering aerial colonies on shoots and rootstock; sticky-trap monitoring to detect aphid movement (upward and downward) and parasitoid activity.

Where feasible, emergence traps were also employed, along with aspiration sampling in bark crevices. Microclimatic conditions (air and soil temperature and humidity) were recorded to identify environmental drivers.

The study addressed the following key ecological questions: (i) whether overwintering populations were restricted to the roots or present in the aerial tissues too; (ii) the relationship between above- and below-ground infestations; (iii) where and in which life stages *A. mali* overwintered; (iv) whether winged aphids emerged from the root zone during the winter months.

This work generated an integrated dataset on the 'hidden half' of *E. lanigerum* and *A. mali* in representative European organic orchards, providing vital insights into their biology and overwintering strategies under climatic changing conditions, contributing to the development of effective biocontrol programs.

Locomotor behaviour of *Dermanyssus gallinae* : effect of the substrate layout, from individuals to population

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Bourgeois THOMAS, Lise ROY

Abstract

Dermanyssus mites are strictly hematophagous mites associated with birds. These ectoparasites live at a distance from their host and are devoid of wings, which imposes significant constraints on their dispersal and access to resources. Characterized by negative geotropism, a lively gait and a tortuous path, these mites are capable of traveling more than ten meters in an hour to locate a host and feed. The orientation of surfaces (vertical or horizontal), their continuity and their physical properties at the mite's scale along the shelter-host route are likely to influence dispersal and foraging success, and, ultimately, the mite population dynamics. *Dermanyssus gallinae* s.s. causes damage in poultry farms, and other *Dermanyssus* species are responsible for human bites in homes harbouring bird nests; however, efforts to manage them face recurring failures. Understanding how substrate layout influences mites' shelter-host routes appears essential from a global health perspective. To characterize how substrate layout affects their locomotor behavior, we studied their movements using specifically-designed experimental setups. At the individual level, we compared the paths traveled in 10 minutes on horizontal and vertical surfaces using electronic trackers. At the group level, we quantified crossings over 1 hour and overnight on four vertical maze models with a minimum path length of 25 cm. At the population level, we studied the effect of two of these models on population growth and spatial distribution by using them as shelter-host routes in avian mesocosms. The results of this study indicate that a forced descents of 3 cm acts as a barrier: while not preventing individuals from crossing the passage, it slows the progression of mite groups and affects distribution within the mesocosms. These results could be useful for limiting the transfer of mites from bird nests to human living spaces, or to manage poultry mites on farms.

A multiscale approach to characterize interactions between two mirid predators in a tropical area.

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Hélène DELATTE, Jean - Sébastien COTTINEAU

Abstract

Nesidiocoris tenuis is a cosmopolitan zoophytophagous miridae used as a biological control agent worldwide, to control whiteflies and leaf miners in tomato greenhouses. Recorded in 1997 in the tropical Island of la Réunion, this miridae was scarce. However, over the last decade, outbreaks of this species have been observed, becoming a threat to tomato production. Indeed, its phytophagy induces necrotic rings leading to floral abscission and plants head breaking, especially when temperatures are raising and/or preys sparse. The consequences are strong, both on crop health, but also on local PBI programs. For more than 10 years, an indigenous biological control agent, the predatory bug *N. volucer* (miridae) has been developed and is locally produced. *N. volucer* doesn't induce damages on crops, but struggles to install and maintain, especially when *N. tenuis* is present. Research works are therefore conducted to better understand the interactions between these two species at different scales.

In lab arenas, we observed that both species adapt their respective behaviour differently in inter vs intra species situations: *N. tenuis* is more mobile than *N. volucer*, and less prone to flee after an interaction. Nymphs in both species are more mobile and tend to be more aggressive. At the plant scale, the intraguild predation is limited, and would even be in favour of *N. volucer*, but *N. volucer* survival is way more dependant of preys' availability compared with *N. tenuis*, leading occasionally *N. volucer* to cannibalism. At the crop scale, *N. volucer* population when pre-installed and fed is not impacted by a delayed *N. tenuis* inoculation, moreover, a barrier effect exists, the stronger when *N. tenuis* is the later to install. Together, these results improve our understanding of the multiscale interactions between the two predatory mirids and provide guidance for optimizing PBI strategies in tropical tomato growing systems.

Affordance-Based Landing on Moving Flowers to Model Decision and Control Mechanisms of Honeybees

Flowers

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Julien SERRES, Antoine MORICE

Abstract

The visual control of landing in flying insects is increasingly understood through the prism of Gibson's Direct Perception Theory. Therefore, the elegant optic flow-based strategy of maintaining the rate of change of τ (τ' , tau dot) equal to -0.5 has been widely adopted to model information-movement coupling and has proven effective in simplified experimental contexts.

The applicability of the tau-dot regulation is compromised in more complex tasks, e.g., when honeybees (*Apis mellifera*) land on flowers swayed by wind. First, the τ' - τ coupling assumes that insects can fully comply with the prescribed τ value, neglecting constraints acting on flying insects—such as limits on speed, acceleration, turning rate, force production, and energetic capabilities—as well as their differential effects depending on the postural demands of flight. Second, successful landings are not guaranteed by this model, even taking into account these constraints on capacity for action.

We propose that a biologically grounded alternative to purely τ' -driven models—affordance-based models, which explicitly take into account the action capabilities of honeybees—offer a better framework to model both bees' ecological decision-making and flight regulation behavior. An affordance-based landing model defines a set of possible landing trajectories bounded by the bee's action capabilities and the flower motion, forming a landscape within which the bees can navigate to control their landing task. The temporal and spatial projections of this landscape create possible landing trigger windows during which landing decisions should be made.

In the affordance-based landing model, τ' information would not necessarily be discarded but used as one of the optical correlates contributing to the perception of landing feasibility. This framework offers new perspectives not only on modeling the natural behavior of insects but also on creating control mechanisms for autonomous robots.

Foraging in the margin: metabarcoding to reveal bird prey use adjacent to production systems

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Erin GRABARCZYK, P.Glynn TILLMAN

Abstract

Insectivorous vertebrates contribute to ecosystem services via biological control of insect pests in many managed systems. However, unlike some arthropod predators and parasitoids, vertebrates such as birds are unlikely to specialize on insect pests alone and consumption of both beneficial arthropods as well as additional arthropod functional groups is relatively unclear. Molecular barcoding provides a tool for monitoring and identifying biocontrol services and disservices by analyzing fecal "biodiversity capsules" collected non-invasively. In this study, we investigated roles of bird communities foraging on the margins of two perennial orchard systems to: 1) identify common birds throughout the year and 2) apply Illumina sequencing to fecal samples thereby revealing dietary composition of arthropod prey. We observed 19 commonly occurring bird species, and amplified arthropod DNA from 257 individuals. Overall, the detection of DNA from arthropod taxa mostly consisted of herbivores and principally, Lepidoptera and Hemiptera taxa with more than 10 species of pest species detected. Other taxa detected indicate feeding on some predatory species and likely secondary detection of parasitoid species present in herbivores consumed by the birds. Lastly, although birds are quite generalist in their feeding patterns, resolved here and in other studies, bird species are using unique taxa from the environment which likely reflects differences in foraging patterns and behavior by species.

Sexual behavior and mating system of the parasitoid *Tetrastichus howardi* (Hymenoptera: Eulophidae)

Christian TORRES (Universidade Federal Rural de Pernambuco, Christian.silva@ufrpe.br)

Adria GALINDO

Abstract

Biological control has grown in integrated pest management as a sustainable, economically viable alternative to chemical pesticides, thereby reducing environmental risks. Among the natural enemies employed, insect parasitoids play a key role in controlling various agricultural pests. In this context, *Tetrastichus howardi* (Hymenoptera: Eulophidae) stands out as a parasitoid with a broad geographic distribution, capable of parasitizing different economically important lepidopterans, and it is easily mass-reared in the laboratory on alternative hosts such as pupae of *Tenebrio molitor* (Coleoptera: Tenebrionidae). But we lack information regarding the sexual behavior and mating system of *T. howardi*, which could affect the mass production of this parasitoid under laboratory conditions. Thus, adults were isolated immediately after emergence, and pairs were formed to allow mating. The results showed that males and females reach sexual maturity shortly after emergence, being able to copulate in less than 24 hours, and that no significant differences were observed in courtship or copulation duration among individuals up to 48 hours old. During courtship, males exhibited more active behavior, with higher frequencies of walking, antennal vibration, abdominal elevation, and physical contact with females, as well as greater copulatory activity throughout the photophase, with a peak between 1:00 p.m. and 2:00 p.m. Furthermore, males can mate multiple times with different females after emergence, whereas females mate only once. The results confirm the hypothesis that male *T. howardi* exhibits a polygamous mating system and that females are predominantly monandrous, and that multiple male copulations are relevant for maximizing reproductive success. Understanding these aspects provides important insights for optimizing mass-rearing protocols in the laboratory, thereby favoring the production of more females for field releases and increasing the efficiency of biological control in integrated pest management programs.

Centipedegrass Pollen: An Overlooked Resource for Foraging Bees

Shimat VILLANASSERY JOSEPH (Department of Entomology, University of Georgia, Svjoseph@uga.edu)

Karen HARRIS-SHULTZ, David JESPERSEN, Daniel IBIYEMI

Abstract

Turfgrasses are commonly perceived as lacking pollinator interactions because they are considered exclusively wind-pollinated. Centipedegrass (*Eremochloa ophiuroides*), a widely used turfgrass in the southeastern United States, produces numerous inflorescences from August through October. This study evaluated the potential of centipedegrass as a pollen resource for bees and examined bee foraging behaviors and pollen utilization within centipedegrass lawns. Bees were observed actively foraging on centipedegrass spikes. Pollen load analysis from species including *Bombus* spp., *Apis* spp., and *Lasioglossum* spp. revealed that Poaceae pollen dominated collections, with significantly higher counts during early flowering. However, overall differences between early and late flowering phases were not significant. Pollen transfer assessments confirmed that bees transported Poaceae pollen to their hives. Feeding trials further demonstrated that bumble bee larvae developed as successfully on centipedegrass pollen as on butterfly bush pollen, indicating its suitability for larval growth. Video-based behavioral observations revealed distinct foraging strategies: *Bombus* spp. exhibited crawling and tongue-protrusion behaviors, while *Lasioglossum* spp. frequently dangled from anthers during pollen collection. Remarkably, bees continued to forage on centipedegrass pollen despite the presence of showy dicot flowers nearby. These findings underscore the ecological role of centipedegrass as a supplemental pollen source for pollinators and provide valuable insights for turfgrass management and pollinator conservation across urban, suburban, and rural landscapes.

Study of genetic structure of Russian populations of the bird cherry-oat aphid *Rhopalosiphum padi* (L.) using phenological observations and SSR-analysis

Fedor EREMEEV (All-Russian Institute of Plant Protection (FSBSI VIZR), 9649233@gmail.com)

Natalia KLIMENKO, Elena GANDRABUR, Alla VERESHCHAGINA, Natalia ALPATIEVA

Abstract

The bird cherry–oat aphid *Rhopalosiphum padi* (L.) is an important pest of cereal crops. The high ecological adaptability of this species is promoted by a complex life cycle that includes parthenogenetic and sexual reproduction (also referred to as holocyclic). However, there are populations that have lost sexual reproduction (anholocyclic) and reproduce parthenogenetically on grasses throughout the year — especially in the southern parts of the area. Initially, aphids were studied using phenotypic methods only, but the development of molecular genetic approaches opened up new possibilities for analysis the genetic diversity of *R. padi*. Microsatellite genotyping has been used for studying the genetic diversity of *R. padi* in different countries, except Russia.

In our study, we used seven nuclear SSR-markers (Wilson et al., 1999; Simon et al., 2001) for genotyping of 44 northwestern (Leningrad region, Saint Petersburg) and 22 southern (Krasnodar region, Kabardino-Balkarian Republic, Karachay-Cherkess Republic, Stavropol region, Dagestan Republic) clones of *R. padi*, collected in Russia. According to phenological observations in model experiments most northern clones were holocyclic aside from 11 ones with dual overwintering strategy (holocyclic life cycle with the possibility of parthenogenesis during winter). The life cycle type of the studied southern clones was determined to be anholocyclic, except for two clones from the Novoukrainskij hamlet with dual overwintering strategy. Five south clones are in progress.

The analysis of nuclear SSR markers using UPGMA, PCoA, and Neighbor-Joining revealed a pronounced genetic structuring of *R. padi* populations associated with both geography (north/south) and life-cycle type (holocyclic/anholocyclic). The genetic isolation of the anholocyclic southern populations was established. It was also established that holocycly promotes genetic mixing and reduces the differentiation of genotypes from different locations in St. Petersburg and the Leningrad Region.

The work was carried out within the framework of the Russian Science Foundation grant No. 24-76-10009.

Susceptibility of *Spodoptera frugiperda* larvae (Lepidoptera: Noctuidae) to commercial microbial agents under laboratory conditions

Anastasia PARASKEVOPOULOU (Laboratory of Biological Control, Scientific Directorate of Entomology and Agricultural Zoology, Benaki Phytopathological Institute, A.paraskevopoulou@bpi.gr)

Olga ANESTIDOU, Eirini ANASTASAKI, Panagiotis MILONAS

Abstract

The fall armyworm, *Spodoptera frugiperda* (Smith 1797) (Lepidoptera: Noctuidae), is a highly polyphagous and invasive pest native to tropical and subtropical regions of the Americas. Following its initial detection in Africa in 2016, the species rapidly spread across Asia and Oceania. It was first recorded in Greece in September 2023. The pest attacks a wide range of host plants, including economically important crops such as maize, rice, cotton, and soybean. Due to its high invasive potential and associated economic losses, *S. frugiperda* is classified as a quarantine pest within the European Union (EU). Within the framework of the EUFAWREADY project (“Enhancing Europe’s Readiness for Managing Fall Armyworm”), this study evaluates the efficacy of commercially available microbial formulations, including entomopathogenic fungi (EPFs) (*Beauveria bassiana*) and bacteria (*Bacillus thuringiensis*). Laboratory bioassays are conducted to assess mortality and susceptibility of *S. frugiperda*. Preliminary results are particularly encouraging, especially in the case of *B. thuringiensis*. Experiments are ongoing, aiming to support the development of sustainable and environmentally friendly management strategies for fall armyworm control in the EU.

The EUFAWREADY project has received funding from the European Union's Horizon Europe research and innovation programme under grant agreement No.101212676.

#11307

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Exploring the role of plant diet on symbiont communities in thrips

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Abstract

Microbial associations are commonly found in insects, particularly herbivorous insects that rely on symbionts to feed on poor or toxic plant diets. In many insect groups, microbes originate from plants so that plant species shape the microbial composition of insect guts. The aim of our experiment was to understand how plant diet can drive bacterial diversity and composition of thrips symbionts. We explored bacterial communities in the pest thrips *Echinothrips americanus* that we reared on different plant diets including kidney bean (*Phaseolus vulgaris*) and cucumber (*Cucumis sativus*). To explore the origin of microbial communities in insects, we also examined the microbial diversity present on the leaves of the host plants. This was achieved using bacterial culture methods and 16S RNA sequencing of microbial communities. This is the first step towards a better understanding of the ecological adaptation of thrips and their symbiotic relationship with bacteria, as well as providing insights into the transmission routes from plant to insect microbial communities.

Floral Resource Diversity Drives Behavioural and Reproductive Outcomes in *Osmia* spp. (Hymenoptera: Megachilidae)

Gabriel ARBONA (Universitat de les Illes Balears, Gabriel.arbona@uib.cat)

Joan AMENGUAL, Cayetano HERRERA, Mar LEZA, Anna TRAVESET, Andreu JUAN

Abstract

In recent years, the use of solitary bees of the genus *Osmia* as managed pollinators has increased substantially, particularly in early flowering crops. These bees are frequently introduced into high-intensity monocultures or into mass-rearing systems where only a single plant species is available during their flying period, in sharp contrast to the heterogeneous floral landscapes they exploit in nature. Floral resource diversity is a key determinant of nutritional balance and developmental performance, whereas monofloral diets can constrain overall physiological condition.

In this study, to be conducted in spring 2026, we will examine how floral resource diversity shapes nesting behaviour and progeny traits in *Osmia* bees exposed to two contrasting flowering systems. Four enclosed greenhouses will be established: two planted with *Sinapis alba* monoculture and two containing a mixed assemblage of Mediterranean flowering species. Cocoons will be released into each enclosure, and nesting behaviour will be continuously monitored using video recording. Once flight activity ceases, all nesting reeds will be collected for assessment of nest architecture, brood development, and cocoon traits.

We expect pronounced behavioural and reproductive divergence between treatments. Bees in monoculture are predicted to display prolonged foraging times and to produce smaller offspring with reduced developmental performance. Sex-allocation patterns may also shift toward a male-biased ratio under nutritionally impoverished conditions.

The implications of this work extend beyond crop pollination. Sustaining robust *Osmia* populations likely requires access to diverse floral resources, not only in cropping systems but also in rearing facilities, where single-species plantings may undermine population quality. The preliminary results presented at the conference will inform more sustainable management strategies for solitary bee pollinators.

Preliminary Insights into Fungal–Beetle Interactions in Loire Valley Vineyards

Ingrid ARNAULT (University of Tours, Ingrid.arnault@univ-tours.fr)

Marlène GOUBAULT, Simon DUPONT

Abstract

Preliminary investigations conducted during the earlier BIOVAL project revealed a large and previously underestimated diversity of mycophagous beetles in Loire Valley vineyards. . Field surveys showed high numbers of the Latridiidae and Cryptophagidae in particular and suggested that their presence is positively correlated with nearby semi-natural landscape features such as hedgerows and woodlands.

Metabarcoding analyses (ITS sequencing) performed on 95 individuals collected in 2016–2017 uncovered a rich and diverse fungal community within the beetles' body. Across several genera (Corticarina, Cortinicara, Melanophthalma, and Atomaria), fungal communities were consistently dominated by Agaricomycetes, indicating strong ecological associations with wood-decay fungi and surrounding environmental mycobiota.

DNA from several major grapevine fungal pathogens was detected inside the beetles. These include trunk-disease agents such as *Fomitiporia mediterranea*, *Stereum hirsutum*, *Trametes versicolor*, and occasional detection of *Eutypa lata*. Common spoilage or opportunistic fungi (*Penicillium*, *Cladosporium*, *Botrytis cinerea*) were also present. Patterns varied across beetle genera, suggesting differences in diet, microhabitat, or exposure. No DNA from downy or powdery mildew pathogens (*Plasmopara viticola*, *Erysiphe necator*) was detected, possibly due to low field pressure during the collection period or a lack of interaction.

Despite the degraded nature of the stored samples, these results clearly indicate that mycophagous beetles interact with a wide variety of fungal taxa, including pathogens. This supports the hypothesis that these insects may act as vectors, regulators, or bioindicators of vineyard fungal dynamics, justifying the scientific direction and objectives of the FONGIVIN project (2026-2028 financed by FranceAgrimer).

Thermal and age-dependent parasitism of Banana Spotting Bug Eggs by *Anastatus* sp.

Lok Nath ARYAL (PhD candidate, Applied Biosciences, Macquarie University, Loknath.aryal@hdr.mq.edu.au)

Syed RIZVI, Bishwo MAINALI

Abstract

Banana spotting bug (BSB), *Amblypelta lutescens lutescens* Distant, is a major pest of horticultural crops such as macadamia and avocado. Increasing regulatory constraints and environmental hazards associated with the use of chemical pesticides to manage BSB have prompted the need for sustainable management tools. *Anastatus* sp. (Hymenoptera: Eupelmidae) is an important egg parasitoid of BSB, and is commercially available in Australia; however, detailed information on its biology and parasitism efficiency on the target pest to support its field application is limited. To address this gap, we investigated age-specific parasitism of *Anastatus* sp. on BSB eggs, and assessed oviposition behaviour, fecundity, developmental duration, and adult longevity under constant temperature regimes. Highest parasitism was recorded in five to 19 days old *Anastatus* females without prior host exposure. The highest female progeny ratio occurred at 17 to 19 days. Unexposed females were observed parasitizing BSB eggs up to 40 days post-emergence, indicating prolonged reproductive activity. Continuous host exposure produced a mean female ratio of $42.65 \pm 9.55\%$, with females biased progeny during the early stage of adulthood. Mean cumulative fecundity per female was 31.60 ± 3.42 eggs, with the highest oviposition at five to seven days after emergence. Developmental duration and adult longevity of the *Anastatus* females increased with a decrease in temperature from 30 to 17 °C, and there was no adult emergence at extreme temperatures (33°C and 15 °C). These findings demonstrate that age of female *Anastatus* and temperature strongly influence its performance and provide practical guidance for optimising release timing and conditions to improve biological control of BSB.

Fighting the Flea Beetle: Genetic Secrets of Resistance in *Sinapis alba*

Amrithapriya BINDU (John Innes Centre, Amrithapriya.bindu@jic.ac.uk)

Coretta KLOEPPEL, Ryan BROCK, Steve PENFIELD, Sebastien FAURE, Rachel WELLS

Abstract

Cabbage stem flea beetles (CSFB) are among the major threats to oilseed rape (OSR) cultivation. The predominant method for CSFB control frequently involves the repetitive and widespread application of chemical insecticides. However, the withdrawal of neonicotinoid seed treatments, combined with the emergence of pyrethroid resistance, has resulted in a lack of effective pest control, serious crop losses, and a 50% reduction in the UK cropping area since 2013. Consequently, there is an urgent need for more sustainable and effective pest management alternatives. Exploiting host plant resistance is one promising strategy, with white mustard (*Sinapis alba*) emerging as a noteworthy candidate due to its expression of both antixenosis (feeding deterrence) and larval antibiosis resistance mechanisms against CSFB. However, there is considerable variation in flea beetle feeding preferences among white mustard lines, and not all of them exhibit the same degree of resistance. Despite this, there remains a significant gap in understanding the genetic foundation and molecular mechanisms underlying this variation. This project aims to improve our understanding of *Sinapis*-CSFB interactions, identify potential resistance genes, and investigate their potential for deployment in other Brassica crops through gene editing or introgression. Ultimately, the findings will support efforts to develop insect-resistant crops.

Roles of the endosymbiont Wolbachia in reproductive manipulation and host plant adaptation of spider mites

Xiao-Li BING (Nanjing Agricultural University, Xlbings@njau.edu.cn)

Abstract

Wolbachia is a widespread endosymbiont renowned for reproductive manipulation across arthropods. Recent evidence also links it to host adaptation, yet mechanisms remain elusive. Here, we investigate its dual roles in the two spotted spider mite *Tetranychus urticae*, a global pest frequently infected by Wolbachia strain wTurt. We show wTurt induces cytoplasmic incompatibility (CI) of variable intensity across populations, shaped jointly by bacterial strain and host nuclear background. The wTurt genome contains two *cif* gene pairs (Type V); despite genomic identity, *cifA2 B2* expression—but not *cifA1 B1*—varies markedly with wTurt density and correlates positively with CI strength. Beyond reproduction, wTurt alters life history: infected mites lay fewer eggs but achieve higher hatching rates. Transcriptomics revealed upregulation of numerous salivary proteins, notably uncharacterized SHOT1s, enriched in feeding stages and mite proterosomes. RNAi silencing of SHOT1s reduced Wolbachia titer, increased oviposition, and lowered hatching, linking salivary protein modulation to symbiont maintenance and reproductive outcomes. Our results uncover how Wolbachia simultaneously manipulates mite reproduction and promotes host adaptation via salivary protein regulation, advancing knowledge of symbiont–host biology and informing biocontrol strategies against agricultural mite pests.

Honey as a window on plant-microbiota-bee interactions ? Shedding light on the diversity of the honey bee microbiome.

Julie BIRGEL (GenPhySE, Université de Toulouse, INRAE, ENVT, Castanet Tolosan 31326, France, Julie.birgel@inrae.fr)

Claire HOEDE, Kamila CANALE-TABET, Thibault LEROY

Abstract

Bees are composed of over 20,000 species worldwide, playing a key role in pollination. Among them, only about 10 species are capable of honey production, including *Apis mellifera*, the most widely used species for beekeeping purposes. These species provide a unique opportunity to explore the agroecological continuum linking plants, bees, and their environment. Indeed, honeys can be viewed as end-products, resulting from the transformation of plant nectar collected in the surrounding environment by a colony. In this way, DNA analysis of honey provides a valuable source of information for understanding the complex ecology surrounding the ecosystem and the diversity of interactions that occur within it.

We analyzed shotgun sequencing data coming from around 500 honeys, including 430 samples from open-access public databases and more than 70 honeys sequenced in our laboratory. Overall, the samples originate from a wide variety of geographical origins (38 countries), honey bee species/subspecies (*A. mellifera*, *A. cerana*, *A. dorsata*), and honeydews, when known (mainly from chestnut, lavender and locust). In total, more than five billion sequencing reads, both paired-end and single-end, were assembled and subsequently organized into metagenome-assembled genomes (MAGs) through a dedicated pipeline (metagWGS). This metagenome has been then used to explore the taxonomic and functional diversity of communities through abundance tables.

Throughout these analyses, we identified more than 1,000 species from 348 families present in honey. Variations in α -diversity and β -diversity of microbial communities were associated with several factors mentioned above, including the genetics of the honey bees, the provenance of honeys, and the plant(s) providing the nectar. We will further incorporate the characterization of metabolic networks associated with identified functions, as well as discuss the potential of this approach for describing ecosystem dynamics.

#11101

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Date Odors Shape Sugar-Foraging Behavior in *Aedes* Mosquitoes

Jonathan BOHBOT (The Hebrew University of Jerusalem, Jonathan.bohbot@mail.huji.ac.il)

Evyatar SAR-SHALOM, Neta KEREN

Abstract

Herbivorous insects rely on plants as essential nutritional resources, and plant–insect interactions play a key role in shaping insect ecology and diversification. Although mosquitoes are best known for their interactions with animal hosts, plant-derived sugars are critical for their survival and daily activity, yet the mechanisms underlying mosquito–plant interactions remain poorly understood. Here, we examine how two major disease vectors, *Aedes aegypti* and *Aedes albopictus*, use plant-derived olfactory cues during sugar foraging. Focusing on date extract, a known mosquito attractant, we combine behavioral assays using custom 3D-printed traps with automated tracking based on YOLito, a fine-tuned object detection model for mosquito detection and trajectory analysis. We observe species-specific behavioral responses that may reflect divergent foraging strategies. Using GC–MS analysis of date extracts from different geographic origins, we identify candidate plant volatiles mediating attraction, highlighting the ecological significance of plant odors in mosquito behavior.

#11259

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Seduced by Scent, doomed by fitness - *Ips typographus*' attraction to an occasional host

Jana Gabriele BURCHARDS (Lund University, Jana_gabriele.burchards@biol.lu.se)

Abstract

Ips typographus is one of the most destructive Eurasian forests pests causing major economic and ecologically losses annually. *I. typographus* typically attacks stressed trees but during mass outbreaks they are able to attack and kill vigorous trees as well. Main host of *I. typographus* is Norway spruce (*Picea abies*) but they occasionally attack trees of other species as well, possibly damaging even more forests. In our study we investigated the possibility of a host range expansion of *I. typographus* to an occasional host, Scots pine (*Pinus sylvestris*). Scots pine is widely distributed over Eurasia and mostly adjacent to Norway spruce, making it geographically a reachable host for the beetles. We performed behavioral laboratory preference assay and tracked reproductive outcome and offspring fitness in the occasional and main host. Additionally, we inoculated spruce and pine logs with symbiotic fungi of *I. typographus* and observed their growth in both trees. We conclude that *Ips typographus* can reproduce in pine trees under given circumstances but suffers fitness consequences.

Cultural, morphological, physiological, and molecular characterization of *Monilophthora roreri*, the causative agent of cocoa moniliasis in the Ecuadorian Amazon

KARINA CARRERA (Universidad Estatal Amazónica, Mcarrera@uea.edu.ec)

Abstract

Cacao is produced in Ecuador, with the largest production located in the coastal and Amazonian regions. Moniliasis is one of the most destructive diseases of cacao. The severity of the pathogen's attack varies depending on the area, time of year, and climatic conditions, with losses reaching up to 60%. This study aimed to characterize isolates of *Moniliophthora roreri* from the Ecuadorian Amazon. Isolates of the pathogenic fungus were obtained from cacao pods collected from six organic farms producing the Nacional cultivar, located in the provinces of Napo, Pastaza, and Morona Santiago. These isolates were subsequently identified through cultural, morphological, physiological, and molecular characterizations. As a result, 20 isolates of *M. roreri* were obtained, whose cultural, morphological, physiological, and molecular characteristics corresponded to the species. All colonies of the isolates were able to grow radially, and their cultural characteristics were similar on modified V8 medium. The identified isolates were able to cover the Petri dish (90 mm Ø) after 12 days of incubation at 26 ± 2 °C. Considerable diversity in color tones was observed, including white, salmon, and brown. Most isolates produced globose spores (7–9 µm in diameter); however, subglobose (8–14 µm in diameter) and ellipsoidal (8–20 x 6–17 µm) forms were also found. pH 6.5 most favored mycelial growth. The temperature of 25 ± 2 °C showed the highest mycelial growth. Dark conditions resulted in the greatest mycelial growth of the pathogenic fungus, unlike ultraviolet light conditions, which resulted in the slowest mycelial growth. 100% of the isolates analyzed were molecularly identified as *M. roreri*.

Life cycle of the spittlebug *Mahanarva andigena* on sugarcane seedlings

KARINA CARRERA (Universidad Estatal Amazónica, Mcarrera@uea.edu.ec)

Segundo VALLE

Abstract

The spittlebug *Mahanarva andigena* stands out as a pest of economic importance for the cultivation of sugar cane of Pastaza by its wide distribution in all the parishes in production. High population levels of the spittlebug cause a reduction in the productivity of sugarcane and the quality of its derivatives, due to the reduction in length and diameter of the stalk and cane, which become shorter and more fibrous. In order to implement studies of the biology of this pest insect associated with the crop, the duration of egg, nymph and adult stages on sugarcane seedlings was determined. In order to determine the first insect status, 90 x 15 mm Petri dishes were used in the Microbiology Laboratory of the Universidad Estatal Amazonica at a temperature of 23 ± 1 °C and relative humidity of $80.20 \pm 5.3\%$. nymph and adult stages in greenhouse at a mean temperature of 23.81 ± 2.59 °C with relative humidity of 80.47 ± 8.36 . For insect feeding in these states, POJ 93 sugar cane seedlings of 30 days of age were used in pots. The duration of the *M. andigena* embryo period was 19 ± 1.58 days, the nymph state was 46.5 ± 1.29 days and the adult state was 19 ± 1 day. The total life span of *M. andigena* in Pastaza was 84.5 ± 3.87 days.

#11339

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Plant-insect-symbiont interaction networks shaped by elevational gradients and landscape composition

Marguerite CHARTOIS (INRAE CBGP, Marguerite.chartois@inrae.fr)

Laure BENOIT, Anne-Laure CLAMENS, Emmanuelle JOUSSELIN, Anne LOISEAU, Bruno MICHEL, Sabine NIDELET, Laure SAUNÉ, Anne XUEREBO, Enric FRAGO

Abstract

Elevational gradients provide a powerful framework to investigate how abiotic conditions constraints the structure of terrestrial communities and to anticipate their responses to ongoing climate change. Although species richness of plants and animals generally declines with increasing elevation, the consequences of elevation for species interactions and the organization of ecological networks remain poorly understood. With elevation environmental uncertainty increases while resource competition is relaxed, leading to the evolution of a broader diet breadth and to networks that are more intertwined or connected. However, these patterns may differ across species guilds and according to whether interactions are mutualistic or antagonistic. Here, we surveyed thrips (Thysanoptera), across replicated elevational gradients by sampling individuals on their host plants. We constructed quantitative interaction networks linking insects to plants, as well as bacteria to insects, to test the prediction that networks will become dominated by generalist species at high elevations. We further assessed how landscape composition influences the structure of these tri-trophic networks. Finally, we discuss how a network-based perspective enhances our understanding of herbivore resilience to environmental perturbations.

From random bacteria in decaying wood ? to specific gut helpers in saproxylophagous caterpillars

Kateřina CZAJOVÁ (Department of Biology and Ecology, Faculty of Science, University of Ostrava, 710 00 Ostrava, Czech Republic, Katerina.czajova@osu.cz)

Petr PYSZKO, Martin ŠIGUT, Pavel DROZD, Miroslav KOLÁŘÍK

Abstract

Caterpillar gut microbiota are often considered transient and unstable, largely derived from their diet. Saproxylophagous lepidopteran larvae feed inside decomposing wood, a lignocellulose-rich, nitrogen-poor, microbially dense substrate already partly processed by resident microbiota. By consuming both wood and its microbial biofilm, these larvae experience a strong environmental microbial signal and provide a model for testing whether gut communities mirror their diet or consistently diverge from it. We collected saproxylophagous caterpillars from decaying wood together with their frass and the wood they fed on, and compared bacterial communities using 16S rRNA gene metabarcoding.

Genus richness was similar in wood and larval guts and slightly lower in frass, showing that larval guts can host communities as diverse as their diet. Bacterial communities overlapped mostly: over 60% of genera were shared by all three sample types, indicating a shared core pool; however, larvae harboured the largest set of unique taxa. Neutral model parameters, which describe the degree of random taxon occurrence within communities, declined from wood to larvae and frass, suggesting that random colonisation dominates in wood whereas host-driven filtering becomes stronger in guts and faeces. Network analysis showed that bacterial networks in wood were simple, whereas those in larvae and frass were more complex. All three sample types shared a (pre)fermentative *Lactobacillus*–*Lactococcus*–*Streptococcus* core, but in larvae this core was further connected to larval-biased taxa such as *Pseudomonas*, *Streptomyces*, *Microbacterium*, *Kocuria*, *Mycobacterium* and especially ZOR0006 (unclassified Bacillota), a strong candidate saproxylophagous symbiont.

Our results indicate that saproxylophagous caterpillars do not simply carry a random pass-through sample of wood microbiota, but assemble structured gut communities containing both shared and strongly larva-specific taxa that may contribute to lignocellulose degradation, detoxification, nutrient supplementation and further microbial filtering within the host, thereby supporting extreme wood-feeding lifestyles in Lepidoptera.

Leaf sodium levels modulate plant defense barriers against phytophagous insects

Ilaria DI LELIO (University of Napoli Federico II - Department of Agricultural Sciences, Portici, Italy, Ilaria.dilelio@unina.it)

Valerio CIRILLO, Paola PUNZO, Giovanni JESU, Maria Giovanna DE LUCA, Marco CEPPARULO, Claudio RUSSO, Nausicaa POLLARO, Antonio MARCIANO, Andrea BECCHIMANZI, Francesco PENNACCHIO, Albino MAGGIO

Abstract

Phytophagous insects substantially reduce crop productivity, and plants mitigate damage through constitutive and inducible defences. An understudied component of these interactions is sodium (Na^+): although Na^+ is not required for growth in many glycophytic crops, it is physiologically important for herbivores, contributing to osmoregulation and neural function. This asymmetry raises the testable possibility that plants may reduce herbivore performance by restricting Na^+ availability in edible tissues; however, mechanistic evidence for inducible Na^+ regulation during attack has been limited.

Using tomato (*Solanum lycopersicum*) and the noctuid *Spodoptera littoralis* as a model, we provide evidence that herbivory is associated with a reproducible redistribution of Na^+ within the plant. Following larval feeding, foliar Na^+ decreases while root Na^+ increases, a pattern consistent with basipetal recirculation through long-distance transport. In parallel, the expression of Na^+ homeostasis/transport genes shifts in a manner indicative of enhanced Na^+ retrieval from aerial tissues and reduced Na^+ delivery and/or retention in leaves, supporting a regulatory “transport switch” during attack.

To evaluate functional consequences, we compared larval performance on plants maintained under standard versus low- Na^+ nutrition. Reduced foliar Na^+ was accompanied by decreased defoliation and impaired larval performance, including slower growth, delayed development and lower survival. Behavioural assays further showed that larvae preferentially fed on Na^+ -richer leaves, indicating that Na^+ availability influences host choice and feeding decisions.

Collectively, these results identify a defence-relevant mechanism whereby herbivory triggers Na^+ reallocation that constrains an essential nutritional resource for insects. More broadly, they suggest that processes typically framed as components of plant salt-stress physiology, Na^+ translocation, redistribution and compartmentalisation, may also have been shaped by selection imposed by herbivores. This sodium-centred axis offers translational opportunities for low-input crop protection and reduced pesticide reliance.

From feeding behavior to population growth: Multilevel impacts of bifenthrin resistance in *Dalbulus maidis* (DeLong & Wolcott, 1923)

Gabriel DIAS (University of São Paulo, Dias.gabriel@usp.br)

Anna Mara MACIEL, Lucas CANUTO, Celso OMOTO, Aline GUIDOLIN

Abstract

The ability of insects to adjust their phenotype in response to environmental factors and the host plant allows them to survive under both biotic and abiotic conditions. The corn leafhopper, *Dalbulus maidis* (DeLong & Wolcott, 1923) (Hemiptera: Cicadellidae), as a specialist herbivore of maize, is adapted to the environments where its host plant occurs. However, in habitats under insecticide selection pressure, resistant individuals are selected. The genotype of resistant insects may compromise their behavior and biology in environments lacking such pressure, thereby contributing to the natural regulation of their populations. This study aimed to evaluate the feeding behavior and some biological traits of *D. maidis* resistant and susceptible to bifenthrin, one of the main pyrethroids used for its control. The feeding behavior was examined using the Electrical Penetration Graph technique, and life table and fertility parameters were evaluated for the resistant, susceptible, and a heterozygous strain, produced by crossing resistant females with susceptible males. The relative cost of resistance and the sex ratio of the strains were also determined, and population dynamics were modeled using a Lefkovich matrix framework. Differences between resistant and susceptible strains were observed in feeding behavior, egg and nymphal development times, egg survival, and female longevity and fertility. Evidence of fitness costs was identified for the resistant and heterozygous strains; both strains also exhibited a higher proportion of females, and this skewed female-to-male ratio influenced population dynamics. An overlap was observed between surviving resistant females from one generation and susceptible males from the subsequent generation; this has direct implications for managing resistant insects in the field. Overall, the results demonstrate that bifenthrin resistance in *Dalbulus maidis* incurs a fitness cost, elucidating key aspects of the species' life-history traits and population dynamics under resistance.

Impact of pea enation mosaic virus 1 and 2 on aphid feeding behavior

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Quentin CHESNAIS, Akiko SUGIO

Abstract

During infection, plant viruses modify plant traits including color, volatiles and metabolites. This can impact interactions of plants with aphids transmitting these viruses, resulting in changes in aphid traits in a way conducive for transmission. The pea aphid (*Acyrtosiphon pisum*) is the most important vector of legume-infecting pea enation mosaic virus (PEMV), a complex of two viruses relying on each other to accomplish the complete infection cycle: the enamovirus PEMV1 requires movement proteins of the umbravirus PEMV2 for systemic plant infection and PEMV2 needs PEMV1 capsids for aphid transmission. However, PEMV2 can be inoculated mechanically and therefore plants can be infected either with PEMV2 alone or with PEMV1+2. This offers the unique possibility to study the contribution of each virus to plant-aphid interactions and consequently to transmission. Peas of the susceptible cultivar Radley and the resistant cultivar Lifter were infected with PEMV2 or with PEMV1+2. Three weeks post-inoculation, aphid population growth was measured and plant choice tests and aphid feeding behavior tests were carried out. Non-infected plants served as a control. The data are currently being analyzed and first results will be presented.

When bacteria strike: behavioral and enzymatic responses of aphids to *Bacillus subtilis*

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Karolina PIECUCH, Tomasz DURAK, Martyna MATEROWSKA, Anna MICHALIK

Abstract

Insects play essential roles in natural and agricultural ecosystems; however, many species act as major crop pests and vectors of plant pathogens. Biological control using natural enemies represents a sustainable and environmentally friendly alternative to chemical insecticides. Bacteria of the genus *Bacillus* are ubiquitous soil inhabitants and are considered safe for humans and non-target organisms, yet numerous studies have demonstrated their entomopathogenic potential against agricultural pests.

This study investigated the effects of *Bacillus subtilis* on mortality, oxidative stress responses, and feeding behavior in three aphid species that are important vectors of plant viruses: *Acyrtosiphon pisum*, *Macrosiphum rosae*, and *Myzus persicae*. Aphids were exposed to several *B. subtilis* strains at different concentrations, and mortality was monitored for 10 days following inoculation.

All tested *B. subtilis* strains significantly increased aphid mortality, with three strains identified as the most effective. No clear relationship was observed between bacterial concentration and mortality, suggesting strain-specific effects. To assess physiological responses, superoxide dismutase (SOD) and catalase (CAT) activities were measured following exposure to the most effective strains. Enzymatic activity increased within the first hours after infection, indicating the induction of oxidative stress. Antioxidant responses differed among species, with significantly higher SOD and CAT activity observed in *M. rosae*. Notably, lower levels of enzymatic defense induced by certain strains were associated with increased aphid mortality.

Feeding behavior was examined using the Electrical Penetration Graph (EPG) technique. Aphids exposed to *B. subtilis* exhibited marked feeding disturbances, including significantly shortened feeding duration on host plants.

Overall, our findings demonstrate that *B. subtilis* infection leads to increased aphid mortality, induces oxidative stress responses, and disrupts feeding behavior, highlighting its potential as a biological control agent for the sustainable management of aphid pests in agriculture.

Project funded by the National Science Centre, grant No. 24 2022/47/B/NZ9/03472.

Biotremology on a tri-trophic system: feeding vibrations of *Liriomyza trifolii* and their role as kairodones

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Abstract

Liriomyza trifolii (Diptera: Agromyzidae) is a leaf-miner larva that causes severe leaf damage, leading to reductions in yield and quality in many crops, such as tomato. Biocontrol of *L. trifolii* is crucial to reduce reliance on chemical pesticides and protect crops. *Diglyphus isaea* (Hymenoptera: Eulophidae) is a parasitoid wasp particularly effective against leaf-miner larvae. The host-searching behavior of *D. isaea* involves the detection of chemical cues from damaged plant tissue. Moreover, some studies suggest that *D. isaea* may detect vibrational cues produced by larval movement within leaf mines. Feeding vibrations could be perceived by parasitoids (kairodones) and used to precisely locate the host (echolocation), but little is known about the possible contribution of vibration detection in the host-searching behavior of *D. isaea*.

In addition, previous studies have reported that chewing vibrations produced by herbivorous insects can induce physiological responses in plants, including the activation of defense pathways and the emission of volatile organic compounds (VOCs). However, the role of leaf-miner feeding vibrations in triggering such plant-mediated responses in tomato plants remains poorly understood.

The aims of this study were therefore: (i) to characterize the feeding vibrations of *L. trifolii* larvae and their propagation through tomato tissues; (ii) to investigate their role in the host-searching behavior of *D. isaea*; and (iii) to assess the potential role of pest-generated vibrations in plant-insect interactions.

The results will provide deeper insight into the propagation of feeding vibrations through a natural substrate and clarify the potential role of substrate-borne vibrations, both in parasitoid host-location and in plant defense responses.

Cereal grasses as alternative host plants for *Rhopalosiphum padi* (L.) in the northwestern and southern parts of the species range in Russia

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Alla VERESHCHAGINA, Andrey FROLOV, Natalia KLIMENKO

Abstract

Changes in the species composition and abundance of grass communities necessitate the control of trophic interactions of *Rhopalosiphum padi* (L.) (Hemiptera: Aphididae), a major pest of cereal crops.

We studied 25 grass species, as host plants of aphids across geographical zones differing in climate and floristic diversity. Reproductive parameters and offspring wing induction were assessed for one southern and two northwestern populations of *R. padi*.

Using a two-factor nonparametric ART ANOVA, we demonstrated significant effects of host plant, regional origin of clones, and their interaction on apterae reproduction ($F = 53.35$, $P\alpha = 2.28 \times 10^{-115}$; $F = 15.93$, $P\alpha = 2.06 \times 10^{-7}$; $F = 3.95$, $P\alpha = 6.60 \times 10^{-15}$ respectively) and on winging formation ($F = 8.27$, $P\alpha = 1.25 \times 10^{-23}$; $F = 5.08$, $P\alpha = 0.0066$; $F = 5.55$, $P\alpha = 9.56 \times 10^{-24}$, respectively).

Application of the Bonferroni correction, Dunn's test allowed us to identify host plant groups that were most favorable (*Poa trivialis*, *Lolium multiflorum*, *Hordeum jubatum*, *H. murinum*) and least favorable (*Leymus arenarius*, *Panicum miliaceum*, *Agrostis tenuis*, *Setaria viridis*, *Elytrigia repens*, *Bromopsis erecta*) for aphid reproduction across three populations. We assessed the adaptation of clones from different geographic zones to host plants with different climatic habitats.

A significant negative correlation between offspring abundance and wing induction in *R. padi* on the plants differing in their food suitability was revealed ($r = -0.49$, $P\alpha = 0.01$). Aphids quickly migrate from unfavorable hosts, where their population sizes were low.

The obtained results can be applied to the management of *R. padi* reproduction and dispersal on alternative hosts in landscapes, as well as to predicting pest status during the breeding of intergeneric cereal hybrids and under changing grass biodiversity.

The work was carried out within the framework of the Russian Science Foundation grant No. 24-76-10009

Agroecological strategies for sustainable management of *Phthorimaea absoluta* in processing tomato: results from a two-year field study in southern Italy

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Domenico Giuseppe CRISPO, Giorgio FORMISANO, Gianluca MELONE, Stefano PARISI, Angelo NAPOLITANO, Valentino Maria GUASTAFERRO, Michelina RUOCCO, Adriana SACCO, Pasquale CASONE, Massimo GIORGINI

Abstract

Reducing chemical inputs in agriculture is essential to limit environmental impacts and preserve water resources. Agroecological crop management offers a sustainable alternative by promoting functional biodiversity both above and below ground. Within this framework, a two-year study (2024–2025) was carried out as part of the PRIMA project “ASTER – Agroecology-inspired Strategies and Tools to Enhance Resilience and Ecosystem Services in Tomato Crop” on a commercial open-field processing tomato farm in Campania, Italy. The study aimed to develop a resilient system to reduce pest pressure, focusing on *Phthorimaea absoluta*, a major pest of processing tomato. The experimental area is intensively cultivated and shows limited spontaneous vegetation. The agroecological approach combined inter-cropping with repellent plants, perimeter flowering strips, and beneficial root symbionts. *Tagetes erecta* was inter-planted along tomato rows for its nematicidal and insect repellent properties. Along the field edges, flowering herbaceous mixtures were sown to provide food and refuge for natural enemies and pollinators, while *Calendula officinalis* and *Verbena hybrida* were grown to support predatory mirids. Selected *Trichoderma* strains were applied to roots to stimulate plant growth and resilience. No insecticides were used. The ASTER plot was compared with a conventional plot managed with synthetic insecticides and lacking vegetation diversification. In 2024, a lower infestation of *P. absoluta* occurred in the agroecological plot, together with a greater abundance and diversity of natural enemies (parasitoid Hymenoptera and predators). No differences in infestation levels of other pests were observed. In 2025, results were consistent with those of the previous year, demonstrating that managing a tomato crop with companion plants, perimeter biodiversity, and root symbionts effectively controls pests while enhancing ecological resilience. These findings support the agroecological approach as an environmentally and economically sustainable strategy for processing tomato production, even in intensively farmed areas.

We're not all the same: Intraspecific differences in the extended phenotype of gall wasps (Cynipidae)

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Abstract

Gall wasps (Cynipidae) and their parasitoids have long been a subject of study in entomology, as a model for interactions between host and parasite. The creation of galls by the host cynipids has been hypothesized to be adaptive against its natural enemies, notably the parasitoids which form a closed biological system with their hosts. This "Enemy Hypothesis" is often used to explain the large diversity in gall morphology, including ornaments, sticky exudates, and complex internal structure, hypothesized to act as defenses against these natural enemies. Yet, despite these structures, many parasitoids act as generalists and are able to overcome the putative defenses of multiple different cynipid species. Studies of this gall-parasitoid relationship have traditionally utilized mean and mode to describe host galls and their defenses. However, gall phenotype can vary considerably within a single cynipid species. Excessive intraspecific variation in gall phenotype may obfuscate the actual relationship between host gall traits and parasitoid community assembly processes. As such, the objective of this study was to examine the degree of intraspecific variation in cynipid wasp galls compared to the level of interspecific variation. Using a more granular system for recording gall traits, we conduct multivariate comparisons of within- and between-species phenotypic variation in putative gall defenses. We demonstrate that considerable variation exists across many gall traits and that caution should be taken in interpreting studies employing more reductive methods of trait assessment.

IPS – Innovative Pest Sustainable Control: Microbiome Responses to Natural Extract Control Formulations in *Ips typographus*

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Martin SCHEBECK, Massimo FACCOLI, Christian STAUFFER, Andrea BATTISTI, Hannes SCHULER

Abstract

Bark beetles account for roughly half of all biotic damage to European forests, and both the frequency and severity of outbreaks have intensified in recent decades, driven by climate change–induced drought stress and storm disturbance. In particular, the Eurasian spruce bark beetle, *Ips typographus*, is regarded as the greatest challenge to forest management in Central and South Europe and has been responsible for killing hundreds of millions of cubic metres of timber across recent outbreaks years. For context, total consumption of industrial roundwood in Europe is around 420 Mm³ per year.

Traditionally, bark beetle management has relied on salvage and sanitation logging, supported by monitoring and modelling of phenological events. More recently, natural plant-derived extracts have shown promise as alternative insecticides; however, their toxic effects on bark beetles remain poorly understood. We hypothesise that the efficacy of these natural extracts may be mediated, at least in part, through disruption or restructuring of the beetle gut microbiome. Increasing evidence suggests that bark beetle fitness, detoxification capacity, and host colonisation success are influenced by symbiotic bacteria and fungi which contribute to nutrient acquisition, degradation of conifer defence compounds, and modulation of host physiology.

We investigate the microbiome of *I. typographus* to evaluate how exposure to innovative formulations, based on plant extracts and mineral trace elements, alters microbial community composition. We characterise bacterial and fungal communities using Illumina short-read amplicon sequencing and Oxford Nanopore long-read sequencing targeting bacterial 16S rRNA genes and fungal ITS regions. This dual-platform approach enables accurate taxonomic assignment whilst improving resolution of closely related taxa.

By linking microbial diversity analyses to treatment assays, this work aims to quantify microbiome shifts following exposure to natural extracts and identify microbial taxa potentially linked to beetle performance, thereby informing the future development of sustainable bark beetle control agents.

Exploring and characterising the role of volatile organic compounds from aromatic plants to disrupt interactions between grapevines and the insect vector, *Scaphoideus titanus*

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Foteini G. PACHALIDOU, Nicolas SAUVION

Abstract

Flavescence dorée (FD) is a devastating phytoplasma disease that threatens European grapevines. The leafhopper *Scaphoideus titanus* is the primary vector of FD, and its management relies only on pesticides. To reduce this reliance, I aim to understand the potential of chemical cues - specifically volatile organic compounds (VOCs) emitted by aromatic plants - to mediate plant defences and disrupt vector behaviour. Unlike most studies focusing on annual crops, during my PhD I will investigate how specific thyme chemotypes influence the behavioural and physiological interactions between grapevine cultivars and *S. titanus*. Thyme chemotypes synthesise large amounts of VOCs that may induce plant defences in receiver plants or directly affect the behaviour of pests. First, I will compare the host suitability of four grapevine cultivars differing in their sensitivity to the vector. Short-term host preference of *S. titanus* will be evaluated using two-choice assays on whole plants and leaf discs. Long-term acceptance and host suitability will be evaluated in cages by measuring different fitness proxies (e.g. survival, developmental time, etc). Second, feeding behaviour of *S. titanus* is a key step in phytoplasma transmission; therefore, I will use electropenetrography (EPG) to evaluate access to and phloem ingestion by *S. titanus* on the four grapevine cultivars and characterise their resistance to the pest. Third, I will assess the effectiveness of aromatic plant VOCs on *S. titanus* behaviour and performance. EPG and performance assays will be repeated on the two extreme grapevine cultivars after pre-exposure to different thyme chemotypes to determine whether aromatic plant VOCs induce resistance in grapevine, leading to altered feeding behaviour or reduced performance of the pest. Overall, my PhD aims to identify cultivar x chemotype combinations capable of improving pest management of *S. titanus*, contributing to more sustainable solutions for modern agriculture.

Effects of drought stress on fall armyworm infestation and oviposition in different maize varieties

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Ismail AYEGBYIN, Astrid GROOT, Mobolade AKINBULUMA

Abstract

The increasing frequency of drought plays an important role in plant-insect interactions, as drought alters plant physiology, herbivore performance and insect preference to host plants. Plants resistant to drought may thus be more or less susceptible to agricultural pests. One of the major invasive pests in sub-Saharan Africa is the fall armyworm *Spodoptera frugiperda*, which poses a major constraint to maize production across the region. We investigated the effects of drought stress on eleven maize (*Zea mays* L.) varieties, comprising five hybrids and six open-pollinated varieties, in relation to their susceptibility to *S. frugiperda* infestation under field and laboratory conditions. In the field, open-pollinated maize varieties had significantly higher foliar damage than the hybrid maize varieties, even though the number of *S. frugiperda* larvae were similar on all maize varieties. The varieties that had been the least and most susceptible to *S. frugiperda* in the field were further tested in the laboratory. Specifically, we assessed the effect of drought on female oviposition behavior by subjecting eight maize varieties to either drought or well-watered treatments. Surprisingly, we found that females laid significantly more egg masses on drought-stressed plants than on well-watered plants in six of the eight tested varieties. These first results indicate a maize variety dependent response in *S. frugiperda* oviposition behavior under varying water conditions. Also, plant vigor traits may influence maize resistance to *S. frugiperda*. How drought may affect plant chemical traits that influence resistance to *S. frugiperda* remains to be investigated.

Buzzing Benefits: Pollinator Diurnal Behaviour and Complementarity Drive Strawberry Yield and Vitamin C

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Sarah ARNOLD, Steven HARTE, Simon SPRINGATE

Abstract

A diverse assemblage of insect visitors can provide functional complementarity within plant pollination due to differences in characteristics such as their physical traits, visitation rate and foraging time of day or year. In a horticultural context, greater functional complementarity may play a crucial role in enhancing fruit yield and quality by improving pollination. We tested whether the identity of the crop pollinators (bumblebee *Bombus terrestris* and hoverfly *Eupeodes corollae*) independently and additively influenced commercial strawberry yield, quality, and nutritional parameters such as vitamin C and sugar concentration. *Fragaria x ananassa* “Malling Champion” plants received pollination treatments of either a) “control”: self-pollination where pollinators were excluded, b) “bee”: bumblebee *Bombus terrestris*, c) “hoverfly”: *Eupeodes corollae*, d) “combined”: both *B. terrestris* and *E. corollae*. Hoverflies and bumblebees exhibited distinct visitation patterns throughout the day, establishing a functional complementary relationship that enhances pollination success and crop output as well as vitamin C concentrations. Strawberries from plants receiving pollination by bumblebees, or bumblebees and hoverflies combined, had higher yields of higher marketable quality. They also had measurably higher vitamin C content than strawberries from plants pollinated by hoverflies alone, or the control (self-pollinating) plants. This study advances our understanding of niche complementarity and its impact on fruit yield and quality. By elucidating the behavioural and temporal dynamics of pollinators, we provide valuable insights for optimizing pollination strategies in agricultural contexts. Our findings highlight the significance of behavioural factors, such as handling time and number of visits, in determining fruit quality.

Aphid-associated bacteria shape both early and long-term dynamics of ant-aphid interactions

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Claire DETRAIN

Abstract

Symbiotic microorganisms can vary widely in their degree of host dependence and in their influence on partners within multitrophic systems. In the plant-aphid-ant system, the bacterial symbiont *Serratia symbiotica* encompasses a wide diversity of strains with contrasted lifestyles. Among them, a free-living gut-associated strain occurs in *Aphis fabae* aphids and can impose fitness costs to its aphid host while providing protection from parasitoids. This bacterial strain has also been detected in the digestive tract of aphid-tending *Lasius niger* ants. Here, we investigated how this bacterium influences both the early establishment and the long-term stability of the ant-aphid mutualism.

Using complementary experimental approaches, we assessed ant responses to *S. symbiotica*-infected aphids through plant-based foraging assays and host-free behavioral tests, disentangling direct bacterial effects from aphid-mediated effects. Olfactometer and feeding assays revealed that ants were attracted at a distance to *S. symbiotica*-infected diets and aphids, while showing reduced food acceptance at high bacterial concentrations. Consistently, infected aphids did not trigger a stronger collective exploitation of honeydew during the early steps of the ant-aphid interaction.

At longer timescales, aphids infected with *S. symbiotica* exhibited reduced population growth, an effect partially mitigated by ant attendance. Furthermore, ants displayed decreased interest in *S. symbiotica*-infected aphid colonies, visiting them less frequently, ingesting less honeydew, and delaying feeding decisions. These results suggest that *S. symbiotica* progressively alters honeydew palatability, likely through changes in its composition.

Overall, our findings indicate that, although *S. symbiotica* may transiently attract ants towards infected aphids during the initial phase of the interaction, it weakens ant exploitation over time and may threaten the persistence of the partnership. This bacterium may therefore contribute to a gradual destabilization of ant-aphid mutualism, with cascading ecological consequences for aphid protection and plant defence.

Aphid-Plant Cross Talk in Gall Formation: Insights into Metabolic Reprogramming and Host Defense Responses

Katarzyna KMIEC (Department of Plant Protection, Faculty of Horticulture and Landscape Architecture, University of Life Sciences in Lublin, Katarzyna.kmiec@up.edu.pl)

Izabela KOT, Hubert SYTYKIEWICZ, Cezary SEMPRUCH, Paweł CZERNIEWICZ, Katarzyna GOLAN

Abstract

Gall-inducing aphids represent a unique group of plant parasites capable of manipulating host physiology and metabolism to create specialized structures that ensure their nutrition and protection. The present study summarizes our long-term research on galling aphids from Eriosomatinae family, and their impact on primary host plants at the physiological and biochemical levels.

Feeding activity of stem mothers significantly disrupted the oxidative balance in host leaves, as reflected by increased hydrogen peroxide accumulation and enhanced activity of antioxidant enzymes. Simultaneously, gall tissues exhibited marked alterations in photosynthetic performance. Our studies confirmed that gall-induced stress correlates with both, local and systemic physiological changes underscoring the spatial complexity of host responses to galling across different aphid–host systems. Biochemical assays demonstrated that aphid-induced galls alter primary metabolism in the host, including the activity of amino acid decarboxylases and the accumulation of biogenic amines — compounds associated with stress tolerance and cell wall modification. Additionally, changes in protein content, phenolic compounds and antioxidant potential reflecting complex adjustments in the host defense system and localized metabolic reprogramming.

These findings provide a comprehensive view of the intricate metabolic responses of woody hosts to gall-inducing aphids. Galls represent functionally specialized plant tissues shaped by intricate molecular crosstalk between the aphid and its host. The consistent findings across different *Ulmus* and *Populus* species indicate that gall formation involves conserved physiological trade-offs, balancing defense activation with the maintenance of metabolic functions that sustain both the plant, and the aphid colony.

Strip cropping soil legacy modifies fertilizer effects on cabbage herbivores

Andi Dirham NASRUDDIN (Wageningen University & Research, Andi.nasruddin@wur.nl)

Misty HU, Maria Rosaria CHIANESE, Luuk CROIJMANS, Dirk VAN APELDOORN, Felix BIANCHI, Erik POELMAN

Abstract

Strip cropping, the practice of growing different crops in side-by-side strips, creates unique soil legacies that can influence how pests interact with plants. We investigated how soil legacies (eight-year monoculture vs. strip cropping) and fertilizer types (organic insect frass vs. synthetic NPK) affect two pest guilds on white cabbage (*Brassica oleracea*): the chewing caterpillar *Pieris brassicae* and the sucking aphid *Brevicoryne brassicae*.

We collected soils from an eight-year field trial with either grass-clover or potato as the preceding crop for cabbage. Strip cropping soil did not directly suppress pests on its own (all main effects $p > 0.5$). However, we found a buffering effect that depended on the previous crop. In grass-clover soils, strip cropping reduced the pest-promoting effect of NPK fertilizer: caterpillar weight gain dropped from +58% in monoculture soils to +35% in strip cropping soils (three-way interaction, FDR $p = 0.030$). This effect did not occur in potato soils and was specific to caterpillars, not aphids ($p > 0.9$). Interface positions where strips meet showed no edge effect (all $p > 0.4$).

Organic insect frass consistently suppressed both pest guilds regardless of soil history. Although nitrogen supply was equalized, frass released it more slowly, resulting in 53% lower leaf nitrogen ($p < 0.001$). Pests on frass-fertilized plants were significantly smaller: aphid colonies were 28% lighter (FDR $p = 0.005$) and caterpillars were 37–45% lighter (FDR $p = 0.002$). Caterpillars on NPK also caused more severe leaf damage (FDR $p = 0.007$), suggesting higher weights came from greater consumption rather than better conversion.

Our findings show that strip cropping legacies can buffer the pest-promoting effects of synthetic fertilizers on caterpillars, while insect frass provides consistent suppression of herbivore performance across both feeding guilds. Combining these strategies offers a complementary approach to sustainable pest management.

#11233

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Spatial Ecology of Aphid Protective Symbionts

Will PAINE (University of Oxford, William.paine@biology.ox.ac.uk)

Ailsa MCLEAN

Abstract

Pea aphids (*Acyrthosiphon pisum*) are infected at intermediate frequencies with endosymbiotic bacteria that offer their host near complete protection from specific parasitoid species at minimal cost. Variation in parasitism risk over time has been thought to explain why these symbionts have not reached fixation in the host population. However, there has been little consideration of variation in space. It is possible unprotected colonies neighbouring protected colonies experience lower parasitism pressure, as their neighbours produce few or no parasitoids. Alternatively, these colonies may see increased parasitism if parasitoids can assess protective status and target unprotected colonies. Using two parasitoid species, *Praon volucre* and *Aphidius ervi*, and their corresponding defensive symbionts, we first assessed whether parasitoids show an oviposition preference when encountering protected and unprotected hosts on the same plant. Then, using experimental foraging assays we evaluated whether parasitoids avoid ovipositing in protected aphid colonies and if unprotected colonies that neighbour protected colonies may benefit from a reduction in parasitism. We found that, when foraging, parasitoids oviposit evenly in protected and unprotected colonies and that the reduced number of parasitoids produced by protected colonies led to a significant reduction in parasitism in neighbouring, unprotected colonies. [AM1.1]Our findings indicate that the spatial ecology of defensive symbionts may have important consequences for their hosts and parasitoids.

Behavior of the pest insect *Caliroa cerasi* (Hymenoptera: Tenthredinidae) in response to endophytic fungi associated with cherry plants.

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Ignacio MATAMALA, Daniel MARTÍNEZ-CISTERNA, Valeria ASECIO-CANCINO, Gabriela GOMEZ, Leonardo BARDEHLE

Abstract

The insect *Caliroa cerasi*, commonly known as the “pear or cherry slug” (Hymenoptera: Tenthredinidae), is one of the main pests affecting cherry trees due to the foliar damage caused by its larvae during the immature stage. This damage compromises plant tissue integrity, reduces photosynthetic capacity, and affects overall plant health, negatively impacting plant development and fruit quality. In particular, key commercial parameters such as fruit size, soluble solids content (°Brix), and ripening stage are affected, directly reducing crop productivity. In this context, the use of endophytic fungi as biological control agents has emerged in the last decade as a promising and environmentally sustainable alternative, especially in horticultural and forage systems. However, their application in fruit crops remains limited worldwide. To contribute to more sustainable pest management strategies and reduce reliance on conventional insecticides, the effects of mycelia and metabolic exudates from endophytic fungi isolated from cherry tissues were evaluated against *C. cerasi* larvae. A total of 23 endophytic fungi were isolated, of which 8 were selected for bioassays by applying them to cherry leaves, which were then offered as food to larvae under controlled conditions. Four isolates caused mortality rates above 30%, while two induced mortality rates exceeding 60% when applied as mycelium on the leaf surface. These isolates also showed an exponential increase in mortality between days 4 and 8 of the assay. Molecular analysis identified the most effective isolates as *Alternaria infectoria* and *Deconica horizontalis*. These results highlight the potential of endophytic fungi as insecticidal agents against *C. cerasi*, although further studies are needed to confirm their effectiveness under field conditions.

Striacosta albicosta (Lepidoptera: Noctuidae) in corn: biology, distribution, management and mitigation of its impacts on mycotoxins production.

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Simon CHAUSSÉ, Tanya COPLEY

Abstract

The western bean cutworm, *Striacosta albicosta* (Lepidoptera: Noctuidae), has emerged as a major lepidopteran pest in corn, in North America, over the past two decades. This species has expanded its geographical range eastward and northward and is now well established across the U.S. Corn Belt and several provinces in Canada. Although this pest is currently restricted to North America, a recent study has shown that other regions in the world, including Europe, also present suitable conditions for its occurrence.

The larvae feed on the reproductive parts of plants, mostly on ears, resulting in significant yield losses. Furthermore, damage caused by larval feeding can also affect the quality, ears being more exposed to pathogens such as *Fusarium* spp. The latter may produce mycotoxins (e.g.: deoxynivalenol) that affect livestock health and performances.

Consequently, the rapid expansion of western bean cutworm and the damage it causes, raise new challenges for integrated pest management (IPM). This presentation will focus on the methods used to monitor and scout the pest. Control options, including foliar insecticides, Bt corn hybrids and trichogrammas will also be presented. Finally, mitigation of mycotoxin risk will be addressed through integrated tactics.

Strong fitness costs of fall armyworm resistance to dual-gene bt maize are magnified on less-suitable host-crop cultivars

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Clebson DOS SANTOS TAVARES, Eliseu José GUEDES PEREIRA

Abstract

We examined the fitness costs of resistance to transgenic Cry1A.105+Cry2Ab2 *Bacillus thuringiensis* (Bt) maize in the fall armyworm, *Spodoptera frugiperda*, a globally invasive pest species. Using Bt-resistant and -susceptible populations of similar genetic backgrounds, we compared insect life-history traits and population growth rates on the foliage of Bt or non-Bt cultivars of maize, soybean, and cotton. We found that (i) the resistance alleles led to a major reduction in insect fitness on seven of the eight cultivars of three host crops studied; (ii) developmental time was the life-history trait that accounted for most of the fitness variation of the armyworm, and (iii) the magnitude of fitness reduction of the resistant individuals was stronger on cotton foliage, on which the insects did not pass the resistance alleles to subsequent generations. These results show that fall armyworm resistance to Cry1A.105+Cry2Ab2-expressing Bt maize comes with strong fitness costs, which were magnified on less-suitable host plants for the insects. Thus, natural selection may help maintain or even restore the insect susceptibility to the pesticidal proteins and perhaps is a significant factor helping manage fall armyworm resistance to Cry1A.105+Cry2Ab2 Bt maize. These findings indicate that fitness costs of insect resistance to multi-toxin Bt crops can be strong, and host plants or conditions that magnify the fitness differential of susceptible insects could be specifically deployed with refuge to improve resistance management to Bt crops.

Manipulation of host plant biology by the pea aphid, *Acyrtosiphon pisum*

Akiko SUGIO (INRAE IGEPP, Akiko.sugio@inrae.fr)

Abstract

The pea aphid (*Acyrtosiphon pisum*) forms at least 15 biotypes, each of which is specialized to feed on one or a few species of legumes and cannot feed on others. For example, the pea biotype feeds and reproduces on peas, but the alfalfa biotype cannot thrive on peas. We hypothesized that the pea-adapted biotype of *A. pisum* (hereafter, pea biotype) secretes a set of salivary proteins that alter the biology of the pea plant and suppresses its defence against the aphids. We tested this hypothesis by a co-infestation experiment of the pea and alfalfa biotypes and demonstrated that the alfalfa biotype increases its phloem feeding time and reproduces better on pea when the pea biotype was present. We also found that the pea biotype induces massive transcriptional reprogramming in peas, which may contribute to the suppression of pea immunity to the aphids. Untargeted metabolomics analyses also showed that infestation of pea biotype changes the quantities of certain pea metabolites.

Some aphid salivary proteins have been shown to interfere with plant immunity. To identify salivary proteins that suppress pea immunity, we did transcriptomics of salivary glands, created a catalog of *A. pisum* salivary genes and examined the transcription levels of these proteins in the pea and alfalfa biotypes. We identified candidate salivary genes that are highly expressed in the pea biotype, suggesting their importance in manipulating pea biology. Although we found some salivary proteins, Ap25 and Ap4, whose ectopic expression increased the fecundity of the pea biotype on pea, we have not found salivary proteins that help the alfalfa biotype feed on pea. Characterization of Ap25 and Ap4 protein functions and new plan of identifying pea-biotype specific salivary proteins will be presented.

#14765

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Soil-dwelling insects as drivers of rhizosphere microbial dynamics

Ayşe TORRES AGAMA (Field Crops Central Research Institute, Aysetorresagama@gmail.com)

Abstract

Soil-dwelling and root-associated insects are usually treated as either pests or biological control agents, but this split does not reflect what they actually do in the rhizosphere. Root feeding changes exudate chemistry and reshapes local microbial communities. In some cases this supports pathogen development, in others it favours beneficial microbes, depending on the plant-insect system and soil conditions. Insect activity is not only physical damage but also a direct driver of microbiome composition. Beyond feeding, soil-active insects also move through the soil and can transport microorganisms, a role that is largely overlooked in crop protection research. This also means even insects not used in biological control may still influence plant health indirectly by modifying the microbial environment around roots. Putting insects inside plant-microbiome interactions, rather than outside them, helps explain inconsistent crop responses and gives a more realistic basis for improving biological control in agricultural systems.

#11701

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Effect of plant-plant comepetition on plant defence and insect communities

Laura ZUIDEMA (Wageningen University & Research, Laura.zuidema@wur.nl)

Gabriel JOACHIM, Maximilien ADAM, Erik POELMAN

Abstract

In order to maximize fitness, plants have to balance growth and defence in a way that allows them to outcompete neighbouring plants and mitigate effects of herbivory. It is commonly believed that the metabolic cost of defence results in a decrease of growth and reproduction and vice versa. This concept is referred to as the growth-defence trade-off. To fully understand the balance between growth and defence in plants, the ecological costs of defence need to be considered. These are costs related to the complex interactions between organisms in the entire ecological context of the plant, such as neighbouring plants, herbivores, natural enemies of those herbivores and pollinators. In this field study, *Brassica nigra* plants were grown in a competitive environment and their growth, reproduction and defence responses were assessed. In addition, the herbivore and natural enemy communities of these plants were monitored. We found that plants that are growing in a competitive environment grow taller, finish their growth cycle much quicker, and produce fewer seeds compared to control plants. Additionally, these plants attract a different composition of the community of herbivores and natural enemies. Plant competition also affected the top down control of herbivores by parasitoids, which suggests that plant-plant competition also affects indirect defence. This field study showed that plants growing under competition change their balance between growth and defence against insects, resulting in different interactions with their environment.

Female-biased captures of Calliphoridae in small-bait traps: Patterns across species and environmental variation

Denis BOUDREAU (Université de Moncton, Edb5864@umoncton.ca)

Lena LUTZ, Gaétan MOREAU

Abstract

Traps are essential tools for insect ecologists, allowing the characterization of population and community dynamics. They are not free of biases, however. For instance, traps baited with decaying animal tissue attract necrophagous flies, particularly members of the family Calliphoridae. One frequently noted bias is its tendency to trap more females than males. To investigate this, baited traps were deployed in Germany and Canada to 1) validate the apparent female bias across the Calliphoridae family, and 2) assess whether sex bias varies among species and in response to abiotic and biotic environmental variables. Sampling was carried out from spring to late fall in both regions to capture most of their period of activity. Sex was determined based on eye size. Results from the Wilcoxon test indicated that the ranked abundance of females was consistently greater than that of males. Female abundance was strongly related to total family density whereas male abundance was less so, as indicated by higher mean absolute percentage errors in regression models for males than females. Analyses of sex-specific counts relative to total abundance revealed two distinct patterns: female abundance followed a power-law relationship, whereas males increased non-linearly. At the species level, G-tests revealed that sex ratio was not consistent among common species, with female proportions ranging from 64-93% in Canada and 67-90% in Germany. Logistic regression models relating female proportion to environmental variables revealed species-specific responses. Seasonality and wind speed effects were common. Wind effects were generally consistent, but weak, whereas seasonal effects varied substantially among species. The strongest patterns observed were pronounced negative effects of family density on female proportions in Calliphora, which were consistent across all species within the genus. The implications of the results are discussed in terms of their practical relevance to forensic entomology and their fundamental contributions to ecology.

Invasion?resistance in experimental Drosophilidae communities: native species limit *Drosophila suzukii* invasion success

Méghan BOULEMBERT (Université de Picardie Jules Verne d'Amiens - Unité de recherche EDYSAN - BIPE, Boulembert.m@gmail.com)

Joan LAURENT, Jules POMART, Aude COUTY, Patrice ESLIN, Olivier CHABRERIE

Abstract

Drosophila suzukii is a fruit fly native to Southeast Asia that has become invasive on most continents. Unlike other Drosophilidae, this highly polyphagous and pioneer fly can lay eggs early in healthy and ripening fruits, causing major economic losses. It also disrupts ecosystem functioning by preempting fruit resources before native species and reducing fruit attractiveness and dispersal. During colder seasons, *D. suzukii* is forced to rely primarily on suboptimal resources such as rotten apples. However, little is known about its interactions with native Drosophilidae species that commonly use these autumnal food reservoirs.

This study experimentally tested the biotic resistance of the native Drosophilidae community to *D. suzukii* invasion using microcosms of decaying apples. We monitored population dynamics of *D. suzukii* and native species (*Drosophila immigrans*, *Drosophila melanogaster* and *Drosophila subobscura*) in decaying apples exposed to 24 adult flies under controlled conditions. Three treatments were tested: (1) *D. suzukii* alone in the fruits, (2) the three native species together and (3) *D. suzukii* with the native flies. Fly composition was monitored up to 16 weeks in microcosms after initial infestation.

Apple represented a suitable reservoir for *D. suzukii* when alone, yielding an average of 54 individuals per fruit. However, its abundance rapidly declined from week 6 in the presence of natives, averaging 1.8 adults per fruits versus 15 when alone. *D. melanogaster* was the only native species exhibiting reduced abundance in the presence of *D. suzukii* and showing an overlap of functional traits. Initially, the invasive species appeared to have facilitated the development of native species by accelerating the decomposition of apples, but this positive effect was subsequently reversed, due to rapid resource depletion. These results offer new perspectives for the conservative biological control of *D. suzukii* by native communities.

A Mechanistic, Spatially Explicit Model of Predator–Pest Dynamics in Heterogeneous Agricultural Landscapes

Andrew CORBETT (University of California, Davis, Andcorbett@ucdavis.edu)

Abstract

Landscape heterogeneity is widely assumed to enhance natural pest control, yet recent meta analyses report inconsistent or even contradictory effects. To clarify the mechanisms underlying these variable outcomes, I developed a mechanistic, spatially explicit model of predator–pest dynamics that enables controlled *in silico* experiments on landscape structure, resource distribution, and species traits. The framework couples a stochastic dispersal kernel with a two dimensional reaction–diffusion system to represent both trivial movement and infrequent long distance dispersal. Adult predator energetics are modelled explicitly, with energy and egg reserves determining movement, survival, and oviposition, allowing resource availability to shape colonization success.

Pest population growth and predation occur on an explicit, dynamically growing crop leaf surface area to capture the temporal structure of annual cropping systems. Predators overwinter in natural habitat patches, which are systematically varied in percent cover, patch size, and spatial configuration. Pest insects and alternate prey overwinter in field margins, and the crop may or may not provide floral resources or alternative prey during the season.

Simulation experiments on 10×10 km landscapes, resolved at 10×10 m, reproduce several of the divergent empirical responses reported in the literature. Preliminary results indicate that although landscape structure can substantially influence pest load, its effect is strongly mediated by the resource environment encountered by predators upon crop entry, including the abundance of the pest. In particular, supplemental prey and floral resources can either amplify or suppress the influence of landscape heterogeneity by altering predator persistence and reproductive output.

These findings suggest that natural control in agricultural landscapes emerges from a nonlinear interaction between landscape configuration, resource availability, and pest population dynamics. Mechanistic models that integrate these components may help reconcile conflicting empirical results and guide the design of landscapes that reliably support biological control.

Investigating factors influencing the outbreak of woolly apple aphid *Eriosoma lanigerum* in apple orchards in South Tyrol (Northern Italy)

Matilde FRASCARI (Free University of Bozen-Bolzano, Mfrascari@unibz.it)

Matilde FRASCARI, Sara BORTOLINI, Martina FALAGIARDA, Manfred WOLF, Hannes SCHULER

Abstract

The woolly apple aphid (WAA), *Eriosoma lanigerum* (Hausmann) (Hemiptera: Aphididae), is a pest threatening apple production by causing a damage to roots and limbs that can significantly weaken the plants. This aphid species currently represents a major challenge for apple growers of many regions of the world especially because of a limited availability of control strategies or their low efficacy. The attack varies greatly from orchard to orchard, and only a few of the factors that may be involved have been studied. Many of the common agronomic practices used in apple orchards, for example, have not been investigated as factors related to the outbreak of this insect. This project aims to identify factors, in particular abiotic factors and agronomic practices, influencing the infestation of the woolly apple aphid and the activity of its host-specific parasitoid *Aphelinus mali* (Haldeman) (Hymenoptera: Aphelinidae), through systematic surveys in apple orchards located in South Tyrol: an important alpine apple-producing area. The data collected, concerning individual factors and degrees of infestation, parasitization and damage in each field, will then be analysed through a comprehensive multifactorial analysis. A model, specific to the South Tyrol region, will be developed with the aim of predicting the incidence of aphid infestation, parasitization and the extent of the final damage in orchards based on abiotic factors and agronomic practices used.

#12050

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Temporal morphological changes in carabid beetle communities in agroecosystems over 3 decades

Yohann GRAUX (IRBI, Yohann.graux@univ-tours.fr)

Sabrina GABA, Stéphane BOYER, Vincent BRETAGNOLLE

Abstract

Insect body size is a key ecological trait. In carabid beetles, morphometric variations may reflect shifts in ecological niche in response to environmental fluctuations. This study investigates temporal changes in carabid beetles monitoring eight morphological traits across more than 1,600 individuals from ten carabid species sampled in oilseed rape (OSR) between 2001 and 2025.

Despite a relatively short time span (25 years), significant changes in morphometric traits were detected in several species. These patterns suggest potential increases in mobility and shifts in prey spectra, likely driven by intense disturbances. Additionally, traits did not vary uniformly, indicating potential changes in body shape over time. Further analyses are required to better understand the environmental drivers underlying these morphometric dynamics.

Diversity and population dynamics of some predatory spiders from district Loralai, Balochistan, Pakistan.

Bilal Saeed KHAN (Department of Entomology, University of Agriculture, Faisalabad, Pakistan., Dr.bilal.saeed@uaf.edu.pk)

Abstract

A complete survey was carried out in four distinct of District Loralai, Baluchistan, Pakistan. Spiders were collected by using different methods such as pitfall traps, hand picking, beat sheet and sweep netting. Collectively a total of 13,894 specimens representing 50 species, 41 genera and 18 families of predatory spiders were recorded. Lycosidae was the most diverse and abundant family contributing 20% of total species richness ($n=12$) followed by Salticidae (11%; $n=4$) while Theraphosidae and Euagridae were least abundant. Menhinick's index indicated the highest species richness in Kili Zengiwal (0.6512), while Margalef's index showed the highest richness in Kach Ahmaqzai (5.334). Shannon-Weiner index recorded the highest diversity of predatory spiders in Kach Ahmaqzai (3.465), whereas Simpson's index emphasised a dominating report as highest value in Kili Zengiwal (0.9635). Pielou's evenness index identified Barnema as the site with the highest species evenness (0.9032). Spider abundance was highest in July while lowest in May and September. There was a positive association between environmental factors and functional spider density particularly with minimum temperature in each locality i.e. Kach Ahmaqzai (0.612**), Kili Sagar (0.621**), Kili Zengiwal (0.626**) and Barnema (0.690**) while other factors have not strong influence on predatory spiders. Landscape diversity and remoteness from urban areas played a key role in determining spider species richness while altitude negatively impacts species richness (-0.0025 , $p=0.025^*$) and abundance (-0.0027 , $p<0.05$). These findings provide valuable insight into diversity, distribution and environmental associations of predatory spiders that highlighted their ecological potential as biocontrol agents from Baluchistan, Pakistan.

Species diversity, population dynamics, and distribution of *Dacus* fruit flies on cucurbits in South Africa

Nomathamsanqa MKHIZE (Agricultural Research Council, Mkhizen@arc.agric.za)

Zolile MASEKO, Pia ADDISON

Abstract

Fruit flies of the genus *Dacus* (Diptera: Tephritidae) are major pests of cucurbit crops (Cucurbitales: Cucurbitaceae) and pose a significant threat to food security and trade. Yield losses of 30–100% have been reported in cucurbit-producing regions due to larval infestations, necessitating costly phytosanitary interventions. The current control measures include attractant-baited traps and other Integrated Pest Management (IPM) strategies, but their effectiveness in controlling *Dacus* populations remains inadequately assessed. This study aims to characterize *Dacus* fruit fly species diversity, population dynamics, genetic diversity, and distribution across South African cucurbit production areas. Data will be collected for two years (2025-2027) using McPhail and sensus traps baited with male lures (Cuelure, Zingerone, and Methyl-eugenol) and food baits (Questlure). Continuous monitoring data will be collected from six identified cucurbit-growing farms in the North-West province, while ad-hoc surveys will be performed nationwide. Specific objectives are to (i) monitor population fluctuations using lure and food attractant-based trapping systems and assess the role of environmental variables in population trends; (ii) employ molecular techniques to evaluate genetic diversity and potential cryptic species of *Dacus* species; (iii) determine host preference and critical life stages susceptible to control measures under controlled temperature conditions; and (iv) update distribution maps to inform pest risk analyses. The findings will serve as a foundation for improving monitoring and control strategies to mitigate these pests' economic and ecological impact. The outcomes will support evidence-based pest management and enhance sustainable control methods. Ultimately, this research will provide critical insights into *Dacus* fruit flies' diversity, ecology, geography, and management, facilitating more effective mitigation strategies to safeguard cucurbit production and international trade.

Preliminary results: 700 fruit fly specimens have been recorded in three cucurbit farms since March 2025.

First evidence of parthenogenesis in Byrrhoidea: The case of *Cytilus sericeus*

Sára ŠEBESTOVÁ (Department of Biology and Ecology, Faculty of Science, University of Ostrava, Czechia, Sarasebestova745@seznam.cz)

Sára ŠEBESTOVÁ, Petr PYSZKO, Kateřina CZAJOVÁ, Oto KALÁB, Veronika LABAJOVÁ, Tomáš PAVLICA, Michaela DRGOVÁ, Pavel DROZD

Abstract

Although parthenogenesis is known in Coleoptera, it remains relatively uncommon (except in Curculionidae) and has not yet been documented within the superfamily Byrrhoidea. During earlier research focused on the trophic ecology of Byrrhidae, we observed that populations of *Cytilus sericeus* (Coleoptera: Byrrhidae) in Czechia consisted exclusively of females. With subsequent rearing in laboratory, we confirmed parthenogenesis. Available data from genetic datasets revealed higher genetic variability among specimens from Northern Europe and the examination of additional material from entomologists confirmed the presence of males in this region. In contrast, available data from the rest of Europe showed lower genetic variability and no evidence of males, but detailed information is limited. As few males have been reported in Czechia from entomological collections summarized by Boukal (2017), this country appears suitable for studying patterns of sexual and asexual populations in *C. sericeus*.

The aims of this study were to (i) obtain environmental data for all records of this species collected in Czechia and correlate these variables with male occurrence. Based on these results (ii) identify relevant regions for targeted field sampling and laboratory rearing to confirm reproductive modes, (iii) assess the presence of potential parthenogenesis-associated bacterial endosymbionts (Rickettsiales), using metabarcoding, and (iv) compare basic cytogenetic characteristics between reproductive modes. We compiled a database of 1,056 records, including 44 males, extracted environmental variables for each locality using the CHELSA dataset, conducted targeted field sampling in ten regions, and initiated metabarcoding and karyological analyses.

Our results show that male occurrence in Czechia is significantly associated with mountainous regions and isothermality. However sexual populations were confirmed exclusively in one of six studied mountain ranges (the Ore Mountains) and in none of four studied lowland regions. These results show ecological patterns in the distribution of reproductive modes, while cytogenetic and metabarcoding analyses are currently ongoing.

Cross-Habitat Movement of the Olive Fly in Mediterranean Mosaics: Evidence for Forest-Associated Thermal Sheltering

Giorgos STAVRIANAKIS (Laboratory of Rural Geography and Precision Farming Systems, Department of Geography, University of the Aegean, G.stavrianakis@aegean.gr)

Stratis SENTAS, Panagiotis DEMESIOTIS, Thanasis KIZOS

Abstract

The olive fly (*Bactrocera oleae*) is a significant insect pest of olive cultivation across Mediterranean regions, threatening both yield and product quality. Traditional management approaches largely concentrate on within grove dynamics. They often overlook the role of surrounding non-agricultural habitats in shaping pest behavior and population persistence. Under climate change, characterized by rising temperatures and more frequent heat extremes, understanding how landscape heterogeneity and microclimatic variation influence olive fly dispersal and survival becomes increasingly important.

This study investigates the dispersal of *B. oleae* beyond olive groves and into adjacent pine forest habitats within a Mediterranean mosaic landscape on Lesbos Island, Greece. McPhail traps were placed along a gradient from grove interior to forest interior (up to 300 m), while temperature was monitored at each sampling point. We assessed spatial patterns of fly abundance and their relationship with microclimate during summer and autumn (2024).

The results of this pilot study showed that olive fly presence was consistently recorded within groves, along grove–forest borders, and up to 100 m inside pine forests, while captures at 300 m were negligible. Forested sites exhibited cooler thermal regimes compared to groves, with a higher proportion of hours within temperatures favorable for olive fly activity and survival ($23^{\circ}\text{C} < T < 31^{\circ}\text{C}$). These findings suggest that nearby forests can function as microclimatic refugia, while deeper forest interiors may act as ecological barriers.

The results challenge the perception of non-agricultural habitats as irrelevant to olive fly management. The importance of adopting an agroecological perspective that integrates cross-habitat interactions, is also highlighted. Incorporating landscape structure and microclimate buffering into integrated pest management strategies may enhance their effectiveness under future climate scenarios, contributing to more resilient and sustainable olive production systems.

How to eradicate an invasive forest pest without clear-cutting

Hongyu SUN (INRAe, Hongyu.sun@inrae.fr)

Christelle ROBINET, Hervé JACTEL, Monique MOURITS, Manuela BRANCO, Wopke VAN DER WERF, Bob DOUMA

Abstract

1. The pine wood nematode (PWN), *Bursaphelenchus xylophilus*, is an invasive species causing high pine mortality in invaded areas outside its native range. European Union (EU) regulations stipulate a 500-m-radius clear-cutting around infested trees to prevent the spread of PWN by the vector beetle *Monochamus galloprovincialis*, yet this measure is costly and not fully effective.

2. We used an individual-based model describing the dispersal of the insect vector and its transmission of PWN, to compare the cost-effectiveness of clear-cutting and selective cutting of only the PWN-infested trees for three different methods for surveillance: visual ground surveys, aerial surveys, and insect trap networks.

3. Both strategies eradicated PWN if intensive aerial surveillance was conducted at a time that all infested trees showed symptoms. Selective cutting reduced costs by up to a factor 200 compared to clear-cutting, mainly due to the preservation of healthy trees. Additionally, selective cutting reduces environmental and societal costs. However eradication is unlikely if symptom expression of infectious trees is incomplete at the time of survey.

4. Policy implications. The results show that selective cutting applied together with modern remote sensing surveillance methods is an environmentally friendly alternative to the mandatory clear-cutting for PWN control in the EU.

Environmental drivers of *Wolbachia* infection and the genomic basis of its dual role in Italian populations of *Philaenus spumarius*

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Valentino Maria GUASTAFERRO, Giorgio FORMISANO, Lorenza ALBANO, Domenico Giuseppe CRISPO, Gianluca MELONE, Adriana SACCO, Luigi IODICE, Marco GEBIOLA

Abstract

The cosmopolitan spittlebug *Philaenus spumarius* has become a serious pest in Europe as the main vector of the dangerous plant pathogen *Xylella fastidiosa*. *Wolbachia* are bacterial symbionts of many insects, able to spread within host populations as reproductive manipulators or by mutualistic relationships. *Philaenus spumarius* is also infected by *Wolbachia*, and based on COI gene sequencing, the populations of southern and central Italy belong to the eastern-Mediterranean (East-Med) lineage, while those of northern Italy are predominantly represented by the western Mediterranean (West-Med) lineage. The north-eastern (NE) lineage is instead confined to the Alpine arc at high altitudes. *Wolbachia* infection rates were assessed in relation to the geographical distribution (longitude and altitude) and genetic diversity of Italian populations of *P. spumarius*. In northern Italy, high *Wolbachia* infection rates occurred in NE and West-Med populations at 1200-2000 m asl; at low altitude, *Wolbachia* prevalence in West-Med populations was low. In Central Italy, *Wolbachia* showed high infection rates in East-Med populations at 1000-1500 m asl. *Wolbachia* was absent in East-Med populations of southern Italy, regardless of altitude. Our results exclude host genotype as a factor influencing *Wolbachia* spreading and suggest that environmental factors play a key role in shaping the symbiont distribution, favored by cold temperatures. We also assembled the draft genome of one of the most frequent *Wolbachia* strain (supergroup B) of *P. spumarius*. Two hypothetical proteins were identified as potential homologs of the cifA and cifB cytoplasmic incompatibility factors: one fully matched the antitoxin structure (7ESX_B), the other perfectly aligned with a ULP protease domain protein (7FIW_A). KEGG annotation revealed genes involved in riboflavin, folate, and lysine precursor biosynthesis, suggesting additional metabolic functions in this genome. Genomic data suggest that *Wolbachia* may spread by inducing cytoplasmic incompatibility and/or by establishing a beneficial relationship with *P. spumarius* under low temperature regimes.

Population-level variations in *Macrosiphum rosae* microbiome

Jagoda KAMINSKA (Jagiellonian University Faculty of Biology, Jagoda8.kaminska@student.uj.edu.pl)

Roma DURAK, Veronika ANDRIIENKO, Małgorzata SEKUŁA, Anna MICHALIK

Abstract

Symbiotic relationships drive key evolutionary processes, including the emergence of eukaryotic cells, plant colonization of land, and insect diversification. Insects rely on symbionts to exploit nutrient-poor diets and colonize novel ecological niches. Given their crucial ecological role, understanding insect–microbe interactions is increasingly important, especially under climate change.

Aphids (superfamily Aphidoidea) are model organisms for studying insect symbiosis due to their obligate association with *Buchnera aphidicola* and rapid population growth. They are also important ecologically and economically—as pests, honeydew producers, and vectors of plant viruses. While *Buchnera* is well characterized, co-obligatory and facultative symbionts are more variable in occurrence and function and remain poorly explored.

We investigated microbiome variation across populations of *Macrosiphum rosae* using high-throughput amplicon sequencing, metagenomics, and microscopy. Molecular analyses of over 130 aphids from nine populations revealed variation in microbiome composition, even among individuals collected from the same host plant. All specimens harbored *Buchnera aphidicola*, which consistently co-resided with *Serratia symbiotica*. Both symbionts were localized in bacteriocytes, specialized cells that maintain, protect and control symbionts. In some populations, facultative symbionts - *Regiella* and *Rickettsiales* were also present.

Metagenomic analyses supported amplicon results and revealed differences in GC content: *Rickettsiales* resembled *Buchnera*, while *Regiella* was closer to the more recently acquired *Serratia*. Genome annotation showed that *Buchnera* retained a consistent set of amino acid biosynthesis genes across populations, sharing some pathways with *Serratia*.

These findings demonstrate that aphid microbiomes are dynamic at the population level, with facultative symbionts likely contributing to ecological adaptability. Understanding these interactions provides insights into symbiont-mediated mechanisms affecting aphid biology and may inform sustainable pest management strategies.

Host trees partially explain the complex bacterial communities of two threatened saproxylic beetles

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Abstract

Microorganisms are integral to ecosystem functioning and host adaptation, yet the understanding of microbiomes in diverse beetle taxa remains limited. We conducted a comprehensive study to investigate the microbial composition of two red flat bark beetle species, *Cucujus haematodes* and *C. cinnaberinus*, and assessed the influence of host taxonomic relatedness and host tree species on their microbiomes. We sampled 67 larvae of two *Cucujus* taxa taken from 11 host tree species. 16S rRNA V4 fragment sequencing revealed distinct microbial communities associated with each *Cucujus* species, with host tree species significantly influencing microbiome composition. Alpha and beta diversity metrics indicated significant differences between microbial communities in both beetle and host tree species. Principal component analysis indicated distinct clustering based on host tree species but not for beetle species. This overlap could be attributed to the similar ecology of both *Cucujus* species. The detection of various bacteria, among which some have already been reported in saproxylophagous beetles, suggests that the red flat bark beetles ingest the bacteria via foraging on other wood-dwelling invertebrates. Our findings show the complex interplay between host taxonomy, microhabitat and microbial composition in *Cucujus*, providing insights into their ecological roles and conservation implications. This research helps to fill the gap in understanding the microbial dynamics of saproxylic beetles, sheds light on factors shaping their microbiomes and highlights the importance of considering both host species and environmental conditions when studying insect-microbe interactions in forest ecosystems.

Differential landscape effects on the microbiota of primitively and fully eusocial pollinators

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Marco FALASCO, Laura MARETTO, Lorenzo MARINI, Luca MAZZON

Abstract

Microbiomes play a key role in many insects, including hymenopteran pollinators, which rely on their gut microbiota for nutrition, health, and immune function. Consequently, factors that alter the microbial associations may have detrimental effects on host fitness. Among these factors, landscape may represent an important contributor to the composition and diversity of insect-associated microbiota, particularly by determining the availability and composition of floral resources that act as microbial reservoirs. Furthermore, because pollinators' microbiota can be transmitted vertically, horizontally, or acquired from the environment, host sociality is expected to influence the composition and stability of these bacterial communities.

In this study, we investigated the microbiota of two key European pollinators, the primitively eusocial *Halictus scabiosae* and the fully eusocial *Bombus pascuorum*, across contrasting landscapes in five European countries. A metabarcoding approach was used to study the microbiota of a total of 1242 samples.

Results showed that the microbiota of *B. pascuorum* is dominated by a stable core bacterial community that appears unaffected by landscape composition and only weakly associated with geographic location ($R^2 = 0.003$, $p = 0.047$, α -diversity metrics $p < 0.01$). Additionally, analyses restricted to Italian *B. pascuorum* populations revealed significant differences in microbiota composition between early- and late-season individuals. In *H. scabiosae*, by contrast, the microbiota is characterized by a narrower core community, with both landscape composition and geographic location associated with variation in bacterial community structure (α - and β -diversity metrics, $p < 0.05$).

These findings suggest that host sociality may shape how landscape influences pollinator microbiota and highlight the importance of considering landscape composition and seasonal variation in pollinator conservation strategies.

The effect of host diet and phylogeny on the microbial communities associated with hoverflies

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Gunilla STÅHLS, Anne DUPLOUY

Abstract

The effect of host diet and phylogeny on the microbial communities associated with hoverflies

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Host-associated microbial communities (i.e., microbiota) can play a key role in pollinator health and conservation. Amidst the global decline of pollinators, research on the microbiota of pollinators has grown, but some key pollinator groups remain understudied. Hoverflies are a unique and highly diverse group of true flies, providing diverse, important ecosystem services. While adults are regarded as the second most important group of pollinators, hoverfly larvae provide natural crop protection and nutrient recycling. Although hoverflies face similar threats to bees, they remain underrepresented in research on pollinators, especially on the characterization of their microbiota and their role in the flies fitness. Here, we aim to fill this gap. Using the metabarcoding approach of the 16S rRNA and ITS genes, we aimed to characterize the richness and composition of the bacterial and fungal microbial communities associated with a selection of 22 Finnish hoverfly species. We questioned whether host phylogeny and diet influenced these microbial communities, and expected that the different hoverfly species would harbor specific symbiotic microbes potentially involved in the digestion of their respective diet types. These findings generate new insights into hoverfly biology and the main drivers of insect microbiota diversity.

Keywords: Symbionts, Syrphidae, Host- microbe interactions, Natural predators, Saprophagous larvae

WICKED – Wolbachia Infection: Corrupted Killers Effects on *Drosophila suzukii*

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Giulia FIORENZA, Martina PAVESI, Giuliano GASPERI, Maria Vittoria MANCINI, Francesco LESCAI, Alberta PINNOLA, Anna Rodolfa MALACRIDA,
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Abstract

Drosophila suzukii is an invasive pest from South-Eastern Asia that has successfully colonized most temperate regions worldwide. This fly represents a major threat to soft fruits, particularly cherries, strawberries, and blueberries. Current control strategies are challenging and rely heavily on broad-spectrum, non-eco-friendly insecticides. The endosymbiont *Wolbachia* represents a promising tool for biocontrol. However, wSuz, the native strain harboured by *D. suzukii*, does not induce Cytoplasmic Incompatibility (CI). Consequently, we are investigating the evolutionary maintenance of wSuz in the absence of reproductive manipulation, specifically exploring potential fitness advantages related to overwintering survival both performing field and laboratory investigations. Concurrently, we aim to understand the mechanisms behind the lack of CI to engineer effective control strategies. To this end, we are analysing the protein structures and molecular interactions of the CI factors (Cifs). Preliminary *in silico* results suggest that, despite high sequence similarity with the CI-inducing wMel strain (harboured in *D. melanogaster*), there are structural differences in the interaction dynamics between CI factors.

A genomic perspective on the evolution of microbial nutritional symbiosis in Triatominae bugs

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Marie MERLE, Elaine FOLLY-RAMOS, Carlos Eduardo ALMEIDA, Myriam HARRY, Jonathan FILÉE

Abstract

Triatominae bugs, the main vectors of the Chagas disease, rely on a microbial nutritional symbiosis that supplies B-vitamins missing from their nutrient-poor hematophagous diet. *Rhodococcus* bacteria have so far been identified as supporting this symbiosis, but diverse metabarcoding analyses have revealed potential additional symbionts for which genomic data and thus potential metabolic capabilities are lacking.

To fill this gap, we generated metagenomic assemblies for 14 Triatominae species (13 *Rhodnius*, 1 *Triatoma*) and recovered 15 complete bacterial genomes belonging to four different genera (*Rhododoccus*, *Wolbachia*, *Symbiopectobacterium* and *Arsenophonus*) infecting nine Triatominae species (8 *Rhodnius*, 1 *Triatoma*). We identified five cases of co-infection, including one involving two distinct *Arsenophonus* symbionts, one of which displaying typical signatures of extensive genome degradation.

For each bacterial genus, symbiont genome phylogenies showed that Triatominae symbiont sequences clustered together in a monophyletic clade, supporting a common (vertical) origin. We used these genomes to annotate vitamin B metabolic genes and predict that most symbionts have incomplete vitamin B pathways, revealing possible cases of metabolic complementation between co-infecting symbionts.

Finally, we searched for bacterial genes laterally transferred into the insect host genomes and found that most of Triatominae genomes harbour numerous genes from all four bacterial genera described above, including those for which a symbiont genome assembly have not been evidenced. These discoveries support recurrent symbiont turn-overs driven by symbiont loss and replacement and/or possible tissue specialization.

Taken together, these discoveries shed new light on the evolution of nutritional symbiosis in this important group of insect vectors and may also help identify new targets for microbiota-based vector control.

Identifying the core and niche-specific microbiota in an invasive polyphagous fly pest

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Abstract

Over the last decade, many studies have demonstrated that the gut microbiota of phytophagous insects can strongly affects essential traits associated with fitness, such as immunity or growth. In specialist holometabolous insects, the larval and adult microbiota often partially overlap but remain distinct. This allows to define a stable core microbiota consisting in taxa consistently shared among individuals and life-stages, and a stage-specific microbiota consisting in taxa which consistently differ between larvae and adults due to differences in diet, physiology, or habitat use between life-stages.

In contrast to specialist holometabolous insects, polyphagous holometabolous insects can harbor both a core, a stage-specific and a niche-specific microbiota, which varies across host plants. The relative importance of the core, stage-specific and niche-specific gut microbiota has rarely been studied in polyphagous insects.

Here we study how these three factors affect the bacterial and yeast community of *Drosophila suzukii*, an exotic invasive fruit pest that infests multiple host fruits. We artificially infested fresh fruits (strawberry, cherry or blackberry) with *D. suzukii* larvae and tracked changes in the bacteria and yeast community using 16S and ITS metabarcoding. We identified the bacteria *Gluconobacter cerinus* as the single taxa forming a core microbiota stable among host fruits and life-stages. We also identified niche-specific yeast taxa that differ among host fruits (i.e. blackberry vs. strawberry or cherry) throughout the developmental stages of *D. suzukii*. We further test the fruit-specific fitness effects of these taxa using mono-associations with *D. suzukii* larvae reared across different fruit media.

Overall, our results indicate that despite extreme dietary breadth, *D. suzukii* maintains a highly reduced but stable core bacterial microbiota while relying on flexible, fruit-dependent yeast microbiota across development. This highlights the central role of niche-specific microbiota in shaping insect-microbe interactions in polyphagous invasive pests and opens interesting perspectives for microbiota-based management strategies.

Wolbachia dynamics across hoverflies (Diptera:Syrphidae) in Greenland

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Piotr ŁUKASIK

Abstract

Symbiotic bacteria play a crucial role in host biology and evolution, often shaping key traits in heterogeneous and rapidly changing environments. *Wolbachia* is a widespread, maternally transmitted insect endosymbiont known to influence nutrition, reproduction, and defense against pathogens. Despite its prevalence, transmission within and among host clades remains understudied. In high arctic ecosystems, such as Greenland, where species diversity is low, *Wolbachia* infections occur across multiple insect clades (Coleoptera, Diptera, Lepidoptera, and Hymenoptera). In this context, hoverflies (Diptera: Syrphidae) represent the most diverse dipteran family and key pollinator group in Greenland. Interestingly, they are also the most diverse *Wolbachia*-hosts, making them an ideal model to study host-symbiont dynamics.

The goal of this study was to uncover the dynamics of host-*Wolbachia* associations across Greenland hoverfly species. Specifically, we asked about a) the diversity of *Wolbachia* genotypes infecting hoverflies and its variation across time and space, b) species-specificity of *Wolbachia* genotypes, and c) patterns of its transmission within the Syrphidae family. We addressed those questions by simultaneously amplifying the COI gene and the 16S-V4 rRNA bacterial marker to confirm the identity of over a thousand flies, and their microbiome profiles, collected in 12 localities from Greenland. Across the surveyed locations, we identified 18 hoverfly species, of which 3 represent new records for Greenland, and 5 *Wolbachia* OTUs. Approximately half of the hoverfly species carried *Wolbachia*. Most genotypes were distributed across hoverfly species, occasionally showing species-specificity. Interestingly, some host species harboured multiple lineages of the endosymbiont. Moreover, infection prevalence and diversity varied by locality, while other species were never found infected. Overall, our results contribute to the understanding of pollinator biodiversity in Greenland and the potential role of their associated microbial communities in shaping it.

Who Gets In? Bacterial Filtering in Ambrosia Gall Midge Fungiculture

Nikola ROJOVSKÁ (University of Ostrava, Department of Biology and Ecology, Nikola.rojovska@osu.cz)

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Abstract

Ambrosia gall midges (AGM; Diptera: Cecidomyiidae) are an overlooked lineage of fungus-farming insects. Their larvae develop inside plant galls and feed on cultivated fungal symbionts, turning each gall into a small, self-contained farming system. In other fungus-farming insects, bacteria are recognized as integral partners, contributing to nutrient cycling, garden protection, and chemical regulation of the cultivated environment. In AGM, however, the bacterial component of fungiculture has remained unexplored.

Here, we present the first insight into bacterial communities associated with AGM sampled from gall surface, gall interior and larvae. We detected 364 bacterial taxa, with a broad shared core (119 taxa) present in all three compartments. Yet, the communities were far from identical. The gall surface harboured the highest richness and the largest number of unique taxa, consistent with strong environmental influences. The gall interior formed a strongly interconnected community, with fewer unique taxa (33), while larvae resembled the interior community but stood out by a clearer host-linked signature, with *Methylobacterium*/*Methylorubrum* and *Aureimonas* emerging as larval indicators (10 unique taxa). Other taxa were compartment-typical as well: lactic acid bacteria and *Erwinia*/*Serratia* were associated with the surface, whereas *Microbacterium*/*Iamia*/*Moheibacter* characterized the interior.

The inner compartments stood out as more strongly filtered than the surface, consistent with increased selectivity toward larvae and the gall interior. Across all three compartments, the genera most consistently exceeding neutral expectations included *Microbacterium*, *Curtobacterium*, *Cutibacterium*, *Delftia* and *Methylobacterium*/*Methylorubrum*.

Together, these results suggest that ambrosia gall fungiculture does not simply accumulate environmental bacteria; it sorts them into compartment-specific communities. While functional roles remain to be tested, such bacteria may contribute to the stability of the fungal garden (e.g., by suppressing antagonists), with consequences for nutrient availability and gall development. This positions AGM as a compact model for studying bacterial integration into insect farming and the evolution of phytomycetophagy.

#12249

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Modeling Host–Microbiota Interactions

Claire RUNSER (Insect Biology Research Institut, University of Tours, Runserclaire@gmail.com)

Lucas MARIE-ORLEACH, Franck DEDEINE

Abstract

Most insects host diverse microbial communities in their digestive tract, which often play key roles in host biological functions such as nutrition, immunity, and development. While host-microbiota co-adaptation is generally considered beneficial to the host, competition among microbial entities may actually be detrimental to the host, inducing conflicts of interest across different levels of selection. These conflicts remain poorly understood. Here, we will develop simulation models exploring key population genetics parameters, including the mode and efficiency of microbial transmission, host mating systems, and natural selection acting at different levels of host–microbiota associations. Our theoretical work aims to better understand how within-microbiota conflicts affect host-microbiota co-adaptation.

#10853

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Wolbachia as a nutritional mutualist

Mathilde SCHEIFLER (Evolution and Ecophysiology Group - Gembloux Agro-Bio Tech, University of Liège, Mathilde.scheifler@gmail.com)

Abstract

Vertically transmitted endosymbionts have a major impact on the physiology, ecology, and evolution of their hosts, but the nutritional bases of symbiotic interactions are not well understood. Wolbachia, a widespread bacterial endosymbiont of insects and other arthropods, has recently been proposed to act as a nutritional mutualist for micronutrients and nucleotides. In this project, we will test the hypothesis that Wolbachia is a nutritional mutualist for fatty acids and fat, key macronutrients for all organisms. We will use the amber wasp, *Leptopilina heterotoma*, one of the best studied insects regarding fat metabolism and a species in which nearly all individuals are infected with Wolbachia in nature.

First, we will compare the metabolic capacities of all Wolbachia strains associated with *L. heterotoma* to infer the evolutionary origin of fat-related mutualism. We will then use *L. heterotoma* inbred lines with selective symbiont curing to determine how wasp genotype and fat content determine Wolbachia density, and reciprocally how Wolbachia influences wasp fatty acid synthesis, fat accumulation, and fitness. Finally, we will unravel the mechanistic basis of this nutritional mutualism by performing dual RNA sequencing to identify candidate Wolbachia modulators and wasp genes involved in fat metabolism, followed by functional validation through RNA interference. This integrative evolutionary, ecological, biochemical, and genomic approach will provide new insights into the role of fat in Wolbachia-insect symbioses.

Tripartite Host-Microbiota-Pathogen Interaction and Pathogen Virulence Evolution in *Tenebrio molitor*

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Maryam KESHAVARZ

Abstract

Tripartite interaction between insect hosts, their gut microbiota and pathogens impacts infection dynamics through apparent competition and immune crosstalk. Host-derived antimicrobial peptides (AMPs) directly target pathogens, while the microbiota exerts apparent competition by modulating the host immune landscape (e.g., AMP expression) and altering pathogen niche accessibility. This interaction forces pathogens to balance evading AMP killing with adapting to microbiota-driven limitations. However, how these interactions influence pathogen virulence evolution remains unclear. To investigate this, *Tenebrio molitor* larvae underwent gut microbiota depletion (antibiotic diet) and RNAi-mediated *Tenebrio molitor* Relish (TmRelish) knockdown to alter AMP expression. Larvae were infected with *Providencia burhodogranariae* B (P.b.B) and passaged serially 10 times. Virulence evolution was assessed through survival assays, bacterial load quantification, and comparative analysis of ancestral versus evolved strains. We anticipate that within hosts with an intact immune system and normal gut microbiota, serially passaged pathogens will exhibit minimal virulence expression. Accelerated virulence evolution will happen in microbiota-depleted hosts with functional immunity. Intact immunity in microbiota-depleted hosts suppresses virulence enhancement compared with immunodeficient hosts. Gut microbiota absence and downregulation of AMPs promote P.b.B virulence during serial passages. Synergistic gut microbiota-immune interactions likely shape pathogen virulence evolution.

The architecture of choice: Network topology mediates the eco-evolutionary dynamics of sexual selection

SOLIMARY GARCIA HERNANDEZ (UNIVERSITY OF SAO PAULO, Solimarygarcia@gmail.com)

Abstract

Intersexual selection strongly shapes phenotypic evolution. Even though many classical models treat female mate preferences as uniform, real populations show variation in what females actually prefer. What we still don't fully understand is how this individual variation interacts with ecological constraints to drive long-term evolutionary trends. To tackle this, we built an individual-based model tracking populations across 100 generations by combining quantitative genetics with bipartite network analysis. We tested a gradient of variation in female preference (σ_p) across four classic preference functions: uniform, Gaussian, sigmoid, and U-shaped. We also restricted how many males a female could sample, simulating real-world ecological search costs. We found that local mating rules create distinct sexual network topologies, which directly drive trait evolution. Under directional selection, populations form highly nested networks. In this hierarchical structure, a few attractive "hub" males secure matings with both choosy and generalist females, fueling extreme trait exaggeration. In contrast, stabilizing selection reveals a clear tipping point. When female preference varies more than the male trait ($\sigma_p > \sigma_z$), the network fragments into isolated modules. This modularity essentially mirrors strict assortative mating—females only mate with males matching their exact preferences. This modular structure shields rare phenotypes from natural selection and rescues the genetic variance of the population. Interestingly, introducing strict ecological sampling costs reveals a fundamental asymmetry in evolutionary resilience. While directional trait exaggeration remains highly robust even when females sample very few males, the modular structures required to rescue genetic variance are extremely fragile. When females cannot properly sample the male pool, assortative mating breaks down, triggering a collapse of genetic diversity back to null-model levels. Given their diversity in mating strategies and ecological search costs, arthropods represent ideal empirical systems to test these predictions. Our framework demonstrates that mating topology is a link translating behavioral variation into long-term evolutionary outcomes.

From phylogenomics to population genomics: the role of geography versus ecology in driving *Coenonympha* butterfly diversification

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Matthew GREENWOOD, Thibaut CAPBLANCQ

Abstract

The role of geographical isolation and ecological adaptation in species diversification is a fundamental question in evolutionary biology. While allopatric speciation has been a paradigm for decades, growing evidences for porous boundaries between closely related species suggest that speciation may occur in the face of gene flow, driven by divergent selection along environmental gradients. In the Northern hemisphere, Quaternary climatic oscillations repeatedly opened and closed migration routes in the geological complex landscape of the Holarctic potentially resulting in a large increase in the number of species that form in areas where impermanent geographical barriers allowed recurrent cycles of isolation and mixing to occur. We explore the drivers of speciation in one of the most species-rich and ecologically diverse butterfly genera of the temperate zone, the genus *Coenonympha* (Satyrinae, Nymphalidae) based on whole genome sequences from 32 species.

By combining phylogenomic, climatic niche and morphological trait evolution analyses, we show that key episodes of species diversification coincided with periods of climatic change and biogeographic dispersal. Focusing on two ecologically divergent sister species, the lowland *C. arcania* and the highland *C. gardetta*, we found little overlap between barrier loci and loci under divergent selection which suggest that reproductive isolation and ecological adaptation are distinct mechanisms. A model of divergence in isolation with secondary contact (geographic speciation) was favored over a model of divergence with gene flow (ecological speciation). Beyond this alpine species complex, allopatric isolation and secondary gene flow appear to be pervasive in the genus, also involving the balkano-caucasian species *C. leander*, the boreal *C. hero*, and the two mediterranean insular endemics *C. corinna* and *C. elbana*.

In conclusion, both macroevolutionary and microevolutionary analyses support the view that alternating phases of geographic isolation and connectivity have been key drivers of speciation in this ecologically diverse genus.

#11133

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Trait evolution, biome shifts, and spatiotemporal diversification in Neotropical tortoise beetles

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Julio SCHENIDER, Marianna SIMÕES

Abstract

Patterns of trait evolution and biome associations offer valuable insights into how lineages diversify across the Neotropics. The tortoise beetle tribe Dorynotini (Chrysomelidae: Cassidinae) spans across rainforest, savannas and seasonally dry habitats of Central and South America, including the Caribbean islands. They also exhibit conserved host-plant associations and convergent evolution of traits that have been linked to drought tolerance and/or defence. However, due to limited molecular sampling, outstanding questions remain on the evolutionary relationships within the group and their historical diversification, making them an excellent system for studying how biome transitions are linked to trait evolution in herbivorous insects.

In this talk, I will outline ongoing phylogenomic work on Dorynotini on low coverage whole genome sequencing data from both fresh and museum specimens. Using this framework, we aim to resolve outstanding taxonomic questions and reveal patterns of the timing and direction of biome transitions by testing the hypothesis that drought associated traits evolved repeatedly and in response to the independent colonisation of dry biomes. By integrating trait, biome, and biogeographic histories, this study throws light on how ecological transitions shape phenotypic evolution and diversification in Neotropical herbivorous insects.

Glutathione-S-Transferases of *Drosophila suzukii*, unveiling unexpected diversity

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Nicolas PETIOT, Fabrice NEIERS, Adrien NICOLAI, Martine MAIBECHE, Thomas CHERTEMPS

Abstract

Glutathione transferases (GSTs) are Phase II xenobiotic-metabolizing enzymes involved in the detoxification of a wide range of endogenous and exogenous compounds. GST diversity and expression profiles vary considerably among insects, reflecting their ecological niches, diets and lifestyle. Conflicting studies have been published regarding the size of GST repertoire in *Drosophila suzukii*, a major invasive pest of soft-fruit production worldwide. The maximum of 22 annotated sequences found in this species, which is low compared to other drosophilids (35-40), suggests that GSTs do not play a major role in the detoxification of xenobiotic compounds. Using genomic and transcriptomic approaches, we re-annotated and identified 42 GST genes in *D. suzukii*, including seven new GST sequences absent in the reference model *D. melanogaster*. Phylogenetic analysis of these GSTs reveals their evolutionary relationships and functional diversification. We also performed an in silico structural analysis of these 42 sequences using AlphaFold to highlight their structural features, particularly at the catalytic site and dimerization interface, revealing original characteristics in some cases. We further characterized the tissue-specific expression profiles of these GSTs under different insecticide or oxidative stress conditions. These findings elucidate the structural and functional complexity of the GST family in this invasive species and provide a basis for identifying functionally specialized GSTs that may contribute to its ecological success and chemical tolerance.

From Nudiviruses and Ascoviruse to Transient Organelles

Brian FEDERICI (University of California, Riverside, Brian.federici@ucr.edu)

Abstract

By 1984, two types of particles produced by female parasitic wasps were known that suppressed the innate immunity of their lepidopteran hosts. These particles were considered virions of symbiotic viruses, referred to as polydnaviruses, belonging to two virus genera, Bracovirus for those that occurred in wasps of the family Bracoviridae, and Ichnovirus for those that produced by species in the family Ichneumonidae. Structurally, the particles resembled, respectively, baculoviruses and ascoviruses. Little was known about their putative genomes other than that they consisted of various double-stranded DNA circles. The most unusual feature of these viruses was that they did not produce progeny virions in their lepidopteran hosts. Thus, my view at that time was that these particles may not be virions, but rather a type of organelle that evolved from the two different types of virions. In 1991, these viruses were accepted by the International Committee on the Taxonomy of Viruses (ICTV), in the family Polydnviridae. Subsequently, thirty years later, after it had been shown that the DNA of bracoviruses and ichnoviruses consisted almost exclusively genes coding for immunosuppressive proteins and others that facilitated the synthesis of the latter, the ICTV disestablished the family Polydnviridae, and replaced it outside the Virosphere, and reclassified these particles as mobile genetic elements named viriforms in the non-viral family Polydnviriformidea. Here, based on their functional role in suppression of host immunity, I justify referring viriform particles as “suppressons,” and the former polydnvirus nucleocapsids as “nucleocassettes,” based on their circular DNA structures and roles in immunosuppression.

Role of cytochrome P450 in the adaptation of Asian and European corn borers to maize

Frederique HILLIOU (INRAE, Frederique.hilliou@inrae.fr)

Mariam EL KHATIB, Gabriela CABALLERO-VIDAL, Julien GIOVANAZZI, Olivier MIGLIORE, Guy PEREZ, Gaëlle LE GOFF

Abstract

With the introduction of corn into Europe and Asia around 500 years ago, Lepidopteran species *Ostrinia nubilalis* (the European corn borer) and *Ostrinia furnicalis* (the Asian corn borer) evolved the ability to feed on corn independently. Another species, *Ostrinia scapulalis* (the adzuki corn borer), is sympatric with the European and Asian corn borer but still favors the original dicot host plant *Artemisia vulgaris* (mugwort). This occurrence presents a unique opportunity to study convergent adaptive evolution and highlight putative independent adaptations in the three *Ostrinia* species.

Cytochrome P450s (CYPs) constitute a superfamily of heme monooxygenase genes involved in metabolizing endogenous compounds such as hormones and fatty acids and detoxifying exogenous compounds such as plant allelochemicals and synthetic pesticides. We have manually curated the annotation of P450 genes on the three *Ostrinia* species genomes. We highlight the differences in the *Ostrinia* CYPs repertoire using phylogenetic analysis between the three *Ostrinia* species and other lepidopteran pests feeding on corn. We also report CYP expression in response to different diets in our three *Ostrinia* species.

By combining our phylogenetic and our mRNA expression data we have highlighted some CYPs in *Ostrinia* species potentially involved in insect adaptation to host plants.

Shared continent, different histories: Comparing movement patterns and population connectivity of the redback spider (*Latrodectus hasselti*) and the Portuguese millipede (*Ommatoiulus moreleti*).

Marta KAROLAK (Curtin University, Marta.karolak@postgrad.curtin.edu.au)

Abstract

Dispersal has major consequences for population viability, gene flow, and species invasions. Despite its ecological importance, quantifying dispersal remains challenging. We have limited information about dispersal to guide management, and this dearth of knowledge is particularly acute for invertebrates – a large and highly diverse group of animals that have suffered massive declines over the last few decades, and which are critical for maintaining the structure and function of natural ecosystems.

In my study I am using ddRAD sequencing to estimate dispersal patterns in ecologically and evolutionarily distinct invertebrates: the Portuguese millipede (*Ommatoiulus moreleti*) and the redback spider (*Latrodectus hasselti*). By quantifying the patterns of gene flow and connectivity for species with different dispersal characteristics, I am trying to develop models of how the environment and species traits interact to drive patterns of dispersal. The Portuguese millipede and the redback spider are two unrelated species with a well-documented history in Australia. Portuguese millipede is a pest introduced to South Australia in the 50s that has spread across the southern part of the continent since, whereas the redback spider occurs nationwide, but its native range remains uncertain. I used these two species to understand the historical population size patterns and current connectivity between their populations.

Using fine-scale sampling across Perth (94 individuals) and broad-scale sampling across six Australian states (87 individuals), I quantified patterns of gene flow and population connectivity. To identify environmental and landscape drivers of dispersal, I applied gravity models and isolation-by-resistance analyses.

This work improves our understanding of invertebrate dispersal by combining species traits, landscape features, and historical demography. The results provide insights into the spread of invasive species, and offer new information on the origins and population history of the redback spider—a species of ecological and medical significance in Australia.

Advancing high-quality genomic resources for the honey bee research community

Thibault LEROY (GenPhySE, Université de Toulouse, INRAE, ENVT, 31326, Castanet Tolosan, France, Thibault.leroy@inrae.fr)

Alain VIGNAL, Sonia EYNARD, Baptiste MAYJONADE, Jérôme GOUZY, Jean KELLER

Abstract

Honey bees are among the most important flower-visiting insects worldwide. Even though this species model receives considerable attention in the insect literature and community, the number of high-quality genomic resources available for honey bees is, quite surprisingly, remarkably limited. Most people working on honey bee research rely on one single reference assembly (HAv3.1), annotated for the gene content and produced in 2018 from a yellow honey bee (*Apis mellifera carnica*).

Here, we report progress from our group in Toulouse (BeeGEES team, UMR GenPhySE) to produce two new high-quality genome assemblies generated with long-read technologies (PacBio SMRT and Nanopore reads). One assembly is a black honey bee (*Apis mellifera mellifera*), and the other a “Buckfast”, a hybrid breeding lineage widely used by beekeepers. Both assemblies are longer than the existing reference (by up to 12%) and show much lower fragmentation. With these improvements, we gain access to more sequence information in highly repeated regions, especially in the centromeric regions of the acrocentric chromosomes. The remaining breaks in the assemblies (*e.g.* 24 contigs for 16 chromosomes in our best one) are mainly linked to contigs that contain almost only repeated content, preventing their integration into the assembly.

Beyond producing these new high-quality references, we combined all assemblies with large RNA-seq datasets to provide gene content for these additional references. This effort covers all available high-quality genomes of *Apis mellifera* (including HAv3.1), but also extends to other *Apis* species. In addition to presenting these resources, the talk will also show some biological insights gained from them, including the apparently limited structural variation at the species level and the remarkably conserved synteny at the genus level and beyond. Based on all this information, bringing these resources together into a genus-level pangenome seems to be the next logical step.

Dynamics of Chromosome Evolution in Termites: Multivalent Chains, Inbreeding and Novel Chromosomal Translocations

Ruth MORAA (Johannes Gutenberg University of Mainz, Moraarut@uni-mainz.de)

Mara JULSETH, Dino MCMAHON, Ann-Kathrin HUYLMANS

Abstract

Dynamics of chromosome evolution in termites: Multivalent chains, inbreeding and novel chromosomal translocations

Termites are diploid eusocial roaches that possess an XX/XY sex-determination system, in contrast to their cockroach ancestors, which exhibit an XX/XO system. Chromosomal rearrangements play an important role in the evolution of sex chromosomes, leading to fast speciation events and further can alter genomic patterns on a population scale.

An intriguing yet understudied feature of termite reproduction is the occurrence of ring chromosomes and multivalent chains during male meiosis, which have been theoretically linked to inbreeding. These multivalent chains consist of varying numbers of chromosomes that differ both between and within species.

Using European species of the genus *Reticulitermes* as our study system, this project aims explore this topic at two contrasting evolutionary scales within the termites. We first target the link between chromosome ring formation and sex chromosome evolution at the origin of termite eusociality, before going on to investigate the evolutionary causes and consequences of ring chromosome formation at the population level

By leveraging publicly available genomic datasets for both termites and cockroaches, we investigated the origin of the Y chromosome in termites within a comparative genomics framework, using the termite X chromosome as a reference. Our findings indicated that sex chromosome turnover events may have occurred during termite evolution. (Publication from part of this work 'Evidence for a Novel X Chromosome in Termites' <https://doi.org/10.1093/gbe/evae265>)

To explore the mechanisms underlying ring chromosome formation and multivalent chains, we employ de novo chromosome-level assemblies from males of both ring- and non-ring-forming species. Ongoing comparative and population genomic analyses will assess the patterns of genetic differentiation and adaptation within and between species.

#11992

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Evolutionary history and host plant adaptation in European *Ostrinia* borers

Pierre NOUHAUD (CBGP, INRAE, CIRAD, IRD, Montpellier SupAgro, Univ Montpellier, Montpellier, France, Pierre.nouhaud@inrae.fr)

Mathieu GAUTIER, Stuart BAIRD, Sabine NIDELET, Louise BROUSSEAU, Philippe AUDIOT, Sylvain SANTONI, Audrey WEBER, Christine TOLEDO, Carole SMADJA, Renaud VITALIS, Réjane STREIFF

Abstract

Phytophagous insects are key models for studying adaptive divergence associated with host specialization. In Western Europe, the genus *Ostrinia* (Lepidoptera: Crambidae) comprises two sympatric lineages (sometimes treated as species) exploiting either wild dicotyledons or maize, which was introduced to the continent about 500 years ago. Through a large-scale European sampling effort and population genomic analyses, we show that (i) these lineages correspond to the two pheromonal races previously identified in the *Ostrinia* system, (ii) the maize-associated lineage likely arose via a recent host shift event from the dicot-associated lineage followed by specialization, and (iii) a large, old, Z-linked inversion may variably contribute to reduced gene flow between lineages across Western Europe. Altogether, our results shed new light on the evolutionary history of a major agricultural pest worldwide.

Exploring the Potential of Non-coding RNA for RNAi-Pest control

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Doga CEDDEN, Gregor BUCHER

Abstract

With the global population projected to reach approximately 10 billion before the year 2050, crop production must rise accordingly. Currently, pests account for 20-40% of losses in major crop yields and their management methods rely mainly on classical pesticides. However, their limited modes of action can drive widespread resistance and harm non-target organisms, including pollinators and natural predators. Pesticides leveraging the RNA-interference (RNAi) pathway have a species-specific mode of action, and represent an environmentally friendly alternative to conventional pesticides. RNAi-pesticides work by the delivery of double-stranded RNA (dsRNA), which are cleaved into small interfering RNA (siRNA) that act as guides for the cleavage of complementary protein-coding mRNA, leading to mortality if the targeted protein is essential for survival. Traditionally, RNAi-based pesticides target protein-coding mRNA, this study, however, explores non-coding RNA as RNAi targets in *Tribolium castaneum*. Cleavage of non-coding RNA may allow for a faster effect of RNAi-insecticides, as they would not require protein already present in the organism to degrade. The spliceosome, essential for development, is used as a target, because it relies on non-coding small nuclear RNA (snRNA) to splice precursor mRNA. The snRNA bind to proteins to form small nuclear ribonucleoprotein complexes (snRNP), which in turn form the spliceosome. These snRNA serve as a test case to test the viability of non-coding RNA-targeting RNAi pesticides. Results indicate that targeting of the non-coding spliceosomal snRNA with dsRNA does not cause significant mortality, even when targeting multiple snRNA at once. This is likely due to multiple factors hindering targetability of snRNA, such as low presence of snRNA in the cytoplasm, and a high number of secondary structures.

Functional innovation in aphid IAPs through expansion, diversification, and morph-specific expression

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Abstract

Inhibitors of Apoptosis (IAPs) regulate cell death and contribute to immunity, cell division, and signaling, yet remain poorly studied in aphids and other hemipterans. Here, we annotated IAP genes across 33 aphid species (3 families, 5 subfamilies), identifying a total of 662 IAPs and revealing a striking expansion in aphids, with some species encoding up to 60 proteins versus only 4-5 in other insects. Phylogenomic analyses grouped aphid IAPs into four groups of paralogs, that we named IAP A, B, C and Deterin, with differing structures. Among them, Groups A, B and C exhibit aphid-specific duplication or loss of canonical IAP domains, including duplication of domains involved in target protein degradation or loss of domains involved in immunity in other insects. Furthermore, Groups A and C have further diversified through lineage- and species-specific gene duplications. Expression analyses of >300 RNA-seq datasets and targeted qRT-PCR experiments demonstrated that many expanded IAPs are expressed in a tissue- and condition-specific manner, suggesting functional diversification. Notably, distinct IAP genes are upregulated in different morphs (male, sexual female, asexual female; winged or wingless) and in response to infection. Moreover, 5 of the 28 IAPs in the pea aphid, *Acyrtosiphon pisum*, are specifically induced during the programmed cell death of bacteriocytes, the specialized cells that harbor the obligate endosymbiont *Buchnera aphidicola*. Three of these belong to Group A, possess aphid-specific domain architecture, and exhibit strong anti-apoptotic activity. RNA interference knockdown of these potent IAPs reduced reproduction in parthenogenetic females and triggered bacteriocyte apoptosis, demonstrating their importance for aphid development. Taken together, these findings demonstrate how the expansion and structural modification of a multigene family have enabled functional innovation and diversification tailored to the distinct lifestyle, morphs and cell types differentiation of aphids.

Genomic innovations underlying plant manipulation: comparative analysis of gall-inducing cynipid wasps

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Patrick SHIH

Abstract

Plant galls represent one of the most striking examples of extended phenotypes, in which insects redirect host plant development to produce complex, species-specific structures. Despite their ecological and morphological diversity, the genomic basis of gall induction remains poorly resolved, especially in the Hymenoptera. Cynipid gall wasps (Hymenoptera: Cynipidae) induce highly organized galls on oaks (*Quercus* spp.), a process hypothesized to rely on secreted effector proteins that manipulate host developmental pathways. We present genome assemblies and gene annotations for three California oak-galling cynipids: *Andricus quercuscalifornicus*, *Amphibolips quercuspomiformis*, and *Callirhytis quercussuttoni*, spanning three genera within the tribe Cynipini. Using a comparative genomics framework that incorporates non-galling parasitoid outgroups as well as cynipid lineages with secondary loss of galling, we perform orthogroup inference to characterize gene family evolution across the phylogeny.

We identify gene families that are significantly expanded in gall-inducing lineages relative to non-galling relatives, consistent with lineage-specific innovation. We also detect orthogroups uniquely shared among galling taxa but absent from non-gallers, defining a set of candidate galling-associated gene families. These loci are enriched for features consistent with secreted effectors and represent strong candidates for plant gall induction. Our results provide a phylogenetically grounded view of gene family dynamics associated with the evolution of gall induction.

Genetic control of *Ceratitis capitata* by combining sex-conversion and female sterilization

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Abstract

The Mediterranean fruit fly (*Ceratitis capitata*) is a globally significant agricultural pest. Genetic control strategies based on gene drive systems offer a sustainable and species-specific alternative to chemical insecticides and the Sterile Insect technique (SIT). Sex-ratio distortion and female sterility are among the most effective approaches for suppressing insect populations. In *C. capitata*, sex conversion can be induced by targeting the transformer gene, enabling the production of fertile XX males. To enhance suppression, we identified *yellow-g2*, a gene essential for eggshell formation, as a suitable target for inducing female sterility. Disruption of *yellow-g2* through CRISPR/Cas9-based gene editing resulted in fully sterile females producing only non-viable eggs. We utilized two constructs: one targeting transformer, integrated into the white locus and carrying Cas9 under a germline-specific promoter, and another targeting *yellow-g2*. In cage trials, the co-release of males carrying both constructs led to efficient gene drive propagation, a strong male-biased sex ratio, and complete sterility in homozygous females. These effects caused a substantial reduction in population size across successive generations. Our results demonstrate the feasibility of the genetic suppression of *C. capitata* populations using gene drives and offer avenues for their further improvement.

Resolving Species Boundaries in *Neptis* (Lepidoptera: Nymphalidae) from Northwest India Using Integrative Taxonomy: Evidence from Genital Morphology and Mitochondrial COI gene

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Gurinder Kaur WALIA, Avtar Kaur SIDHU

Abstract

Resolving Species Boundaries in *Neptis* (Lepidoptera: Nymphalidae) from Northwest India Using Integrative Taxonomy: Evidence from Genital Morphology and Mitochondrial COI gene

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The genus *Neptis* represents a taxonomically challenging group of butterflies due to subtle external morphological variation, often complicating accurate species identification. The present study examines selected *Neptis* species collected from Northwest India using detailed genitalic morphology and mitochondrial cytochrome c oxidase subunit I (COI) data. Genitalia of selected species were studied and illustrated for the first time, highlighting diagnostic characters useful for species delimitation. COI sequences were generated and supplemented with reference data from public repositories to support species-level identification and comparative analysis. The combined use of morphological and molecular approaches provides a more robust framework for distinguishing closely related taxa within the genus. This study emphasizes the significance of genital morphology in resolving taxonomic ambiguities and demonstrates the complementary role of DNA barcoding in integrative taxonomy. The findings contribute baseline information for future systematic, ecological, and conservation-oriented studies of *Neptis* in the northwestern region of India.

Molecular basis of migrant induction in the bird cherry-oat aphid

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Abstract

Host alternation occurs in 10% of aphid species and involves an obligate migration between two taxonomically distinct host plants, typically a primary woody host and a secondary herbaceous host. This life-cycle strategy depends on tightly regulated developmental transitions and the production of a specialized migrant morph, yet the molecular mechanisms governing this switch remain largely unknown. The bird cherry–oat aphid *Rhopalosiphum padi* alternates annually between *Prunus padus* (primary host) and Poaceae (secondary hosts). A crucial developmental transition occurs early in larval development, during the first and second larval instars (L1–L2), when specific conditions on the primary host trigger the production of the migrant morph. Previous work has shown that *P. padus* leaf maturity alone can induce this developmental pathway.

To elucidate the molecular basis of host alternation in *R. padi*, we conducted a fine-scale kinetic analysis of L1 and L2 larvae reared on defined *P. padus* leaf maturity stages and performed a transcriptomic time-course study. This approach enabled us to capture the earliest gene-expression changes associated with the induction of host alternation. We identified candidate genes potentially involved in initiating the migrant morph development, along with finely tuned regulatory responses related to aphid–plant interactions (e.g. salivary effector candidates, detoxification pathways) and stress responses. Together, these results provide new insight into the initial molecular events underlying host alternation and shed light on how aphids perceive and integrate environmental cues to control morph determination.

Long term adaptation of *Bemisia tabaci* to a plant at the margin of the host range

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Abstract

Although generalist insect herbivores can exploit a wide range of host plants, colonization of hosts at the margins of the species' host range often reduces performance and fitness. How long-term adaptation to such marginal hosts evolves, and whether it is stable when selection is relaxed, remains largely unknown. Our study examined the long-term adaptation of the generalist phloem-feeding whitefly *Bemisia tabaci* to Habanero pepper (*Capsicum chinense*), a marginally suitable host, in comparison to cotton (*Gossypium hirsutum*), a suitable host. Multigenerational whitefly populations were established and maintained for more than 70 generations on either Habanero pepper or cotton. In the first generations, the survival of the Habanero pepper population was extremely low (5%) and its egg to adult development period was significantly longer than on cotton plants. During the 70 generations period, the Habanero Pepper population evolved to perform similarly on cotton and Habanero pepper plants. To test the stability of adaptation, the Habanero pepper adapted population was transferred to cotton, and its performance was examined using survival and development assays. In addition, the feeding behavior both on cotton and Habanero pepper plants was documented using the Electrical Penetration Graph (EPG) technique. In parallel, transcriptomic analyses were conducted to identify gene expression changes associated with long-term adaptation to the marginal host, and the functionality of selected genes was examined using RNA interference (RNAi). The results obtained so far suggest that the high adaptation to Habanero pepper is stable and maintained even after more than 15 generations on cotton, with no apparent fitness costs. The EPG feeding behavior assays suggest that adaptation is related to reduced duration of phloem-feeding on Habanero pepper. These findings provide first insights into the mechanisms that generalist phloem-feeding insects utilize to maintain their "generalists" ability while overcoming periods in which suitable host plants are not available.

Unraveling the molecular basis of the Orco-ORx assembly

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Abstract

Olfaction is one of the oldest sensory systems insects use to interpret their environment. To detect airborne chemicals, insects rely on several types of receptors, including olfactory receptors (ORs). In winged insects, the OR signaling complex is a heterotetramer composed of two subunits: the highly conserved co-receptor Orco and a more rapidly evolving tuning OR.

While Orco shows strong conservation across insect species, tuning ORs can diverge by up to 80% within a single species' repertoire. Despite this variation, Orco can still assemble functional complexes with many different ORs. Recent structural studies have revealed the overall architecture of Orco and ORs, identifying both the interacting domains between subunits and the ligand-binding site. However, it remains unclear how Orco accommodates such diverse OR partners to form active complexes.

Our research seeks to address this question by integrating phylogenetic analyses of Orco across insect lineages, computational modeling of Orco-OR complexes, and electrophysiological recordings. By comparing the interactions between Orco and a range of divergent, functionally distinct ORs, we aim to uncover mechanisms that enable complex formation despite high sequence variability. This work will advance our understanding of the molecular principles that govern assembly of the Orco-ORx signaling complex.

Temperature affects the transmission efficiency of *Xylella fastidiosa* by the spittlebug *Philaenus spumarius* on olive plants

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Abstract

Temperature is a key abiotic factor influencing interactions among plant pathogens, insect vectors, and their hosts, ultimately affecting transmission efficiency. The spittlebug *Philaenus spumarius* is the main vector of the xylem-limited bacterium *Xylella fastidiosa*, the causal agent of Olive Quick Decline Syndrome (OQDS) in Southern Italy. Understanding how temperature modulates *X. fastidiosa* transmission by *P. spumarius* is essential for predicting disease dynamics under current and future geographical extent and climatic conditions.

We evaluated the transmission efficiency of *X. fastidiosa* ST53 by *P. spumarius* by isolating insect batches for a 3-day AAP on infected source olive plants and subsequent 3-day IAP on olive plantlets under controlled conditions (i.e. phytotron) across five ranges of temperatures (averages between 17–35 °C, with day/night fluctuations of 4–8 °C).

Acquisition rates were higher at 24 and 28 °C ($\approx$ 85% of insects Xf-positive), lower at 17 °C (65%), and dropped sharply above 30 °C (<20%). Inoculation rates peaked at 24 °C (61% of recipient olive plantlets) and were significantly lower at both cooler (17 °C: 33%) and warmer temperatures (28 °C: 39%), with few successful inoculations above 30 °C (< 5%). Insect survival remained high up to 28 °C (85–95%) but decreased markedly at higher temperatures.

These findings demonstrate that temperature strongly affects *X. fastidiosa* ST53 transmission efficiency and *P. spumarius* survival, highlighting its critical role in OQDS epidemiology. Further studies under semi-field conditions should explore how temperature shapes the tritrophic interactions of the OQDS pathosystem to effectively evaluate the influence of seasonal variability and climate change on disease spread.

Effects of insecticides applied against *Scaphoideus titanus* on leafhopper communities in North-eastern Italy

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Abstract

Recently, a resurgence of Flavescence dorée (FD) has been reported in vineyards located in the Veneto region (north-eastern Italy). FD, a disease belonging to grapevine yellows, is associated with a phytoplasma (FDp), which is primarily transmitted by the leafhopper *Scaphoideus titanus*. FD control is mandatory and relies on insecticide applications against the vector and preventive cultural measures. Chemical control against *S. titanus* has evolved over time, as many previously used active ingredients have been withdrawn. Current management in many Italian regions is based on two insecticide applications: first, typically involving systemic insecticides (e.g., flupyradifurone, acetamiprid), is suggested when the third instar nymphs of *S. titanus* are dominant; second is carried out approximately two weeks later, using pyrethroids (e.g., tau-fluvalinate, deltamethrin). It has been suggested that the frequent use of insecticides accelerates the selection for resistance strains and promotes the proliferation of secondary pests (e.g., spider mites and leafhoppers). Different chemical control strategies against *S. titanus* on leafhopper communities were compared here: i) a systemic insecticide application (timing A), followed by a pyrethroid application (timing B); ii) two pyrethroid applications (timing A and B); iii) a single systemic application (timing A); iv) a single pyrethroid application (timing B). Tested products were based on flupyradifurone and tau-fluvalinate, or deltamethrin. Leafhopper abundance was assessed through leaf sampling conducted before and after insecticide applications. Yellow sticky traps were also employed to monitor the abundance of adult leafhoppers and parasitoids of economic importance (*Anagrus* spp.). Higher densities of the leafhoppers *Hebata vitis* and *Zygina rhamni* were recorded in plots subjected to single or double pyrethroid applications. Lower densities of *Anagrus* spp. were found in plots treated twice with pyrethroids. Field investigations and laboratory bioassays using a dose-mortality approach are needed to confirm these trends and identify the mechanism underlying higher pest densities in pyrethroid-treated plots.

Tracing Flavescence dorée vectors: Auchenorrhyncha communities in the viticulture of South Tyrol, Italy.

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Abstract

Flavescence dorée (FD) is one of the most destructive phytoplasma- associated diseases in European viticulture. While the primary epidemic vector, *Scaphoideus titanus*, is well studied, recent findings increasingly highlight the role of additional Fulgoromorpha and Cicadomorpha species, as well as wild host plants, in sustaining FD epidemiology. In South Tyrol (Italy), *S. titanus* was first detected in 2010. Six years later, in 2016, the first symptomatic grapevines were recorded in Valle Isarco, followed by 12 infected plants in Salorno in 2018 and 16 plants in the Bassa Atesina region in 2019. Since then, an annual increase in vines exhibiting FD symptoms has been observed. Although *S. titanus* is considered the main vector of FD, several other Auchenorrhyncha species, such as *Orientus ishidae* and *Dictyophara europaea*, are reported as confirmed or suspected FD-vectors. To address these emerging dynamics, a multi-scale project will elucidate local drivers of FD epidemiology, with a focus on Auchenorrhyncha communities. A previous survey of Auchenorrhyncha communities conducted in 2006 across South Tyrolean vineyards provides a historical baseline for evaluating subsequent faunal changes. Twenty-four vineyards across the region were selected based on altitude, ecotone characteristics, and vineyard management type to assess the distribution and composition of leafhopper and planthopper assemblages. The resulting species inventory will evaluate spatial patterns of Auchenorrhyncha communities in relation to vineyard structure and FD incidence. Targeted molecular analyses will further clarify which species harbor the phytoplasma and thus have the potential to act as vectors. Overall, this study will provide new insights into the epidemiology of FD at a local scale, evaluate the role of additional phloem-feeding species, and contribute to the development of effective and innovative management strategies.

Occurrence and prevalence in Central and Southern Italy of *Ooctonus vulgatus* Haliday (Hymenoptera Mymaridae), an egg parasitoid of *Philaenus spumarius* L. (Hemiptera Aphrophoridae)

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Abstract

Members of the family Mymaridae are tiny wasps occurring in all terrestrial habitats, and in freshwater streams and ponds. Since their minute size, mymarids are often overlooked, and many species remain mostly unknown. This is the case of *Ooctonus vulgatus* Haliday, an egg parasitoid of the spittlebug *Philaenus spumarius* L., which is considered the main European vector of the plant pathogenic bacterium *Xylella fastidiosa*. The need for sustainable control strategies against *P. spumarius*, has intensified interest in its natural enemies and their potential role in regulating vector populations.

In the current study, the presence and prevalence of *O. vulgatus* in Central and Southern Italy has been assessed using sentinel eggs in the period 2023-2026. *Philaenus spumarius* eggs, laid on pine needles, were deployed in multiple sampling sites across Tuscany and Apulia regions to assess the occurrence of *O. vulgatus* (2 sampling years per region for a total of 51 monitored sites). Sites were selected according to different ecological gradients (the percentage of semi-natural habitats in a 1 km buffer, altitude, and management). *Philaenus spumarius* eggs were exposed in November and left in the field until January. Then, pine needles carrying the eggs were placed in a thermostatic chamber at a temperature of 20 ± 2 °C and 70% relative humidity, awaiting the potential emergence of parasitoids. In the first year, only few *O. vulgatus* specimens emerged from eggs, revealing a quite low prevalence (0.63 - 7.50%) but confirming the occurrence of this species in Central Italy (Tuscany region). No parasitoids emerged from eggs exposed in Southern Italy (Apulia region) in the first year. Upon completion, our study will help elucidate spatial differences in the occurrence and prevalence of *O. vulgatus* between central and southern Italy, as well as potential environmental drivers such as landscape composition, altitude, and management practices.

Early detection of insect-mediated apple proliferation disease

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Abstract

Apple proliferation (AP) is one of the most important diseases affecting apple trees, caused by phytoplasmas. This bacterium is transmitted from one plant to another by phloem-feeding psyllids, primarily *Cacopsylla melanoneura* and *Cacopsylla picta*. Infected trees become permanent sources of infection, allowing the disease to be spread by these psyllids. As no effective treatment exists for this disease, current management strategies rely on controlling vector populations or eventually removing infected plants. Therefore, early detection and subsequent eradication of infected plants is essential to prevent an outbreak of this disease.

To quantify and monitor disease spread, we will combine: (i) extensive mapping through visual field surveys and drone-based georeferencing of infected (symptomatic) plants, and (ii) the application of a molecular biology method on plant tissues that quantifies phytoplasma and assess the health status of neighbouring trees that might be infected but are asymptomatic. The monitoring and molecular analyses will be extended to the insect vectors populations collected from the affected areas.

Here we present a protocol using droplet digital PCR (ddPCR), which enables the detection and precise quantification of extremely low DNA concentrations. This high sensitivity allows the early identification of phytoplasma DNA, when no clear sign of infection is yet visible. Additionally, this approach enables a precise comparison of bacterial loads between symptomatic and asymptomatic trees, as well as between the two vector species populations.

Neophilaenus campestris and Philaenus spumarius (Hempitera: Aphrophoridae) plant preference: push-pull strategy to control Xylella fastidiosa disease.

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Abstract

Xylella fastidiosa (*Xf*), an invasive insect-borne plant pathogen, represents a major threat to Mediterranean agriculture, impacting key crops such as olive, almond, and grapevine. The spittlebugs *Philaenus spumarius* and *Neophilaenus campestris* are the primary vectors of *Xf* in Europe. In Mediterranean agroecosystems, cover crops—whether naturally occurring or planted between woody crops—offer a range of ecosystem services, including fertility enhancement, pest control, erosion prevention, and biodiversity conservation. During spring, spittlebug nymphs feed on these herbaceous plants before migrating to woody crops in the summer, where they transmit *Xf*. A promising approach for controlling the disease is “the push-pull strategy”: to modify cover crop communities to make them less favourable for vector establishment.

This study aimed to assess the plant preferences and performance of the nymphs of these two majors *Xf* vectors. We selected 13 plant species from nine different families for experimentation, exposing nymphs to these species in both choice and non-choice assays. Our results revealed that *N. campestris* showed a strong preference for Poaceae family with different performance depending on the species, while *P. spumarius* exhibited a more polyphagous feeding behaviour, with notable preferences for the families Caryophyllaceae, Lamiaceae and Apiaceae. These findings offer valuable insights into the potential use of cover crops management to control *Xf* transmission in Mediterranean agricultural systems.

Differentiation of 16SrIV Group Phytoplasmas in the Caribbean Basin Using High Resolution Melt Curve Analysis of 16S and secA Genes

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Melody BLOCH, Brian BAHDER

Abstract

Palm lethal decline is a phytoplasma disease that is always fatal to infected palms and is caused by three species of phytoplasma in the Caribbean basin: '*Candidatus* Phytoplasma palmae', '*Ca. P. aculeata*', and '*Ca. P. hispanola*'. Movement of these pathogens throughout the Caribbean has been documented since their discovery in Jamaica. Current protocols utilize quantitative PCR (qPCR) for rapid amplification and distinction of the phytoplasma using TaqMan probes and high-resolution melt-curve analysis (HRMA) of the 16S rRNA gene. These assays either do not detect all three phytoplasmas (HRMA) or do not distinguish between the three (TaqMan). In this study, a new qPCR-HRMA assay is developed that amplifies and distinguishes between all three phytoplasmas currently known to infect and kill palms in the Caribbean. Efficiency for the primer set secA614F/secA759R was shown to be consistent for all species at each concentration and yielded distinct melting temperature ranges for amplicons of '*Ca. P. palmae*', '*Ca. P. aculeata*', and '*Ca. P. hispanola*'. This assay is a useful new tool, not only for the diagnostics that will contribute to monitoring and management programs, but will also aid in basic research by allowing rapid screening of large samples in the context of vector surveys or identification of reservoir hosts.

BYDV incidence and aphid seasonal dynamic along a climatic longitudinal gradient in Europe

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Abstract

Climate change is reshaping plant disease dynamics by modifying the distribution, abundance, and phenology of viral vectors, which exacerbates the emergence and impact of plant viruses. Among these, Barley yellow dwarf viruses (BYDVs, genus *Luteovirus*) represent a major threat to cereal production and food security. Their primary aphid vectors, *Sitobion avenae*, *Rhopalosiphum padi* and *Metopolophium dirhodum*, now exhibit increasing winter activity and earlier summer recolonization, extending the period during which virus transmission can occur. Despite their importance, the temporal dynamics of BYDV species between autumn and spring remain poorly understood, and no study has compared the viral species present in these seasons, even though symptom severity and epidemiological patterns depend heavily on viral composition and vector phenology. Moreover, the emergence of recombinant forms, such as BYDV-SOS, raises new questions about their distribution and impact.

This study aims to update knowledge on BYDV prevalence across Europe, with a focus on the newly identified recombinant BYDV-SOS. We investigate its distribution alongside BYDV-PAV and BYDV-PAS, whose distinction has often been overlooked in past assessments. The study of a longitudinal climatic gradient enables to examine the influence of extreme climatic events, landscape structure, and vector abundance on virus dynamics to identify key drivers of epidemiological change. We hypothesize that seasonal alterations may allow multiple infection waves involving different viral species, potentially resulting in distinct winter and spring prevalence patterns

Preliminary results reveal the presence of BYDV-PAV, BYDV-PAS, and BYDV-SOS across the European transect. Notably, BYDV-SOS, once restricted to Brittany, is now detected in Belgium, Germany, and the Czech Republic. Viral prevalence changed throughout the cereal growing season, with a more diverse viral community in spring and higher BYDV-SOS prevalence. Species-specific drivers emerged: *M. dirhodum* abundance influenced BYDV-SOS presence, while BYDV-PAV was shaped by climate, landscape composition, and *R. padi* abundance. No tested factor affected BYDV-PAS.

Investigation of *Phaenops cyanea* (F.) (Col., Buprestidae) and *Pissodes* spp. (Col., Curculionidae) as potential vectors of phytoratogenic fungi using massively parallel sequencing approaches

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Liva LEGZDINA, Dainis Edgars RUŅĪS

Abstract

One of the pest species causing pine tree dieback is *Phaenops cyanea* (F.). *P. cyanea* is the primary colonizer of pine trees weakened by various factors, yet still relatively viable. Unlike bark beetle infestations, trees infested by *P. cyanea* can remain asymptomatic for extended periods.

Several cases have been recorded in which species such as *P. cyanea* and *Pissodes* spp. were the most aggressive first colonizers. Wood damaged by the larvae of *P. cyanea* and *Pissodes* spp. often exhibits blue staining.

It has been proposed that these insect species can vector plant pathogenic fungi of Ophiostomataceae, *Heterobasidion* and other genera. Since the insects feed at different developmental stages and on various parts of the tree (crown, stem), we hypothesize that their mycobiome will also differ. Therefore, to gain a more comprehensive understanding of the interactions among insects, fungi, and host trees, metabarcoding of the fungal communities in larvae, pupae, adults, and infected wood is needed.

Over 370 samples of adults and larvae from both insect species, as well as damaged wood, were collected. To create a massively parallel sequencing (MPS) library, DNA was isolated from adults (*P. cyanea* - 52, *Pissodes* spp. - 23) and larvae (*P. cyanea* - 50, *Pissodes* spp. - 93), as well as from 51 blue-stained wood samples from *P. cyanea*-infested trees.

MPS will be performed on an Ion GeneStudio S5 Plus instrument or an integrated Oxford Nanopore P2 instrument.

We would like to invite you to collaborate on this project and would be happy to receive laboratory samples for this project or other information about the harmfulness of insects in your country. Instructions for collecting insect samples in the forest have been written and can be found on the institute's website:

(<https://www.silava.lv/en/research/projects/mycobiome-of-insect-pests-of-scots-pine-phaenops-cyanea-and-pissodes-spp>).

Acknowledgement: This research was funded by the European Regional Development Fund postdoctoral research aid (grant number 1.1.1.9/LZP/1/24/047).

High-throughput behavioural screening to uncover plant genes involved in host and vector manipulation by plant viruses

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Véronique BRAULT, Quentin CHESNAIS

Abstract

Plant viruses can manipulate the behaviour of their insect vectors to enhance their acquisition, retention, and transmission, a phenomenon known as vector manipulation by plant viruses. These behavioural changes are frequently mediated indirectly through virus-induced alterations of the host plant metabolism, and their nature often depends on the virus transmission mode, suggesting an adaptive strategy. For example, phloem-restricted viruses induce longer feeding (phloem sap ingestion) phases, whereas non-phloem-restricted viruses tend to trigger rapid dispersion after probing phases. Although some viral proteins involved in these effects have been identified, the underlying plant genetic and molecular mechanisms remain mostly unknown.

To improve our understanding of virus-induced deregulation in planta, we will use a high-throughput video tracking tool to quantify aphid behaviour on a SNP-mapped collection of *Arabidopsis thaliana*, comparing healthy vs. virus-infected plants. The behavioural data will be integrated into genome-wide association studies (GWAS) to identify candidate plant genes potentially involved in these host and vector manipulation by plant viruses.

A key preliminary challenge is to determine which behavioural parameters are the most relevant for GWAS. We therefore conducted initial tests on *A. thaliana* Col-0 using three viruses differing in their modes of transmission: turnip yellows virus (TuYV, circulative persistent), turnip mosaic virus (TuMV, non-circulative non-persistent) and cauliflower mosaic virus (CaMV, non-circulative semi-persistent). These experiments enabled the identification of behavioural traits of *Myzus persicae* that are specifically modified by each virus. These results provide the methodological foundations of the upcoming large-scale behavioural phenotyping across the *Arabidopsis* collection. They will enable the potential identification of plant genes involved in virus-mediated manipulation of vector behaviour, and contribute to a deeper understanding of plant-virus-vector interactions.

RNA interference in the meadow spittlebug reduces vector survival and impairs *Xylella fastidiosa* transmission

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Monica MARRA, Luciana GALETTO, Daniele CORNARA, Domenico BOSCO

Abstract

RNA interference (RNAi) is a sequence-specific gene regulation mechanism in eukaryotes and represents a promising tool for insect pest management through the delivery of exogenous double-stranded RNA (dsRNA). In Europe, *Philaenus spumarius* L. (Hemiptera: Aphrophoridae) is the main insect vector of *Xylella fastidiosa* (Xf), the causal agent of Olive Quick Decline Syndrome (OQDS) in southern Italy, where effective control strategies are lacking and sustainable alternatives are required.

In previous study we confirmed the presence of an active RNAi machinery in *P. spumarius*, and optimized dsRNA delivery methods. Here, a literature-based screening was conducted to identify potential RNAi targets, resulting in the selection of six candidate genes mainly involved in essential physiological processes. Retrieved gene sequences were screened in silico to minimize potential off-target effects on pollinators.

Corresponding dsRNA molecules were synthesized and individually delivered to adult spittlebugs by microinjection. RNAi efficiency was assessed through target transcript downregulation and survival monitoring. All tested dsRNAs induced significant transcript reduction. However, silencing of the proton ATPase gene resulted in more effective knockdown and significantly higher mortality compared to the other targets and to insects treated with dsRNA targeting Green Fluorescent Protein (dsGFP), used as a control.

Based on these findings, dsRNAs targeting proton ATPase (dsATPase), as well as TRPML (dsTRPML), which caused intermediate mortality, were further investigated to assess their potential effects on *X. fastidiosa* transmission. dsATPase reduced insect's lifespan and bacterial load in *P. spumarius* foregut.

Overall, these results demonstrate the functionality of the RNAi pathway in *P. spumarius* and highlight promising molecular targets for the development of RNAi-based strategies aimed at controlling spittlebug populations and limiting the spread of *X. fastidiosa*.

Can vibrational signals reduce phytoplasmas' transmission? Insights from *Scaphoideus titanus* and Flavescence dorée

Letizia PRODI (Centro Ricerca e Innovazione - Fondazione Edmund Mach, Letizia.prodi@fmach.it)

Giulia LUCETTI, Rachele NIERI, Cristina MARZACHÌ, Domenico BOSCO, Valerio MAZZONI

Abstract

Flavescence dorée (FD) is a major grapevine disease in Southern Europe, caused by a phytoplasma. FD transmission to grapevine plants relies mainly on the American grapevine leafhopper, *Scaphoideus titanus* (Hemiptera: Cicadellidae), which is a *Vitis* specialist in Europe. *S. titanus* is considered a phloem-feeder, and proper feeding is essential for efficient pathogen acquisition and inoculation. Recent studies on *Philaenus spumarius*, vector of the bacterium *Xylella fastidiosa*, showed that the application of disruptive vibrations to the host plant can alter its normal feeding pattern. For *S. titanus*, specific “disruptive vibrational signals” (DVS) are used to accomplish vibrational mating disruption, a method that interferes with the natural mating behavior of insect species that primarily communicate by means of sexual substrate-borne vibrations, recently referred to as pherodones. This technique of pest control has been experimentally applied to *S. titanus* for more than a decade to control the population density in commercial vineyards and is nearing commercial application.

This study tested the hypothesis that DVS can also interfere with feeding behavior, and how this could affect the FD transmission. Newly emerged adults were placed on infected plants for the acquisition access period (AAP), followed by a latency period (LP) under different DVS protocols, and then transferred to healthy plants for the inoculation access period (IAP) for a total duration of 21 days per cycle.

We expect a significant reduction of FD transmission and/or of phytoplasma load in both plants and insects, measured by RT-qPCR, compared to the non-vibrated control. These findings will be discussed in the context of using vibrational feeding disruption as a novel strategy to prevent phytoplasma acquisition and limit its spread in vineyards, along with future research directions.

#14823

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Disentangling multipartite symbiont and phytopathogenic associations in a leafhopper plant pest

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Abstract

In Central Europe, *Pentastiridius leporinus* (Hemiptera: Cixiidae) is a major vector of two phytopathogens, namely *Candidatus Arsenophonus phytopathogenicus* and *Candidatus Phytoplasma solani*. The plant pathogens and the cicada have proven difficult to manage as the Cixiid pest has rapidly expanded its host plant range and its affected areas.

In addition to the two aforementioned plant pathogenic bacteria, the insect host further harbors three ancient primary symbionts and two additional bacterial species of unknown function, thus creating a multipartite system of unusual complexity. In this intertwined system of many moving parts, we slowly disentangle the roles of the many endosymbionts as well as the disease mechanisms of the vectored phytopathogens. We use metagenomic sequencing, multiRNAseq analysis, and bacterial fluorescence *in situ* hybridization, to unravel the host-microbe-microbe interactions within *P. leporinus* through the different life stages, that make this pest so difficult to control.

Epidemiology of the Apple Proliferation phytoplasma: insights at different regional levels

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Marine PALLEZ, Lapo RAGONIERI, Erika CORRETTO, Wolfgang JARAUSCH, Imen KHARRAT-JARBOUI, Carmelo RAPISARDA, Alexander WEIGAND, Hannes SCHULER, Michael EICKERMANN

Abstract

Psyllids are key vectors of phytoplasmas affecting economically important crops. Among them, *Cacopsylla melanoneura* and *Cacopsylla picta* are the main vectors of 'Candidatus Phytoplasma mali', the causal agent of Apple Proliferation (AP), a serious disease of apple in Europe. Both species are univoltine, phloem-feeding insects that overwinter as adults on shelter plants (mainly conifers) and migrate to apple in spring, where the AP-phytoplasma epidemiological cycle continues. However, their natural infection rates and vector competence vary markedly across Europe, as confirmed in recent findings within the PsyPhyPaths2 project in Luxembourg. The project assessed the distribution and prevalence of fruit-trees phytoplasmas in plant hosts and their main psyllid vectors, indicating a wide distribution of the AP-pathosystem in Luxembourg. In particular, 25% of *C. picta* specimens resulted positive to APp. These observations align with current knowledge on AP epidemiology. *C. picta* dominates where it occurs, while *C. melanoneura* is the main vector where *C. picta* is absent or rare, highlighting regional differences in vector competence. Increasing evidence indicates that these differences are driven by interactions among phytoplasma genotype and titre, as well as the genetic background of the vector. A transnational project - VectoRise - aims to assess the ecological risks and regional specificities of the apple-psyllid-phytoplasma pathosystem under current and future climate. By integrating surveys and experimental studies from Luxembourg, Germany, and Northern Italy, the project focuses on the acquisition dynamics of AP phytoplasma by geographically distinct populations of *C. melanoneura*. The project is structured around three pillars: (i) field surveys and comparative genomic analyses of both pathogen and vector; (ii) experiments on acquisition efficiency involving different phytoplasma strains and insect genotypes; and (iii) experiments to evaluate the effects of future climate on transmission. The outcomes will support the development of region-specific management strategies and improve risk assessments for apple production.

Development of RNAi-Based Biopesticide: dsRNA-Mediated Gene Silencing in *Tenebrio molitor* and Evaluation of dsRNA Biosafety

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Angharad GATEHOUSE, Catriona ANDERSON, Martin EDWARDS

Abstract

Sole reliance on chemical pesticides for insect pest management has led to the development of resistant pest populations, creating significant challenges for control and increasing environmental costs. A sustainable alternative is the development of biopesticides, particularly those utilizing RNA interference (RNAi) technology—a sequence-specific gene-silencing mechanism mediated by double-stranded RNA (dsRNA). This research aims to develop a biopesticide with enhanced RNAi efficacy by improving dsRNA stability through nanoparticle-mediated delivery and to evaluate the biosafety of dsRNA molecules using bumblebees. As a proof of concept, the small-conductance calcium-activated potassium channel gene (*TmSK*) in *Tenebrio molitor* was targeted. Gene expression analysis revealed that *TmSK* was expressed at all life stages of the insect, with the highest expression in the head. Injection of 2 µg dsRNA into larvae (0.008% of body mass) resulted in reductions of 15.0% and 10.0% in *TmSK* mRNA levels at 2 and 7 days post-treatment, respectively, and reduced survivability by 33.3% at 15 days. Additionally, the study assessed the non-target effects of ds*TmSK* on the pollinator insect bumblebee, which showed no mortality at a dose of 4 µg ds*TmSK*. The study will also explore product formulations, such as integrating dsRNA with functionalized cationic polymers, to enhance dsRNA stability, uptake, and efficacy, thereby promoting this approach as an effective and sustainable solution for crop protection.

Oral delivery of γ ZcCOPI leads to severe physiological abnormalities and increases susceptibility to β -cypermethrin stress in the melon fly, *Zeugodacus cucurbitae*

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Momana JAMIL

Abstract

The melon fly, *Zeugodacus cucurbitae* Coquillett (Diptera: Tephritidae), is a notorious quarantine pest. It poses a significant risk to fruits and vegetables in tropical and subtropical regions, affecting crops like cucumber, zucchini, muskmelon, bitter gourd and pumpkin. The rapid development of insecticide resistance necessitates the alternative strategies to manage this pest. RNA interference (RNAi) offers a promising and innovative approach for controlling major agricultural insect pests and has recently been approved for use in controlling the *Leptinotarsa decemlineata*. In this study, the essential gene, coatamer complex subunit gamma (γ COPI), was assessed as an RNAi target using an oral feeding delivery method. Z γ COPI was most abundant in eggs and 2nd instar larvae in developmental stage dependent expression analysis, while tissue wise expression showed its highest expression in larval midgut. Exposure of *Z. cucurbitae* to the corresponding dsRNA of Z γ COPI significantly reduced gene expression leads to larval melanization, larval-pupal transition delay and larval mobility. Additionally, adults that emerged from Z γ COPI knockdown larvae exhibited spotless wings, reduced phenoloxidase (PO) activity, and increased susceptibility to β -Cypermethrin exposure. These results demonstrated that Z γ COPI plays a role in the development and regulation of innate immunity, offering a promising target for insect pests management through RNAi.

Assessing the impact of different botanical insecticides against Wheat Aphid (Hemiptera: Aphididae)

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KHANSA SALIK

Abstract

Five botanical insecticides were tested against wheat aphids (*Schizaphis graminum* R. and *Sitobion avenae* F.) in a field in Gehlan Hithar, Tehsil Chunian, district Kasur: onion and garlic (*Allium cepa* and *Allium sativum*), banana peel (*Musa paradisiaca*), hot pepper (*Capsicum frutescens*), turmeric (*Curcuma longa*), and bitter gourd (*Momordica charantia*). Wheat aphids were purposely exposed to the botanical extracts listed above, and the quantity of functioning and dead aphids was monitored to estimate the average aphid population and aphid mortality %. The plant-based pesticide had multiple impacts on aphid infestations. The combination of onion and garlic spray repeatedly wiped out the most aphids (83.5%), followed by bitter gourd (74.40%) and hot pepper (71.17%). The outcomes of these botanical insecticides on wheat aphids were investigated in an attempt to reduce the use of pesticides and insecticides mainly to provide us with pure and good wheat that does not harm human health and is also clean and free of harmful chemical residues.

Field Evaluation of Semiochemical Deterrents for the Management of *Ips typographus*

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Werner TIRLER, Alessandro ANDRIOLO, Enrico TOMELLERI, Sergio ANGELI

Abstract

The European spruce bark beetle, *Ips typographus* (L.), is a major threat to Norway spruce stands, capable of causing extensive forest mortality during critical mass population outbreaks. Current management techniques—pheromone trapping and sanitation logging—are only partially effective and entail ecological drawbacks. In this study, we evaluated chemical ecology-based deterrent strategies under field conditions, using capture counts as a proxy for compound repulsiveness. A large-scale experiment was conducted in South Tyrol, Italy, using 81 pheromone-baited Theysohn traps across 3 one-hectare plots. Traps were assigned to nine treatments, consisting of two controls (aggregation lure alone and with carrier) and seven deterrent blends containing either synthetic anti-aggregation compounds (verbenone, isophorone, 1,8-cineole, 3-octanol, (+)- α -pinene) or essential oils from non-host species, as *P. mugo*, *P. cembra* and *P. sylvestris*. Beetles were sampled across two generations (May–June; July–August 2025), and counts were analyzed using negative binomial GLMs, as well as mixed-effects models to account for subplot variability. Results indicated strong treatment effects. Control traps consistently caught the highest numbers, while the multi-component blend T9 (1,8-cineole, 3-octanol, and (+)- α -pinene and verbenone) reduced captures to <5% of control levels during peak activity. Synthetic blends (verbenone alone, verbenone plus isophorone, isophorone alone) also effectively reduced catch rate up to 7% of the control, whereas essential oil treatments (T6–T8) produced only moderate deterrence (ca. 50%). Due to the abnormally wet July, there was a large decline in beetle activity from the first to the second generation, but relative treatment effects remained consistent. Mixed-effects models confirmed minimal spatial heterogeneity, and treatment efficacy was robust across replicates. These findings demonstrate that chemical ecology-based deterrents have the potential to substantially reduce *I. typographus* aggregation in pheromone-baited traps under field conditions. The study highlights the potential of deploying such deterrents in integrated strategies to mitigate bark beetle damage.

SAGROPIA: Reducing Chemical Insecticide Use in Potato and Sugar Beet through Biological Control–Based Integrated Pest Management

Carlos BERNARDES (Rovensa Next, Carlos.bernardes@rovensanext.com)

Abstract

Insect pests such as aphids (*Myzus persicae*), Colorado potato beetle (*Leptinotarsa decemlineata*), and soil dwelling wireworms (*Agriotes* spp.) remain major constraints in European potato and sugar beet production. Their management still largely relies on chemical insecticides, including candidates for substitution such as Pirimicarb, Lambda Cyhalothrin and Esfenvalerate, which pose risks to non target organisms and accelerate resistance development. In line with the European Farm-to-Fork strategy, the SAGROPIA project aims to significantly reduce chemical insecticide use by embedding biological insecticides into robust, field ready Integrated Pest Management (IPM) strategies.

SAGROPIA is a consortium of eleven academic and industry partners that is evaluating a portfolio of thirteen biological and low risk Plant Protection Products, including five biopesticides derived from botanical extracts and entomopathogenic microorganisms, several of which are already marketed for other crop systems. Rather than pursuing one to one replacement of chemical insecticides, the project applies a system level IPM approach, combining multiple biological solutions with complementary modes of action and existing agronomic practices to maintain efficacy under diverse pedoclimatic conditions.

The project is assessing insect pest control efficacy of individual and combined biological insecticides under controlled conditions, followed by their integration into region specific IPM strategies. These strategies are subsequently validated in participatory, large scale on farm trials across five European regions, targeting key insect pests in both crops. Performance is evaluated in terms of pest suppression, yield stability, operational feasibility, and cost–benefit ratios, alongside comprehensive environmental sustainability assessments.

By targeting a 50% reduction in chemical insecticide use while preserving crop productivity, SAGROPIA will demonstrate that biologically based insect control, when deployed at IPM level, can provide an effective, scalable and environmentally sound pathway for sustainable management of insect pests in European row crops.

Current Status of *Tuta absoluta* (Lepidoptera: Gelechiidae) Infestation in Chungcheongnam-do, Korea, and the Potential for Eco-Friendly Pest Management

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YounGyung SEO

Abstract

ShareGreen and the Smart Agriculture Headquarters have recently undertaken joint efforts to develop eco-friendly strategies for managing *Tuta absoluta* (Tomato leafminer), which has emerged as a serious agricultural issue in the Republic of Korea. We conducted field surveys in two farms suffering severe infestation in Gongju, Chungcheongnam-do, as well as at the ShareGreen farm located in Yesan-gun, Chungcheongnam-do, to investigate the occurrence of *T. absoluta* and to evaluate the control efficacy of an organically derived agricultural input currently under development.

T. absoluta was detected in all surveyed fields from summer through early winter, indicating a strong tolerance to low temperatures. The pest caused substantial foliar damage, whereas fruit damage did not increase markedly until later in the season. Although foliar damage and fruit damage were positively correlated ($p < 0.001$), the explanatory power of this relationship was low ($R^2 = 0.076$). This suggests that, despite a statistically significant positive association, foliar damage alone does not adequately explain variation in fruit damage. Such variation is likely influenced by multiple agronomic and environmental factors, including cultivation site, production practices, and surrounding ecological conditions.

Field evaluations of the newly developed organic agricultural input conducted in the two affected farms demonstrated a clear reduction in *T. absoluta* density following application, with the control effect persisting over time.

Non-thermal plasma technology as an innovative approach for controlling *Tribolium* spp. infestation and improving early growth in wheat

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Abstract

Stored-product beetles of the genus *Tribolium* (Coleoptera: Tenebrionidae), especially *Tribolium castaneum* and *T. confusum*, are key pests in wheat storage, and safer non-chemical control tools are increasingly needed. In the present study, supported by collaborative project ADER 2.1.7, we report on the application of non-thermal plasma treatments as an alternative disinfestation method while enhancing the wheat early growth. The experiments were performed at INFLPR by using a linear DBD plasma curtain-jet of 10 cm width/2 mm length generated at using 50 W RF power (13.56 MHz) in flowing Argon. The plasma source was translated horizontally above the seeds, which also contained insects (50 g of seeds and 30 adults/repetition), within a semi-enclosed setup designed to retain the insects while exposing them to plasma environment during scanning, for total exposure times of 3, 9 and 15 min. This accounted for direct plasma exposure of 14.25% of treatment time, and respectively to continuous exposure to reactive plasma species.

The treatments efficacy was assessed regarding insect mortality, at ICDPP, and wheat plants development (USAMV), respectively. The results demonstrated the insect mortality proportionality with the treatment time, reaching 77% for 15 minutes of exposure. The oxygen addition during treatment was particularly effective for suppression of immature stages, with 100% mortality upon 3 min exposure. In parallel, wheat (*Triticum aestivum* L., cv. Glosa) seed compatibility was assessed by monitoring germination dynamics, seedling vigor, growth, and basic physiological indicators. Across plasma-treated seed lots, early germination and emergence were maintained or improved, final germination reached ~98–99% by day 9, and seedling height at ~1 month was comparable to the control. Photosynthetic pigment profiles remained within physiological ranges, supporting the absence of phytotoxic responses. The final contribution will integrate insect efficacy, plasma dose metrics and seed safety endpoints to support efficacy of cold plasma treatment for stored-wheat protection.

Repellent effects of essential oils on *Tetranychus urticae*

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Sofia DERVISOGLOU, THEODORE STATHAKIS, Anna KARANTONI, Zacharoula ZAMPETI, Ioanna PITTEROU, Anastasia DETSI

Abstract

Tetranychus urticae is a cosmopolitan mite pest which causes serious economic damages on an extremely high number of crops. Essential oils (EOs) hold a promise in the control of several agricultural pests including *T. urticae*. Our study aims to investigate the repellent effects of basil (*Ocimum basilicum*), lavender (*Lavandula officinalis*), laurel (*Laurus nobilis*), bergamot (*Citrus bergamia*) and mandarin (*Citrus reticulata*) EO emulsions on *T. urticae* adults. The chemical profile of each EO was determined using GC-MS technique. Repellency bioassays were conducted by placing 10 female individuals in the central vein of a tomato leaflet, which had been dipped in the emulsion (1%) by one side and in deionized water by the other side. The number of adults on each side of a tomato leaflet was recorded 1h, 2h, 4h and 24h after treatment (n=10). Results showed that among the tested EOs lavender had the highest repellent effect (76%, 76%, 58%, and 46%, 1h, 2h, 4h and 24h after treatment, respectively), followed by laurel EO (62%, 64%, and 54%, 1h, 2h, 4h and 24h after treatment, respectively). Finally, basil showed a moderate repellency (36%, 44%, and 36%). The citrus EOs emulsion demonstrated lower levels of repellency (2–26% for mandarin and 10–17% for bergamot). Therefore, the EO of lavender showed a high repellent effect and further studies should extensively explore its potential in the control of *T. urticae* under more field-related conditions.

This abstract has been produced with the financial assistance of the European Union under the Interreg NEXT MED Programme within the framework of Project No. A_T_1.1_0167-EONANOBIOPS ‘Essential Oil-derived Next Generation Nano-Biopesticides for Sustainable Eco-Friendly Agriculture’.

Harnessing self-DNA autotoxicity for selective agricultural pest control

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Silvia CACCIA, Maria Rosaria CHIANESE, Andrea BECCHIMANZI, Stefano MAZZOLENI, Silvia GIGLIOTTI, Francesco PENNACCHIO

Abstract

Fragmented extracellular DNA has emerged as a highly species-specific inhibitor of growth and development across different taxa, including plants, insects, nematodes and microorganisms. These findings suggest the existence of an auto-toxicity mechanism mediated by self-DNA, although the underlying molecular pathways remain poorly understood. Here, we investigated the translational potential of this conserved phenomenon for selective agricultural biocontrol using the invasive crop pest *Spodoptera littoralis* as a model target species. Oral delivery by gavage of fragmented self-DNA to larvae led to a marked reduction in growth compared to controls receiving heterologous DNA and ultimately resulted in significant mortality over development. These effects were reproduced under a more realistic exposure scenario by feeding larvae tomato leaves sprayed with self-DNA, thus confirming its potent inhibitory impact. Collectively, our findings support the concept that fragmented self-DNA could be exploited as a novel, environmentally sustainable tool for pest management.

Side effects of nanoformulated essential oils on *Encarsia formosa*

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Dejan MARČIĆ, Antonio BIONDI, Lucia ZAPPALÀ, Orlando CAMPOLO, Michele RICUPERO

Abstract

Botanicals provide a broad source of active compounds for developing effective pesticides for agricultural use. However, the inclusion of new potential bioinsecticides in Integrated Pest Management (IPM) programs depends not only on their efficacy against key pests but also on their safety for beneficial arthropods. This research focused on the compatibility of five nanoformulated plant essential oils (EOs) with the whitefly parasitoid *Encarsia formosa* (Hymenoptera: Aphelinidae). Under laboratory conditions, we evaluated the lethal and sublethal effects on life history traits of the F₀ and F₁ generations of *E. formosa* following topical exposure of pupae to EOs, each tested at three selected lethal concentrations (LC₁, LC₁₀, LC₅₀). These concentrations were previously estimated through acute toxicity bioassays on the parasitoid host *Trialeurodes vaporariorum* Westwood (Hemiptera: Aleyrodidae). Results showed that only the LC₅₀ values caused significant acute toxicity in the parasitoid pupal stage. After exposure to LC_{1s}, only garlic EO significantly reduced the total parasitism of surviving wasps. Similarly, in the exposure bioassay to LC_{10s}, only garlic EO significantly prolonged the development of juveniles in treated pupae, while only lavender and garlic EOs significantly affected the longevity of adult wasps compared to the control. All nano-EOs applied at their LC_{50s} significantly prolonged juvenile development (by 10.9 to 16.6%), reduced longevity (by 17.7 to 37%), and decreased total parasitism from 43.2 to 71.6%, with garlic EO having the most detrimental effects on the parasitoid, followed by peppermint, lavender, fennel, and rosemary EOs. However, none of the tested LCs significantly affected the adult emergence rate in F₁ generation wasps. Overall, our findings suggest that all the tested EOs can be detrimental to *E. formosa* even at low doses and should be avoided when pupae are present in the system. Future field studies are warranted to validate the ecotoxicological consequences of EOs within the agricultural context.

Age Dependent Effect of Solanaceae Glycoalkaloids on the Retrocerebral Complex in *Tenebrio molitor* Beetle

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Abstract

Neuroendocrine system regulates many different physiological processes in insects, including reproduction, growth, development, diapause. One of the major neurosecretory organs is the retrocerebral complex, which consists of *corpora cardiaca* and *corpora allata*.

Plants frequently contain secondary metabolites, for example glycoalkaloids, which have a large spectrum of biological activity. Since several years, researchers have provided evidence of the harmful effects of glycoalkaloids on insects, such as disruption of energy metabolism through modulation of key enzymes of glycolysis, the Krebs cycle and fatty acid beta-oxidation. Glycoalkaloids also induce oxidative stress and impair the antioxidant system, bind to cholesterol causing cellular membrane damage and inhibit acetylcholinesterase and butyrylcholinesterase in the nervous system.

Our knowledge concerning the effect of glycoalkaloids in insect neuroendocrine system is limited. Therefore, the aim of this study was to detect structural changes of the retrocerebral complex induced by *Solanaceae* glycoalkaloids, including both the assessment of organ damage and adaptive changes arising from compensatory mechanisms.

Firstly, *Tenebrio molitor* adult beetles were injected with alpha-solanine or alpha-chaconine at concentrations of 10^{-7} M and 10^{-5} M to evaluate their effects on mortality. Next goal was to analyse the morphology of the retrocerebral complex in three time points – 24h, 48h, 72h post-injection that showed changes in length and width of *corpora cardiaca* and *corpora allata*. This study pointed that *Solanaceae* glycoalkaloids affect the size of the retrocerebral complex in the 7- and 30-day-old adult beetles. Our experiments showed that the 7-day-old beetles exhibited greater sensitivity to glycoalkaloids than the 30-day-old insects. Observed malformations of the retrocerebral complex by tested glycoalkaloids may alter activity of this organ, leading to serious disturbance in insects' development. These findings might be helpful in searching for new bioinsecticides based on plant derived substances.

This study was supported by project number 2023/51/B/NZ3/01550 from the National Science Centre, Poland

Sustainable RNA interference approaches to control the Japanese beetle *Popillia japonica*: target genes selection and innovative dsRNA producing platform

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Abstract

Strategies based on RNA interference (RNAi) emerged in crop protection against fungi, viruses and insect pests. Here, double-stranded RNAs (dsRNAs) were newly designed and synthesized to silence essential genes of the Japanese beetle *Popillia japonica* (Coleoptera: Scarabaeidae), a highly polyphagous quarantine invasive species that cause severe damages to crops. Nine genes of *P. japonica* were selected as potential candidates able to induce lethal phenotype, based on previous wide-genome screenings on other coleopterans. To avoid off-target effects, genes showing over 80% identity with pollinator homologs were excluded and *P. japonica* dsRNAs were designed in the least conserved portions according to alignments with *Apis mellifera*, taken as representative of beneficial arthropod species. In an ex-vivo degradation assay, dsRNAs were not degraded when incubated in *P. japonica* midgut juice. This confirmed the possible persistence of such molecules in the digestive canal of adult beetles and indicated that RNAi-based approaches are worth exploring for this species. Different delivery strategies were attempted to administer dsRNAs to larvae (by injection, soaking and soil drench) and to adults (by injection and plant-mediated feeding assays). Such protocols allowed to test five candidate genes and select the most effective in increasing mortality. Following injection of dsRNAs, all the tested specific transcripts were significantly reduced up to 21 days post treatment, as also supported by the sequencing of smallRNA libraries obtained from treated samples. In adults, RNAi-mediated depletion of a transcript encoding a 26S proteasome subunit reduced survival and prolificacy rates. Moreover, *Chlamydomonas reinhardtii* and *Synechococcus* sp. were used to explore the possible use of microalgae and cyanobacteria for cost-effective and suitable production and delivery of dsRNAs. These data pave the way for the possible use of RNAi approaches to control the Japanese beetle, proactively waiting for the EU approval of exogenously applied dsRNAs.

Clove essential oil nano-formulation: a potential bio-acaricide for beehive protection

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Abstract

Effective management of *Varroa destructor* remains a major challenge in beekeeping, as infestations contribute significantly to colony collapse disorder (CCD). Along with its direct damage inflicted on bees during its trophic activity and the suppression of host immune responses, *V. destructor* poses an additional threat to honeybees by transmitting multiple viruses, which can potentially lead to colony death. Mite control relies on multiple strategies, but it is still largely dependent on synthetic acaricides, whose extensive use has led to resistance phenomena, as well as the contamination of apicultural products. As an alternative, several botanical-based formulations are currently authorized for *V. destructor* management in various countries.

Here, an innovative acaricide containing clove [*Syzygium aromaticum* (L.) Merr. & L.M.Perry] EO has been characterized, formulated, and evaluated in laboratory and field conditions to assess toxicity against *V. destructor*, as well as the impact on adult *Apis mellifera* (L.) survival and behavior. Clove EO was chemically characterized by GC-MS and then formulated using different surfactants to assess the adequate hydrophilic-lipophilic balance (HLB). Among the obtained nano-emulsions, the one with the best stability and physical characteristics (165.4 ± 3.17 nm, 0.224 ± 0.035 PDI, -28.5 ± 1.4 mV) was selected and used for the following experiments. In laboratory trials, *S. aromaticum* EO caused significant mortality in mites, with a dose-dependent trend, while acute toxicity on worker bees was negligible. Furthermore, hive treatments with the nano-formulation did not significantly impact bees' orientation and homing ability. Overall, our results suggest that the *S. aromaticum* EO nano-formulation could be a valuable and safe tool in controlling *V. destructor*.

Essential oil–entomopathogenic nematode interactions in laboratory bioassays for combined truffle beetle biocontrol

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Abstract

The truffle beetle (*Leiodes cinnamomeus*) represents the main insect threat to black truffle (*Tuber melanosporum*) orchards. Among alternative control strategies, entomopathogenic nematodes (EPNs) show potentialities against adults and larvae of this beetle, while essential oils (EOs) have recently been proposed as botanical insecticides targeting adult stage. The joint use of both tools within Integrated Pest Management programs could improve pest suppression. However, their combined application requires prior evaluation of EO effects on EPN performance.

In this study, we assessed the compatibility of three insecticidal and nematicidal essential oils (*Allium sativum*, *Mentha suaveolens* and *Satureja montana*) with three EPN species (*Steinernema feltiae*, *Steinernema carpocapsae* and *Heterorhabditis bacteriophora*). Laboratory bioassays were conducted to examine lethal and sublethal effects, fumigant toxicity and chemotactic responses, measuring nematode survival, infectivity, reproduction and behavioural attraction.

Allium sativum EO produced the strongest adverse effects, causing high mortality in all EPN species after 24 and 72 h through both direct exposure (97–99%) and fumigation (40–42%), and significantly reducing their infective capacity against *Galleria mellonella*. *Satureja montana* EO induced moderate but significant mortality after 72 h and acted as a repellent for *S. feltiae* and *H. bacteriophora*. In contrast, *Mentha suaveolens* EO showed negligible effects on nematode survival, pathogenicity and reproduction.

These results indicate that *M. suaveolens* EO is the most suitable candidate for combined use with EPNs in truffle beetle management strategies. Nevertheless, further validation under field conditions and in the presence of *L. cinnamomeus* is necessary to confirm the practical applicability of these findings.

Laboratory assessment of hydrogel and nano-formulations of some selected synthetic insecticides against fall armyworm *Spodoptera frugiperda* (Lepidoptera: Noctuidae)

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Abstract

The fall armyworm *Spodoptera frugiperda* (Lepidoptera: Noctuidae) has been a challenging pest of maize crop worldwide. Novel target-oriented approaches are needed to mitigate the damage of *S. frugiperda*. Farmers rely predominantly on extensive use of synthetic insecticides, but have unsatisfactory control because of the cryptic feeding style of the pest's larvae and rapid decomposition of the applied insecticides. This study aimed to screen out available synthetic insecticides being used against different lepidopterous pests including *S. frugiperda* under field conditions and then the two most effective insecticides were further formulated with silver nanoparticles and with sodium alginate hydrogel beads and were bioassayed against the third larval instar of *S. frugiperda* under laboratory conditions using the standard leaf-dip method. Treatments included normal and nanoformulated commercial formulations of emamectin benzoate and chlorantraniliprole (@ 90 mL/acre), and of emamectin benzoate and lufenuron formulation (@ 400 mL/acre). According to the results, the nanoformulated recommended dose of the emamectin benzoate and lufenuron formulation manifested the highest mortality (100%) at 24 h, followed by the nanoformulated recommended dose of the emamectin benzoate and chlorantraniliprole formulation (100%) at 48 h post-treatment. In another bioassay, alginate beads loaded with the recommended dose of emamectin benzoate and lufenuron formulations caused up to 50% more larval mortality compared to beads loaded with emamectin benzoate and chlorantraniliprole formulations, which resulted in 40% higher larval mortality than the control treatments. The findings suggest that nanoparticle-based and hydrogel bead formulations can be viable and eco-friendly alternatives to the conventional administration of insecticides, offering improved larval mortality, controlled-release of insecticidal compounds, and reduced environmental impact. Future research should focus on upscaling these formulations for practical implications and for assessing their compatibility with other integrated pest management (IPM) strategies under diverse agroclimatic conditions.

Targeting aphid symbionts: Effects of *Bacillus subtilis* on aphid microbiota

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Abstract

Controlling insect pests remains a major challenge for modern agriculture and global food security. While synthetic pesticides are highly effective, their use poses multiple risks, including ecosystem contamination, biodiversity loss, and development of resistance in phytophagous populations. Consequently, alternative strategies based on microorganisms or their secondary metabolites are gaining attention, offering greater selectivity and environmental safety.

Aphids are major crop pests, causing direct feeding damage and transmitting numerous plant viruses. Their persistence on host plants is partly supported by symbiotic microorganisms, which provide essential nutrients and enhance stress tolerance, complicating control efforts. In this study, we evaluated the impact of three *Bacillus subtilis* strains on the abundance and organization of obligate and facultative symbionts in *Myzus persicae*, *Acyrtosiphon pisum*, and *Macrosiphum rosae*. Spray treatments were most effective against *A. pisum* and *M. rosae*, with high levels of *Bacillus* detected within aphid bodies. Infection reduced the absolute abundance of the obligate endosymbiont *Buchnera aphidicola*, accompanied by progressive degeneration of symbiont cells. Microscopic observations revealed substantial alterations in *Buchnera* cell architecture: initial cytoplasmic reorganization, followed by cell shrinkage, fragmentation of the perisymbiotic membrane, and ultimately amorphous or crescent-shaped symbiont cells. In contrast, the facultative symbiont *Serratia symbiotica* remained unaffected.

These effects are likely mediated by antimicrobial secondary metabolites, particularly surfactin, encoded by all analyzed *B. subtilis* strains. Our results suggest that obligate symbionts, often overlooked in studies of biological pest control, play a key role in aphid survival under the influence of entomopathogenic bacteria. This study highlights the potential of *B. subtilis* as an ecological alternative for aphid management and underscores the importance of targeting symbiont-mediated pathways in sustainable pest control strategies. Project funded by the National Science Centre, grant No. 24 2022/47/B/NZ9/03472.

RNAi-based biotechnological approaches for *Halyomorpha halys* (Stål) control

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Abstract

Halyomorpha halys Stål (Hemiptera: Pentatomidae) is an insect native of eastern Asia, but in the last three decades it has spread to Europe, North Africa, North and South America. It is highly polyphagous, with more than 300 reported hosts. In addition, its rapid expansion in recent years was facilitated by its ability to adapt to local environmental conditions and by the absence of natural antagonists in the new habitats. *H. halys* causes significant agricultural losses to many fruits, vegetables and crops. Currently, pest management is mainly conducted by chemical control with broad-spectrum insecticides, but since chemical pesticides are strongly limited by the latest regulations (e.g. Europe), management relies on Integrated Pest Management (IPM). Furthermore, in recent years there has been a growing interest in biological control through the use of parasitoids and in biotechnological innovative strategies. RNA interference (RNAi) mediated by double-stranded RNA (dsRNA) is an emerging powerful tool against pest insects. This approach is triggered by dsRNA and leads to the selective degradation of a specific target mRNA and consequently to reduced levels of the coded protein. In this research, genes encoding for proteins involved in essential activities for the insect's survival have been chosen as RNAi targets, in order to limit their expression levels possibly induce mortality. Juvenile and adult stages of *H. halys* were topically treated with dsRNAs complementary to target genes to measure the silencing effect and the subsequent mortality. Moreover, dsRNAs complementary to transcripts of salivary proteins have been also investigated to induce changes in feeding behavior studied by electropenetrography technique (EPG). These strategies have shown encouraging results, validating the potential role of dsRNAs in *H. halys* control.

Method-driven variation in fungicide–herbicide compatibility with entomopathogenic fungi

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Abstract

Integrating entomopathogenic fungi (EPF) into crop protection and pest management programs requires ensuring their compatibility not only with insecticides but also with herbicides and fungicides to enable simultaneous applications and reduce operational costs. Compatibility is typically assessed by incorporating pesticides into growth media and measuring toxicity through germination, growth, and sporulation (Biological Index, BI). However, field applications mainly expose conidia directly to pesticides, potentially leading to mismatches between laboratory and real-world outcomes. Here, we evaluated the compatibility of five fungicides (copper oxychloride, fosetyl+proamocarb, potassium phosphonate, difenoconazole and fluopyram+tebuconazole) and four herbicides (diflufenican, oxyfluorfen, MCPA, and glyphosate) with two EPF strains (selected to be developed against olive fruit fly) comparing the conventional medium-amendment approach (MAA) with a direct conidial–pesticide mixture method (CPM), and relating both to in vivo performance. For *Metarhizium brunneum*, only one of four herbicides was compatible using MAA (BI > 60), whereas CPM classified all four as compatible. Of the five fungicides, MAA classified three as compatible and two as toxic, while CPM classified three as compatible and two as moderately toxic (BI 42–66). In vivo bioassays using adults of the tephritid model *Ceratitis capitata* (Wied.) confirmed that CPM results aligned more closely with observed efficacy. *Beauveria bassiana* showed a similar pattern, albeit with lower virulence and slightly lower fungicide compatibility, again with CPM reflecting in vivo performance more accurately. CPM better predicts EPF compatibility under realistic conditions than MAA, supporting the safe co-application of several agrochemicals with EPF to reduce field operations, soil disturbance and overall management costs.

Assessment of cyantraniliprole for olive fruit fly control: novel bait formulation and novel high precision UAV aided applications

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Abstract

The olive fruit fly (OFF), *Bactrocera oleae*, is a major pest of olives in the Mediterranean region. Pest control is mainly based on regional baited insecticide applications and/or canopy sprays. Complex and often unpredictable population dynamics, synergy with fungal pathogens and development of resistance in key insecticidal compounds in the olive orchards of Crete have resulted in devastating damages by OFF over the past years. The diamide insecticide cyantraniliprole (cyazypyr®), formulated as a suspension emulsion (SE), has recently been registered for OFF control under the trade name Exirel® for both canopy and baited sprays. Exirel® is now considered an established OFF control solution; however, bait sprays require tank-mix with commercial insect attractants (hydrolyzed proteins / urea). For this reason, a novel ready-to-use bait formulation for cyantraniliprole has been developed under the trade name Atraxis®. Within the frame of the present work, the new product was evaluated under laboratory and field conditions. Utilizing a lab bait-feeding bioassay system for OFF adults, Atraxis® was compared to Exirel® at the label rate against 19 field collected populations from Crete. On average, the novel formulation exhibited significantly higher % mortality levels compared to the tank-mix (Exirel®/attractant). Under field conditions, Atraxis® was applied in commercial orchards in Crete using a high precision UAV aided application protocol, namely GreenJet® and its performance was compared to the established tractor based ground applications. The OFF population density and fruit damage were monitored through the cropping season for 11 weeks using McPhail traps and random fruit sampling (6 August - 23 October). No significant differences were observed between the two applications methods with regard to pest population density levels; however, the fruit damage was reported significantly lower in the Atraxis® UAV plots, providing positive indications for the use of UAV technologies in bait applications.

Improving the efficacy of registered products for *Phthorimaea absoluta* control: combining oil-based adjuvants with the insecticide spinosad

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Abstract

The South American tomato pinworm, *Phthorimaea absoluta* (Meyrick) (Lepidoptera: Gelechiidae), has spread across most Afro-Eurasian countries, posing a major threat to global tomato production. Its control has become increasingly challenging due to the development of resistance and the ban of many insecticidal compounds under European regulations. The spinosyn insecticide, spinosad remains one of the few effective active ingredients available. However, optimizing the performance of product is crucial for integrated resistance management. This study evaluated the efficacy of spinosad alone and in combination with two adjuvants: Adigor, a methylated rapeseed oil-based adjuvant, and Clavitus, a fatty acid potassium salts-based formulation, against different strains of *P. absoluta* in an attempt to establish a pathway for improving the efficacy of registered pest control products. Leaf dip bioassays using the IRAC 022 method were conducted in the laboratory on four populations, and mortality rates were recorded. At the label rate (120 ppm), spinosad exhibited mortality levels ranging from 50.5% to 73%, and at a low rate (40 ppm) mortality levels ranged from 43% to 56.9%. The combination of spinosad at label rate with Adigor, increased mortality by 2% to 25.8%, while the addition of Clavitus resulted in an increase of 27.9% to 45.2%. Similarly, at the low spinosad rate, the addition of Adigor and Clavitus improved efficacy by 10.8% to 32%, and 21.6% to 49.4% respectively, indicating a significant enhancement of spinosad's activity in all cases. The combination of spinosad with Adigor and Clavitus enhanced pest control level, providing a valuable strategy for managing *P. absoluta*. Given the increasing regulatory restrictions on registered chemical insecticides, integrating adjuvants into pest management programs could contribute to the sustainable control of key agricultural pests.

Occurrence, Parasitism, and Control of the Strawberry Blossom Weevil (*Anthonomus rubi*) in South Tyrol, Italy

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Abstract

The strawberry blossom weevil (*Anthonomus rubi*) is an important pest of strawberries as well as raspberries, blackberries, and other small Rosaceae. Adults damage flower buds by laying eggs into them and severing the flower stalks. Larvae subsequently develop inside buds, leading to bud loss and significant yield reductions.

The occurrence of *A. rubi* was monitored in two valleys of South Tyrol, Italy, during the 2023–2025 growing seasons. Beetle presence, damage intensity, and flight activity were assessed using yellow sticky traps baited with pheromones. In addition, the adulticidal efficacy of the active ingredients spinosad, acetamiprid, tau-fluvalinate, cyantraniliprole, and deltamethrin was evaluated. Potential biological control agents were investigated through the collection and identification of parasitoids.

The results demonstrated that the traps were suitable for monitoring purposes; however, only a small proportion of the existing population was captured. Peak flight activity occurred in July and August, and the yellow traps predominantly attracted males. Among the tested insecticides, spinosad exhibited a moderate level of efficacy against adult beetles. Parasitism rates in strawberry fields were generally very low. Although entomopathogenic fungi caused 100% mortality under laboratory conditions, their practical application in the field is limited by environmental factors. Among the once-bearing strawberry varieties, some proved to be less suitable to *A. rubi*, with significantly fewer damaged flowers observed.

These findings confirm that the strawberry blossom weevil is a key pest in strawberry production in South Tyrol, Italy. While individual control measures can significantly reduce infestation, effective long-term management will require the integration of multiple complementary strategies.

The Biotalys AGROBODY Foundry™: A Novel Platform for Insect Pest Management

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Abstract

Insect pests represent a major threat to global agricultural productivity and food security, causing significant crop losses and economic harm through their destructive feeding and rapid reproduction. Addressing this challenge requires innovative pest management strategies that reduce dependence on chemical pesticides. Biotalys offers a novel solution with its AGROBODY Foundry™ platform, which enables the fast development of antibody-derived, protein-based biocontrol agents. These AGROBODY™ bioactives introduce unique modes of action to combat biological threats in agriculture and food systems. The platform is based on the discovery of heavy-chain-only antibodies in Camelidae, which naturally lack light chains and the CH1 domain but retain full antigen-binding functionality through a single variable domain (VHH). These VHH domains have been widely studied in pharmaceutical and diagnostic fields, though their use in agriculture has been limited by lack of study, scalability and cost barriers. Biotalys is working to overcome these hurdles by strain engineering VHH-based AGROBODY™ bioactives tailored specifically for crop and food protection. Combining the precision and robustness of antibody-derived proteins with scalable production technologies, this innovation is expected to offer a sustainable and effective alternative to conventional pesticides. The AGROBODY Foundry™ platform thus is being developed to mark a breakthrough in biological crop protection, with broad implications for advancing sustainable agriculture and ensuring global food security.

Ozone as a Residue-Free Component of Integrated Wax Moth Management during Storage

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Abstract

The greater wax moth, *Galleria mellonella* L. (Lepidoptera: Pyralidae), is a major pest in apiculture, causing substantial damage to honeycombs and stored beekeeping equipment. Current control methods are often labor-intensive, temperature-dependent, or associated with chemical residues and risks to honey bees, highlighting the need for residue-free control options during storage. The efficacy of gaseous ozone against larval stages of *G. mellonella* was evaluated under controlled laboratory conditions. Larvae of two developmental groups (3rd and 4th instars) were exposed to a constant ozone concentration (70 ± 2 ppm) for periods ranging from 10 minutes to 2 hours for small larvae and from 10 minutes to 5 hours for big larvae. Ozone was generated using an ozone generator and continuously monitored with a portable ozone analyser. Mortality was assessed immediately after treatment and over three subsequent days. Mortality of *Galleria mellonella* larvae increased strongly with ozone exposure time and across post-treatment days, while controls remained at 0%. Small larvae were more susceptible, reaching 23–46% mortality after 60 min and 46–86% after 2 h, whereas big larvae showed lower mortality at equivalent times (up to 33% at 60 min and 46% at 2 h) but increased sharply with longer exposure, reaching 50–97% after 3 h and 100% after 5 h. The results demonstrate that ozone is an effective biofumigant against *G. mellonella* larvae, with efficacy strongly dependent on exposure duration and larval stage. The findings support the potential integration of ozone-based treatments into storage-focused wax moth management strategies, particularly for honeycombs and beekeeping equipment, while avoiding chemical residues.

Contribution to the identification of necrophagous insects in the Guelma region and the effect of sun/shade conditions on insect succession on carcasses.

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Abstract

Forensic entomology, a discipline linked to legal medicine, involves estimating the date of death. More precisely, it is referred to as the post-mortem interval (PMI).

In this study, we were interested in studying the necrophagous insect fauna associated with rabbit carcasses in the Guelma region during the spring season. We also applied three types of sacrifice (slaughter by exsanguination, slaughter by exsanguination with acidification, and euthanasia) and examined the effect of two conditions sunlight and shade on carcass decomposition and insect succession during this season.

Our study was conducted at the National Institute of Criminalistics and Criminology. Six rabbits were sacrificed. There was a diverse succession of necrophagous insects. Diptera of the Calliphoridae family were the first colonizers and the most predominant. Both adults and larvae were collected. Climatic data were recorded, and the PMI was calculated using the Accumulated Degree Days (ADD) method.

The first colonizers were Diptera from the Calliphoridae family (*Lucilia sericata* and *Calliphora vicina*). The PMI calculation provided an estimate close to the actual time of death.

Thus, the results obtained in this study can help improve our fundamental knowledge and understand the existing relationship within the diversity of necrophagous insect fauna in Algeria.

ForentLM; A NotebookLM-Powered Chatbot for Forensic Entomology

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Abstract

Large Language Models (LLMs) have been widely applied across various disciplines; however, their reliability in forensic science remains limited due to issues such as hallucination and the black-box problem. To address these limitations and enhance systematic knowledge management and practical usability in forensic entomology, this study developed a NotebookLM-based ChatBot system specialized for this domain. Unlike general-purpose LLMs, our approach integrates the NotebookLM environment with verified academic datasets, enabling domain-specific inference tailored to forensic applications. Approximately 1,700 forensic entomology papers from NCBI PubMed, validated experimental data, developmental models (accumulated degree hours, isomegalen and isomorphen diagrams), and molecular datasets were integrated into the NotebookLM platform. Based on these sources, the system summarizes and interprets the literature to support estimation of minimum and maximum postmortem intervals (PMIs) when users input insect species, larval length, and ambient temperature data, while providing supporting references to ensure transparency. In addition, a reference database was constructed using cytochrome c oxidase subunit I (COI) sequences from 48 forensically important arthropod species obtained from NCBI. The system applies a COI similarity alignment approach optimized for forensic entomology datasets, enabling molecular species identification analyses to be performed directly within the ChatBot environment. The developed web interface (<http://forentlm.kr>) allows users to access the ChatBot via Google login. Although hallucination remains an inherent limitation of large language models, this study mitigated hallucination-related issues through iterative updates. Response guidelines were established to ensure conservative and transparent outputs, whereby the ChatBot avoids definitive conclusions when essential input information is insufficient and instead indicates additional data required for reliable interpretation. Through this conservative response strategy, the system enhances both reliability and interpretability in forensic entomology applications. Overall, this work represents the first application of a domain-specific LLM in forensic entomology, demonstrating its potential as an interactive knowledge hub bridging academic data and practical forensic analysis.

Diagnostic Pitfalls in Forensic Pathology: Postmortem Facial Lesions Mimicking Trauma Caused by Pharaoh Ants (*Monomorium pharaonis*)

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Abstract

Misinterpretation of insect-related postmortem artifacts as traumatic injuries remains a critical diagnostic challenge in forensic pathology, particularly in enclosed indoor environments. We report a case involving a deceased adult male found indoors with multiple superficial perioral and facial lesions initially suspected to be perimortem trauma. However, based on photographic evaluation by a forensic entomologist, the lesions were identified as likely caused by postmortem activity of *Monomorium pharaonis* (pharaoh ants), a synanthropic species commonly found in human dwellings. Numerous ant eggs and larvae were subsequently discovered in the folds of the decedent's clothing, and the lesion morphology was consistent with postmortem necrophagy rather than true antemortem injury. This case represents the first formally documented instance in South Korea in which pharaoh ant-induced artifacts led to the avoidance of an erroneous forensic interpretation of violence. The findings highlight the importance of considering insect activity in the differential diagnosis of soft tissue lesions and demonstrate how inconspicuous insect activity can mimic violence-related injuries. Integration of entomological expertise—particularly early in scene evaluation—is essential to prevent unnecessary autopsies and medicolegal errors.

Influence of Reforestation Age on Insect Community Structure, Diversity and Abundance in a Tropical Rainforest

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Melody GIPANAO, Lerma MALDIA

Abstract

Forest succession plays a crucial role in shaping species richness and habitat complexity, particularly within tropical ecosystems. This study aims to evaluate how insect communities differ in structure, diversity, and abundance in reforestation areas. We categorized the reforestation areas into three age groups: 10, 15, and 20 years since planting (from 2001 to 2015). We collected insects using four methods: pitfall traps, malaise traps, beating sheets, and opportunistic sampling across the different reforestation age groups. A total of 2,733 individual insects were recorded, covering 9 orders, 36 families, and 94 species. The results showed that the 20-year-old stand had the highest species richness with 95 species, followed by the 10-year-old stand with 73 species, and the 15-year-old stand with 63 species. Omnivores, particularly ants (Formicidae), were the most common in all stands. We also found that the number of herbivores and detritivores increased with the age of the reforestation, showing increased functional diversity. Ordination analysis revealed distinct differences based on age group, suggesting that each stand supports a unique group of insect assemblages. Our results showed that species richness and diversity were not significantly affected by the age of the stands, but insect abundance. These findings emphasize that longer reforestation periods tend to support greater insect richness, functional diversity, and ecological stability. The observed patterns highlight the ecological importance of older forest stands in restoring insect communities and enhancing biodiversity in reforested areas.

Dung Beetle Assemblages Across Select Forest Types of Mount Makiling Forest Reserve, Philippines: Implications for Biodiversity Conservation and Sustainable Forest Management

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Czarine Mae GUZMAN

Abstract

The expansion of plantation forestry in the Philippines has raised concerns about its impact on biodiversity, particularly in relation to dung beetle assemblages, which are highly sensitive to forest management practices. There is a lack of studies on dung beetles in the Philippines. Our study explored the effects of various forest management types—natural forest, native tree plantation, and exotic tree plantation—on dung beetle assemblages in the Mt. Makiling Forest Reserve (MMFR), an important ASEAN Heritage Park in the Philippines. A total of 181 individuals belonging to 12 species were collected from the three forest types in MMFR. A pictorial key was created to illustrate the morphological differences among the species, some of which exhibited phenotypic plasticity. The composition of dung beetle species varied significantly across the different forest types. The natural forest displayed the highest species richness, along with a relatively high level of diversity and a balanced community structure. In contrast, the native tree plantation had moderate species richness, but its diversity was skewed, and it showed the lowest abundance. While the exotic tree plantation had the highest abundance, it was dominated by a fewer number of species. These differences can be attributed to variations in forest structure, ecosystem complexity, and litter production. The findings emphasize the importance of dung beetles as effective biological indicators of forest ecosystems. They highlight the ecological value of conserving natural forests and suggest that plantations, through their physical characteristics and gradual naturalization, can also contribute to biodiversity conservation and sustainable forest management.

Disturbance shapes bat fly diversity: community turnover across montane ecosystems of northern Peru

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Jhon Darly CHERO, Anthony ALMEYDA, Gustavo GRACIOLLI

Abstract

Bat ectoparasitic flies are highly specialized dipterans that feed on blood and remain associated with their hosts throughout their entire adult life. In northern Peru, the expansion of agricultural crops such as coffee and cacao has transformed extensive areas of montane ecosystems, where the diversity of these parasites remains poorly studied. To evaluate how habitat disturbance influences bat fly diversity and community composition, we surveyed four conservation areas representing different levels of disturbance: conserved forests (Site 1), crop-disturbed forests (Sites 2 and 3), and secondary regenerating forests (Site 4). Each site was sampled using a standardized mist-netting effort to capture bats and collect their ectoparasites.

We recorded 41 fly species associated with 30 bat species, with *Trichobius joblingi* being the most abundant species across all sites. Crop-disturbed forests showed higher observed species richness (Site 2 = 17 spp.; Site 3 = 21 spp.), whereas the regenerating forest (Site 4 = 14 spp.) and the conserved forest (Site 1 = 11 spp.) exhibited lower richness. However, Simpson diversity revealed a contrasting pattern, with higher values at Sites 1 and 2 ($1-D = 0.81$ and 0.84 , respectively), indicating greater community evenness. Chao1 estimated richness was highest at Site 3, suggesting a greater number of rare or undetected species, and lowest at Site 1, a pattern consistent with differences in host diversity among sites. Bray–Curtis dissimilarity indicated low similarity among communities (< 0.5), with Site 1 supporting the most distinct assemblage. Overall, bat fly communities varied along the disturbance gradient: crop-disturbed forests sustained relatively high diversity, whereas conserved forests appeared important for maintaining rare species.

Monitoring Scolytinae (Coleoptera, Curculionidae) communities in Mediterranean botanical gardens: a two-year survey in the Ligurian region (NW Italy)

Francesca BOERO (Department of Earth, Environmental and Life Sciences (DISTAV), University of Genoa, Italy., Francesca.boero@edu.unige.it)

Elena ZAPPA, Mauro MARIOTTI, Massimo FACCOLI, Stefano VANIN

Abstract

Botanical gardens serve as critical "sentinel sites" for the early detection of invasive alien species, as they often act as hubs for the introduction of non-native organisms. This study aimed to characterize the Scolytinae fauna in two distinct Ligurian environments: the Hanbury Botanic Gardens (HBG) in Ventimiglia, a semi-natural Mediterranean site, and the Genoa Botanical Garden (GBG), an urban site with high anthropogenic pressure.

Monitoring was conducted during 2024 and 2025 using black multi-funnel traps baited with a multi-component lure (ethanol, α -pinene, α -copaene, and quercivorol). The sampling effort reflected the size of each garden, with four traps at HBG and one at GBG. The sampling period was extended in the second year (April–November) compared to the first (May–November) to better intercept spring flight activity.

Significant differences in species richness and abundance were observed: 5.067 individuals from 20 species were recorded at HBG, whereas 201 individuals from 9 species were identified at GBG. Despite these differences, *Xyleborinus saxesenii*, a species of ancient introduction in Europe, was the most abundant species at both sites. The cosmopolitan *Hypothenemus eruditus* was also consistently present in both locations. At HBG, other dominant native taxa included *Orthotomicus erosus*, *Hylurgus ligniperda*, and *Crypturgus cribrellus*.

Five alien species were detected at HBG: *Xylosandrus crassiusculus*, *X. germanus*, *X. compactus*, *Dactylotrypes longicollis*, and *Coccotrypes dactyliperda*. Flight activity patterns for *Xylosandrus* species showed distinct peaks in late spring (April–May), which were more effectively intercepted during the second year. In the urban context of GBG, fewer exotic species were intercepted (*D. longicollis*, *X. compactus*, *X. germanus*), and overall diversity was markedly lower.

These results demonstrate that even small urban botanical gardens can host exotic scolytins, while larger gardens serve as key monitoring points for biosecurity and the protection of botanical heritage.

Do remnant late-seral forests still preserve forest fauna?

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Louka TOUSIGNANT, Billie CHIASSON, Gaétan MOREAU

Abstract

Forest management has reduced the occurrence and size of late-seral forests, a successional stage with distinctive structural attributes that provides essential habitats for many animal species. Here, we tested the hypothesis that landscape-scale forest management affects the integrity of ecological processes that structure animal communities within fragments of late-seral forests. Beetle communities were sampled using flight intercept traps placed away from edge influences in 20 large late-seral secondary forests located in managed or conservation landscapes. A total of 27,914 beetle specimens from over 280 species were collected over three study years. Both beetle richness and abundance were higher in late-seral forests embedded in conservation landscapes. Differences in community composition were driven primarily by abundance, which was nearly three times higher in late-seral forests embedded in conservation landscapes than in those located within managed landscapes. Beetle community attributes varied mainly in response to local resources (softwood biomass and necromass) and landscape-scale management. Overall, our results suggest that conservation landscapes promote more abundant and structured animal communities, thereby supporting ecological processes characteristic of late-seral forests.

Russian olive functions as an egg-killing trap tree for the Asian longhorned beetle through oviposition-induced gum defense

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Ren LILI, Gershenzon JONATHAN, Luo YOUQING

Abstract

Trees can defend against wood-boring insects before larvae ever enter the stem, yet anti-egg defenses in woody tissues remain poorly understood. Russian olive (*Elaeagnus angustifolia*) presents a striking case: adult Asian longhorned beetles (*Anoplophora glabripennis*, ALB) readily attack and oviposit on this tree, but their eggs rarely develop successfully. This apparent mismatch between adult host acceptance and offspring survival suggests that Russian olive may function as a dead-end trap tree.

In ALB oviposition scars, Russian olive secreted abundant gum that enclosed the egg chamber and caused egg mortality, with the egg-killing rate reaching 99.27%. This response was much stronger than that induced by insect-generated scars without eggs or by mechanical wounding. Gum mass in oviposition scars was 1.65 times higher than in mechanical scars, and the polysaccharide content was 2.22 times higher. Anatomical observations further showed wound-induced gum ducts at oviposition sites, indicating that gum secretion was part of a localized tissue defense rather than a passive wound response. The gum defense was closely associated with host carbohydrate reprogramming. ALB oviposition promoted sustained sucrose mobilization, increased glucose-6-phosphate and UDP-glucose levels, depleted several free monosaccharide pools, and enhanced sucrose synthase cleavage and phosphoglucomutase activities. Carbohydrate-related genes, including *SUS1* and *PGM1*, were linked to the regulation of sucrose, glucose-phosphate intermediates, and UDP-glucose supply. Although oviposition-dependent microbial shifts were detected, metatranscriptomic evidence did not support a coherent microbial carbohydrate pathway driving gum formation.

Together, these findings show that Russian olive redirects host carbon metabolism toward polysaccharide-rich gum production after ALB oviposition. This localized anti-egg defense explains the dead-end trap-tree function of Russian olive and may inform trap-tree strategies for managing invasive wood-boring pests.

Regional Variations in Host Preference of the Asian Spongy Moth Estimated by Satellite Image Analysis in South Korea

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Park YONGHWAN

Abstract

The Asian spongy moth (*Lymantria dispar*) is a highly polyphagous forest defoliator, and its host preferences have been reported to vary among ecological variants and geographic regions. In 2020, a large-scale outbreak exceeding 4,000 ha occurred in South Korea, causing severe defoliation across diverse forest types. This study aimed to assess regional differences in host preference by analyzing outbreak areas delineated through remote-sensing defoliation maps and a national forest-type map consisting of seven stand categories (*Pinus densiflora*, *P. koraiensis*, *Larix kaempferi*, other coniferous species, *Quercus* spp., other deciduous species, and mixed forests). Defoliation severity was quantified using Landsat imagery by calculating changes in the Normalized Difference Moisture Index (NDMI) relative to a three-year pre-outbreak baseline. Based on defoliation severity (Severe, Moderate, Light, None), ten severely affected regions were delineated via spatial clustering, and host preference was estimated using a proportional host-preference index derived from severely and moderately defoliated areas relative to forest-type availability. Our results revealed substantial regional variation in host preference. Other deciduous forests and mixed forests were preferentially defoliated in seven regions, whereas *Larix kaempferi* exhibited the highest preference values in two regions. These results indicate that host preference of *L. dispar* is spatially heterogeneous in South Korea, potentially reflecting regional variation in forest composition and differences among genetic lineages within the *L. dispar* species complex. Satellite-based NDMI analysis proved effective for quantifying defoliation severity and identifying host preference at landscape scales, providing valuable information for risk modeling and regional forest-pest management.

Assessment of the relevance of *Agrilus biguttatus* for local oak decline following drought and heat in South-East Germany

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Samira TERZENBACH, W. Andreas HAHN

Abstract

In response to global change and altered climatic conditions, the relevance of forest pests is changing due to range expansion, invasion, as well as shifts of secondary pests toward more primary behaviour contributing to tree mortality. European oak species (*Quercus petrae*, *Q. robur*) are important because of their expected tolerance of drier climate, their provision of habitat for numerous insects, including those that live inside or on the bark, as well as their valuable timber. The two-spotted oak borer (*Agrilus biguttatus*) is commonly perceived as a secondary species, with its larvae colonising the strong branches of old oak trees. However, during periods of intense tree stress (e.g. after repeated defoliation), it has been observed to undergo mass outbreaks and is assumed to be a contributing factor to oak mortality. In this study, we investigated the relevance of *A. biguttatus* for oak decline incited by drought and heat in Bavaria (south-east Germany). Areas affected by *A. biguttatus* are concentrated in the northern parts of Bavaria (Lower and Central Franconia). Stem samples were taken from infested oaks in two stands and kept in rearing cages for two years. Wood- and bark-boring insects were collected at regular intervals. *Agrilus biguttatus* was predominantly found in the lower parts of the trees (mean DBH: 35±5 cm) and was the dominant burprestid species. Several other bark and ambrosia beetles were present in significant numbers, as were several cerambycid species. Surprisingly, large numbers of the otherwise rare weevil *Gasterocercus depressirostris* were also detected. The relevance of *A. biguttatus* for forest protection is discussed in the context of an integrated management approach, with a view to identify research gaps that need to be addressed to prepare for future mass outbreaks.

Scots pine at risk: the rapid spread of *Ips acuminatus* in changing climates

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Elza GRICJUS, Natālija BURNEVIČA, Dārta KĻAVIŅA, Agnis ŠMITS

Abstract

The rapid expansion of the sharp-toothed bark beetle *Ips acuminatus* (Gyllenhal) over the past decade—driven by climate change—has greatly increased the extent of Scots pine *Pinus sylvestris* (L.) stands damaged by this pest across Europe. A warming climate may further elevate outbreak risk by increasing the frequency and intensity of disturbances such as storms and forest fires, which weaken forest stands and create favorable conditions for colonization. In Latvia, several unprecedented weather events and human-caused forest fires have triggered localized outbreaks of *I. acuminatus*. Additionally, *I. acuminatus* is commonly associated with blue stain fungi that increases tree mortality and decreases the timber quality of affected trees. This highlights the need for timely detection and forest management strategies aimed at removing infested trees at an early stage of invasion. Recent technological advances have greatly improved the detection of tree stress and the monitoring of canopy vitality using spectral vegetation index. The potential of remote sensing to detect infestations at their earliest stage—before any physiological disruptions occur—is currently being evaluated. This abstract seeks to provide an overview of the most recent research developments and current understanding regarding this pest in Latvia.

This study was partially funded by the JSC Latvia's State Forests project 'Effect of climate change on forestry and associated risks' No. 5-5.9.1_007p_101_21_78, and State research program 'Forest4LV – Innovation in Forest Management and Value Chain for Latvia's Growth: New Forest Services, Products and Technologies' No. VPP-ZM-VRIIILA-2024/2-0002.

Short-term effects of wildfire on termite in Mediterranean cork oak forests of northern Morocco

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David HERNÁNDEZ-TEIXIDOR, Ahmed TAHERI

Abstract

Wildfires are major disturbances in Mediterranean ecosystems, yet their effects on soil-dwelling insects such as termites remain poorly documented. This study assessed the short-term impact of wildfire on termite nest density and microhabitat use in cork oak (*Quercus suber*) forests of northern Morocco (Rif region). Termites were sampled in 2022 (immediately after fire) and in 2025 using a standardized transect method in burned and unburned plots across three cork oak forests. All potential microhabitats were systematically searched, including surface soil, dead wood, standing dead trunks, and buried wood. Termite encounters were recorded per section, and nest density was analysed using generalized linear models (Poisson distribution), testing the effects of year, fire treatment, forest identity, and their interactions. In 2022, burned plots showed a drastic reduction in termite nest density (0.13 ± 0.06) compared with unburned controls (1.33 ± 0.35). Three years later, nest density in burned plots increased markedly (1.10 ± 0.21), approaching values observed in control plots, which remained stable between years. Statistical analyses revealed significant effects of year, fire treatment, forest, and a strong interaction of the year and fire, indicating a pronounced initial impact of fire followed by rapid recovery. Microhabitat use also differed between treatments. Immediately after fire, all nests in burned plots were restricted to subterranean habitats, whereas by 2025, wood-associated nests reappeared (~28%). In contrast, unburned plots showed stable microhabitat proportions across years (~70% subterranean, ~30% wood). These results demonstrate that wildfires strongly affect termite populations in the short term but that termite communities exhibit a rapid recovery within three years, highlighting their resilience and the importance of subterranean refuges in post-fire environments.

Rapid increase of the *Orthotomicus erosus* bark beetle population following a windthrow caused by a microburst event in the Marjan Forest Park, Split

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Abstract

At the beginning of July 2025, the Marjan Forest Park (Split) was struck by an extremely severe storm accompanied by strong wind gusts (microburst) that, within a short period, broke or uprooted around 4,000 Aleppo pine (*Pinus halepensis*) trees. In certain parts of the forest, the timber mass was completely destroyed. Due to the large quantity of accumulated woody material, its removal could not be carried out in a short time, which increased the risk of bark beetle population development.

Orthotomicus erosus, along with wildfires, has been considered the key problem in Aleppo pine forests in the Mediterranean region of Croatia. In light of that experience, the need for rapid removal of destroyed material from the forest was well understood; however, due to legal constraints, removal began only in early 2026. The bark beetles were monitored through field observations and by installing 20 pheromone traps.

After the windthrow, nearly all the material consisted of healthy trees with no signs of bark beetles. In September 2025, it was determined that beetle activity had begun immediately after the windthrow, with extremely high intensity, and bark beetles and their galleries were easily detectable. A new population assessment in October showed significant progression: entry and exit holes were observed on the fallen material, and nearly all the windthrown timber had been attacked. Consequently, standing physiologically weakened trees also became targets.

The initial catches in pheromone traps were expectedly low at the beginning. However, the October trap results showed a sharp increase in the number of captured individuals, corresponding to the population growth observed in the field. Climate change further prolongs the vegetation season, enabling the development of a greater number of generations per year, thereby increasing the risk of an explosive population surge in 2026.

#11000

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Host preference and chemical ecology of *Saperda tridentata*

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Jon SWEENEY, Deepa PURESWARAN, Kate VAN ROOYEN, Peter MAYO, Alberto SANTINI, Francesco PECORI, Davide RASSATI

Abstract

Saperda tridentata (Olivier, 1795) (Coleoptera: Cerambycidae) is a longhorn beetle species which has gained importance after recent interceptions at Italian ports on rough wood elm logs imported from North America. This beetle feeds on leaves and bark of young twigs of elms, laying eggs on weakened stems in which larvae develop. However, its potential host range in Europe is unknown. Given the likelihood of further introductions of *S. tridentata* in Europe, there is an urgent need to characterize its behavior and potential impact on European trees, as well as to develop efficient monitoring strategies. To address this knowledge gap, we carried out choice and no-choice feeding and development bioassays on ten species of European broadleaved trees. Our findings indicate that *S. tridentata* feeds readily on foliage of European elm species, but not on European species of maples and poplars. In addition, *S. tridentata* is capable of ovipositing and developing from egg to adult on stem sections of European elms. Trapping experiments showed that adults, particularly females, were significantly attracted to stressed elms vs. healthy elms. Chemical analyses are ongoing to determine which host volatiles elicit attraction and whether males emit sex/aggregation pheromones. Our efforts aim to provide a more comprehensive understanding of *S. tridentata* host preference and chemical ecology, offering valuable insights for the development of effective surveillance strategies.

Lure type effectiveness and sample quality thresholds in tortrix moth surveillance in Northern Ireland.

Florentine SPAANS (Agri-Food and Biosciences Institute, Florentine.spaans@afbini.gov.uk)

Ryan WEIR, Joanna KIRBAS, Ciara ISAAC, Peter WILLIAMS, Archie MURCHIE

Abstract

Several micromoth species belonging to the family Tortricidae are listed as Union Quarantine Pests (UQP) under EU plant health regulations and require surveys to confirm the absence of these hosts in EU territories. A general approach can be taken by using light traps or a more targeted approach by using lure-baited traps. The UQPs include species of genera *Acleris*, *Choristoneura*, and *Grapholita*. Several native species of these genera are also present in Ireland. While targeted pheromone lures are available for some of the regulated species, it is expected that these will also attract other closely related species. These could therefore be used as positive controls to determine trapping effectiveness.

Here we present the findings from tortrix moth surveillance in Northern Ireland with a focus on sample collection timing and its impact on sample quality as well as an assessment on the efficacy of targeted lures. Our study suggests that lures containing 11-tetradecenyl acetate are more effective for catching native tortrix moths than a standard light trap in terms species richness and abundance and surveying effort. We further determined that a sample collection timeline of two weeks generated samples of acceptable quality in 80% of instances.

Managing wooded-pasture and high-elevation spruce stands under climate warming and bark beetle risk

Camille TABARY (Camille.tabary@outlook.fr)

Philippe BINET, Loïc ANGONIN, Carole BEGEOT, Anne-Claude GABIOT, Sébastien NAGELEISEN, Marie-Laure TOUSSAINT, Coralie BERTHEAU

Abstract

In France, bark beetle outbreaks have intensified in recent years, particularly affecting spruce stands where *Ips typographus* is the main agent of decline. This situation results from changing environmental conditions—most notably repeated droughts and heatwaves—which are gradually altering population dynamics. This intensification raises concerns about an increased potential for spatial and altitudinal expansion. These developments call for a reassessment of the capacity of mountain environments to act as effective environmental barriers against large-scale infestations. The objective of this study was to characterize the composition and dynamics of bark beetle communities in an altitudinal context historically considered unfavorable to outbreaks. To this end, a three-year trapping campaign was carried out at the “La Boissau” site (Franche-Comté, Doubs) in a wooded-pasture landscape dominated by Norway spruce—a typical setting of Jura mountain environments. The results show a substantial presence of *I. typographus*, accompanied by notable captures of *Pityogenes chalcographus*. The attacks observed on the study plot led to the near-total mortality of spruces, confirming a strong colonization activity despite the high-elevation context. This initial phase was followed by a marked increase in *Crypturgus cinereus*, a saproxylic species typically associated with advanced stages of wood decay. This succession pattern, well documented in lowland areas, is now also occurring at higher elevations. These observations suggest that high-altitude wooded pastures may be just as vulnerable to bark beetle outbreaks as lowland forests, highlighting the need to include these environments in forest monitoring and management strategies.

From Laboratory to Semi-Field Validation: Advancing the Sterile Insect Technique for *Drosophila suzukii* in Québec

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Elisabeth MÉNARD, Kim OSTIGUY, Annabelle FIRLEJ

Abstract

Since its first detection in Québec in 2010, *Drosophila suzukii* has continuously expanded its geographical range, affecting an increasing number of crops, including lowbush blueberry, a species of high patrimonial and commercial value. Overall, the economic and environmental impact of *D. suzukii* is substantial, as this invasive pest can infest a wide range of developing fruits such as cherries, raspberries, strawberries, and blueberries. Management of *D. suzukii* populations has relied primarily on repeated applications of broad-spectrum insecticides.

The sterile insect technique (SIT) represents a promising complementary approach for the integrated management of *D. suzukii*. A first laboratory phase evaluated the effects of different gamma irradiation doses applied to pupae on key biological traits of irradiated individuals and their progeny, including adult emergence, male deformities, longevity, fecundity, and fertility. A subsequent semi-field proof-of-concept demonstrated that yields of marketable fruit were comparable between plots protected using SIT and those treated with conventional insecticides, highlighting the strong potential of this approach.

Current research efforts focus on improving SIT efficiency by addressing three major challenges: (i) producing insects with enhanced compatibility with wild populations; (ii) increasing mass-rearing output by maximizing oviposition through analysis of olfactory and visual cues involved in oviposition site selection; and (iii) achieving male-only releases by targeting the last pupal stage, when males ($n = 267$; 1.31 ± 0.12 mg; 1.08 ± 0.12 mm wide) can be reliably distinguished by visible sex combs and separated from larger females ($n = 358$; 1.61 ± 0.15 mg; 1.17 ± 0.13 mm wide).

Addressing these challenges will enable optimization of the sterile insect technique and support its large-scale implementation in integrated fruit production systems.

A potential biocontrol agent of the key European vector of *Xylella fastidiosa*? *Ooctonus vulgatus* (Hymenoptera: Mymaridae) in Italy

Domenico BOSCO (Dipartimento di Scienze Agrarie, Forestali e Alimentari, Università degli Studi di Torino, 10095 Grugliasco (TO), Italy, Domenico.bosco@unito.it)

Francesco VOLPE, Luigi IODICE, Guillaume MARTEL, Pierre ROYER, Stefano DEMICHELIS, Francesco TORTORICI, Vincenzo CAVALIERI, Crescenza DONGIOVANNI, Nicola BODINO

Abstract

The meadow spittlebug *Philaenus spumarius* (L.) (Hemiptera: Aphrophoridae) is the primary vector of *Xylella fastidiosa* in Europe. Controlling this vector is essential to limit pathogen spread, but current strategies, relying on tillage and insecticides, are often unsatisfactory. Egg parasitoids as biological control agents represent a promising approach to reduce *P. spumarius* populations prior to adult stage and pathogen transmission, potentially improving vector management and tackle the bacterium spread in Europe. This study investigates the presence and biological characteristics of egg parasitoids associated to *P. spumarius* in different regions of Italy (Liguria, Piedmont, and Apulia), through a 3-year field survey and laboratory experiments. Several field sampling techniques, including sentinel egg methods and direct eggs collection, were employed in different agroecosystems (olive groves, vineyards, fallows) during autumn-winter period. Overall, more than 13,500 *P. spumarius* eggs were retrieved after exposition in field and 806 *Ooctonus vulgatus* Haliday (Hymenoptera: Mymaridae) emerged, identified using morphological and molecular tools. Across all regions, *O. vulgatus* was consistently the only egg parasitoid found. Parasitism was widespread and highly variable between sites and years (in average 5–25 % of egg parasitized, up to 60% of the parasitoid emergence rate). The higher parasitism efficiency in field was obtained on sentinel eggs directly oviposited in survey's sites, suggesting that recently laid eggs were more prone to be parasitized. This was confirmed in laboratory parasitisation trials, where the few emergences occurred on freshly oviposited diapausing eggs only. Additionally, the adult parasitoid's short lifespan (9.8 ± 4.7 days) and low emergence rates limit its potential for mass rearing. In conclusion, *O. vulgatus* seems to play a limited role as a standalone biological control agent against *P. spumarius*. Future research should investigate the ecological and phenological factors that may improve its effectiveness within a conservative biological control framework

#11265

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Understanding Long-Lasting Aphid Control with Bayer's SeedGrowth Product BUTEOstart

Christoph Andreas BRAUN (Bayer AG, Christophandreas.braun@bayer.com)

A. Michael KLUEKEN

Abstract

Aphids are key vectors of plant viruses in various plant species, e.g. sugar beet, making early-season infestations a critical concern for yield stability. The introduction of Flupyradifurone as the SeedGrowth product BUTEOstart offers systemic protection, but questions remain about its residual efficacy and the timing of subsequent foliar treatments. We conducted a controlled-environment study to examine how soil moisture, soil type, and dose rates influence aphid suppression by BUTEOstart compared to the seed treatment product Gaucho (active ingredient: imidacloprid). Our findings reveal how physicochemical properties and translocation dynamics of seed-applied insecticides affect aphid population development and virus transmission risk. Combined with IRAC (Insecticide Resistance Action Committee) resistance management principles, these insights support integrated strategies for sustainable aphid control—optimizing product choice, application timing, and minimizing resistance pressure.

Can service plants decrease aphid infestations and virus transmission in sugar beet crops?

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Héloïse LESAGE, Marie HÉDAN, Quentin CHESNAIS, Fabienne MAUPAS, Sylvia ANTON, Audrey FABAREZ

Abstract

Service plants show promise as a means of controlling insect pests in a variety of crops. However, field demonstrations of their efficacy are scarce, despite being needed to propose agroecological alternatives to insecticides. Aphids are major pests of many crops worldwide, particularly in sugar beet, where they transmit several viruses that cause severe yield losses. Here, we present the results of field experiments conducted over three successive years, which assessed the potential of service plants to control the primary vectors of yellows viruses in sugar beet: *Myzus persicae* and *Aphis fabae*. We tested dissuasive and attractive service plants using a push-pull design, with rough oat (*Avena strigosa*) acting as a dissuasive plant and various brassicaceous plants or fava beans (*Vicia faba*) acting as attractive plants, depending on the aphid species targeted. Our results show that rough oat is an effective push service plant, decreasing infestations from both species, while attractive plants alone, or in combination with the dissuasive plant, have a minimal impact on infestations. The presence of rough oat delayed the appearance of yellows symptoms, but did not affect the overall presence of viruses in sugar beet plants. This calls for further studies on the mechanisms of yellows virus epidemics.

Biocontrol or bio-oops : letal and sublethal effects of surfactin on pest and crop auxiliaries.

Louise DUMONT (Interaction Ecology and Global Change, University of Mons, Louisedumont02@gmail.com)

Léa POIRIER, Clément TOURBEZ, Kévin TOUGERON

Abstract

Ectothermic organisms are highly vulnerable to climate change, which disrupts the trophic interactions between plants, crop pests and their natural enemies, thereby challenging the efficiency of biological control. In addition, rising temperatures may also alter the effectiveness of biomolecules, further limiting the success of sustainable pest management strategies. Among these biomolecules, lipopeptides, extracted from the genus *Bacillus*, are promising candidates for controlling crop pests. In particular, surfactins, exhibit insecticidal properties. Yet, little is known about their lethal and sublethal non-target effects on natural enemies of pests, and consequently about their compatibility with biological control under changing climatic conditions.

This study aims to investigate the lethal and sublethal effects of surfactin on both pests and their natural enemies. We focused on the cereal aphid *Sitobion avenae* and one of its key predators: the seven-spotted ladybird *Coccinella septempunctata*.

The effect of surfactin on mortality were assessed by topical application for *S. avenae* and, for *C. septempunctata*, by topical application and ingestion of contaminated aphids, under two temperature scenarios representing IPCC climate change projections.

We hypothesize that surfactin is not fully pest-specific and may exert negative effects on *C. septempunctata*, with outcomes depending on both exposure pathway and temperature. By combining ecotoxicology and thermal ecology, this study aims to assess whether surfactin can be integrated into sustainable pest management strategies without undermining essential ecosystem services provided by crop pest predators.

Beating greenhouse pests with blooms: Supporting natural enemies with functional plants

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Gerben MESSELINK, Felix BIANCHI

Abstract

This PhD research explores the potential of functional plant strips around greenhouses and plant islands within greenhouses to enhance biological pest control of aphids, with a particular focus on green lacewings (Neuroptera: Chrysopidae). Aphids are a major pest in sweet pepper cultivation, leading to yield losses and increased pesticide use. *Chrysoperla carnea*, the most popular lacewing species used in protected sweet pepper systems, is a potential effective natural predator of aphids, but establishing and sustaining their populations in greenhouse environments remains a serious challenge.

By integrating biodiversity-based interventions, this study investigates how functional plant strips and islands can attract, sustain, and support lacewing populations, thereby improving their efficacy in pest control. Through field and greenhouse trials, the research will assess the impact of these plant-based strategies on lacewing fitness, establishment and abundance. We will also study their movement and effectiveness in reducing aphid populations. This project will provide practical guidelines to enhance lacewing biocontrol and support more resilient, biodiversity-based greenhouse systems.

#10718

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

The start of research on pea pests in Latvia

Janis GAILIS (Latvia University of Life Sciences and Technologies, Institute of Plant Protection Research 'Agrihorts', Janis.gailis@lbtu.lv)

Ieva ENGELSONE, Agnese KOLODNICKA, Sabine MOCANE, Sannija RODINA

Abstract

Pea (*Pisum sativum*) cultivation in Latvia had been in decline for several decades, but in recent years its area has been increasing again. Additionally, peas and other legumes are being incorporated into cover crop mixtures, which are also gaining popularity. This raises concerns about the expansion of pests. Therefore, in 2025, we launched a study to determine which insect species could potentially be harmful to peas under the agro-ecological conditions of Latvia.

Previously, it was believed that pea moth (*Cydia nigricana*), pea leaf weevil (*Sitona lineatus*), pea aphid (*Acyrtosiphon pisum*), pea thrips (*Kakothrips robustus*) and pea beetle (*Bruchus pisorum*) are major pea pests in Latvia. However, at least 15 more *Sitona* species and four polyphagous aphid and thrips species feeding on peas and other legumes in various European countries are found in Latvia.

In the first phase of our research, we began studying the potential pest fauna, species phenology and harmfulness in conventional and organic pea fields and in cover crop areas. During the first research season, we observed *Sitona lineatus*, *Sitona ambiguus*, *Sitona striatellus*, pea moth and potato aphid (*Macrosiphum euphorbiae*) in pea fields. The pea beetle and thrips were not observed. Only the pea moth can be recognized as a locally significant pest for now. In most of the study areas, the proportion of its damaged seeds in the harvest was 1...2%, but in some places it reached 14...20%. Some *S. lineatus* individuals and *M. euphorbiae* colonies were detected in cover crop areas in the fall. Therefore, these biotopes could have the potential to promote the proliferation of some pea pests.

It is still too early to say which species might be significant pea pests and what effect cover crop areas have on their populations. Therefore, we plan to continue our study for several more years.

Prediction of seasonal population dynamics of *Anarsia lineatella*, Zeller, 1839 (Lepidoptera: Gelechiidae) in stone fruit orchards in North Macedonia

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Stanislava LAZAREVSKA, Sterja NACESKI

Abstract

Anarsia lineatella, Zeller, 1839 (Lepidoptera: Gelechiidae), is one of the most economically significant pests of stone fruit in North Macedonia (average damages range from 17.5 % to 38 %, depending on the crop and the locality). The successful management of this moth depends on the precise forecast of its adult activity. Because the seasonal dynamics vary between years and crop cultivar, it's difficult to schedule the control measures. The seasonal population dynamics of *A. lineatella* was determined using the accumulated degree-days (DD) obtained from automated meteorological stations and pheromone traps in two regions in the country (Sirkovo, Vardar and Hamzali, Southeastern region) in orchards with mixed stone fruits. The study of this pest was established in 2025 in order to determine the start of pest activity, the period of the moth population peak, and the most critical period of its appearance. The results showed that the first captured male adults of *A. lineatella* on the locality in Sirkovo were observed on 21.04.25 at 160.94 DD and in Hamzali on 22.04.25 at 122.79 DD (lower temperature threshold: 10 °C). The first peak of the pest in Sirkovo was observed on 29.04.25 at 224.04 DD and in Hamzali on 03.06.25 at 384.07 DD. The peaks of the subsequent moth flights were observed on 27.05.25 at 413.8 DD, on 19.08.25 at 1727.36 DD and on 30.09.25 at 2237.58 DD in Sirkovo and on 12.08.25 at 1426.24 DD and on 30.09.25 at 1996.62 DD in Hamzali. The highest number of caught male moth of *A. lineatella* in the season in Sirkovo was observed on 30.09.25 at 2237.58 DD and in Hamzali on 03.06.25 at 384.07 DD. These degree day risk thresholds can be used for more precise treatment timing and to implement automated real time decision support systems in establishing Integrated Pest Management in stone fruit orchards.

Assessment of extreme temperatures for insect control in dried fruits under laboratory and commercial storage conditions

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Maria SAKKA, Marios VASILEIOU, George VLONTZOS, Christos ATHANASSIOU

Abstract

Dried fruits are particularly prone to insect infestation during storage, resulting in quality loss and economic impact across major production regions. This study assesses the insecticidal efficacy of extreme temperature treatments against *Oryzaephilus surinamensis* (L.) (Coleoptera: Silvanidae) and *Plodia interpunctella* Hübner (Lepidoptera: Pyralidae) by combining laboratory experiments with trials carried out under commercial storage conditions. Laboratory experiments evaluated insect mortality and progeny production in treated dried fruits subjected to cold temperatures ranging from 5 to −15 °C and heat treatments ranging from 35 to 55 °C, applied for varying exposure durations. Field trials assessed the effectiveness of moderate cold treatments at 4 and 9 °C and heat treatments from 35 to 55 °C under commercial storage conditions, emphasizing the influence of temperature distribution within storage units on treatment outcomes. Across both experimental environments, exposure to extreme temperatures substantially reduced insect survival, at intervals that ranged among the different temperature levels. Real-world evaluations further highlighted the role of spatial heterogeneity within large, stored product masses, demonstrating that insect position within the commodity can affect the uniformity of disinfestation efficacy. The current findings support extreme temperature treatments as an effective, residue-free disinfestation strategy for insect management in dried fruits. The study highlights their potential for integration into sustainable post-harvest practices and emphasizes the need to consider temperature penetration dynamics when implementing thermal disinfestation at commercial facilities.

Keywords: thermal disinfestation; stored-product insects; dried fruits; extreme temperature treatments

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Engineering an early development sex separation toolkit for Mexfly, *Anastrepha ludens*

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Junru LIU, Ting YANG, Nikolai KANDUL, Evan BRASWELL, Omar AKBARI, Angela MECCARIELLO

Abstract

The Mexican fly, *Anastrepha ludens*, is a major pest insect of the fruit industry in the Western hemisphere. The economic and agricultural effects of Mexican fly's widespread presence have created the necessity for population control and prevention of future invasions. Effective strategies have been applied through the years to suppress *A. ludens* population, including the classic Sterile Insect Technique (SIT) approach, using the genetic sexing strain (GSS) black pupae. Nevertheless, Mexfly continues to be a huge economic threat to crop production. Additionally, the absence of an early developmental stage sexing sorting system, impacts tremendously the efficiency of the existing GSS, and the probability of the robust transfer of these approaches to other species. Here, we show the effective application of a new method based on a sex specific *transformer* gene intron tested previously in *Ceratitis capitata* (SEPARATOR). This system relies on both male and female fluorescent marker expression and removes the barrier of the early developmental stage selection by generating a more precise and efficient approach for sex sorting. Both male and female specific SEPARATOR strains have been characterized and presented the desired phenotype outcomes, facilitating the establishment of new improved Genitic Sexing Strains in non-model organisms.

Understanding Genetic Resistance to Cabbage Stem Flea Beetle in Oilseed Rape

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Emmanuel SOLOMON, Rachel WELLS

Abstract

As one of Europe's top sources of vegetable oil and a key element of many crop rotations, oilseed rape (OSR; *Brassica napus*) has high economic importance. Despite this, acreage dedicated to its growth has steadily declined in the UK over the last decade due to challenges faced during cultivation, such as the increasing pressures from insect pests. One of the most economically significant oilseed pests is the cabbage stem flea beetle (CSFB; *Psylliodes chrysocephala*), a specialist Brassica pest. Adults feed on the cotyledons, weakening plants and threatening crop establishment, larvae then mine the stem and petioles creating further damage. Previously controlled by neonicotinoid seed treatments, losses have intensified since the EU's 2013 neonicotinoid ban and the subsequent rise of resistance to pyrethroid insecticides that have been used in their stead, resulting in a pressing need to develop oilseed rape cultivars resistant to CSFB to combat yield losses.

This project aims to understand the genetic control of adult *P. chrysocephala* feeding variation in *B. napus* by phenotype validation of candidate genes identified in previous associative transcriptomics and gene expression studies. Using the genetic tools available in *Arabidopsis thaliana* to efficiently screen a range of mutants for CSFB feeding, we will confirm genes of interest that could contribute to resistance breeding efforts. The effect of knocking out these genes on adult CSFB feeding will be used to assess their roles in plant-pest interaction and facilitating CSFB resistance.

As a primary level of defence in an Integrated Pest Management strategy, resistant plants are key to help protect yields without negatively impacting non-target organisms, unlike the currently used chemical sprays which harm beneficial arthropods. This work will contribute to the understanding of Brassica resistance CSFB, with a view of helping reduce CSFB pressures in the field, supporting a transition away from chemical pesticides.

Effectiveness of Citrus clementina peel and leaf powder in managing Sitophilus zeamais

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Abstract

The maize weevil is a significant economic pest of stored maize worldwide, with well-documented devastating impacts, particularly in developing countries due to limited resources and budget allocations available for farming. Farmers rely mainly on chemical pesticides to manage this pest. Synthetic pesticides are known to successfully control the activities of this destructive pest. Excessive use of these pesticides harms non-target organisms, increases pest resistance, poses health risks to humans, and contaminates the environment. The drawbacks of synthetic pesticides have led to a demand for safer, effective alternatives like botanical pesticides. Hence, the aim of this study was to investigate the effectiveness of Citrus clementina in managing Sitophilus zeamais on stored maize grains. The results showed C. clementina leaf powder to be more effective in preserving stored maize than peel powder. Further, results revealed that maize treated with 15g and above of C. clementina peel and leaf powder had low number of emerging weevils compared to untreated (0g) maize, which indicated that peel and leaf powder inhibits the development of S. zeamais. The findings of this study demonstrate that C. clementina powder has potential insecticidal properties. However, the efficacy of C. clementina peel and leaf powders decreases with time. Hence, the current study recommends constant reapplications of fresh C. clementina leaf and peel powder at 2-month intervals to maintain its effectiveness.

Developing stress resilient crops by understanding host herbivore interactions under multiple stressors.

RUPESH KARIYAT (University of Arkansas, Rkariyat@uark.edu)

Abstract

Developing stress resilient crops by understanding host-herbivore interactions under multiple stressors.

Global climate change has exacerbated the need to develop stress resilient crops to feed the growing population. In agroecosystems, plants are often under stress from biotic and abiotic factors. While their individual and independent effects have been well studied, their concurrent and temporal effects warrants further investigation. Using Soybean (*Glycine max*) as the model, we examined how insect herbivory and drought affects plant-insect interactions, and whether these effects transcend to progeny. Ecophysiology, plant defense, herbivore growth, development, and survival traits were examined under a combination of drought and herbivory stress with 2 herbivores; Soybean looper (*Chrysodeixis includens*), a dominant herbivore in Soybean, and fall armyworm (*Spodoptera frugiperda*), a polyphagous herbivore. We show that drought and herbivory has synergistic negative effects on soybean yield, and these effects are more pronounced in progeny with strong growth-defense tradeoffs in a phenology dependent manner. Collectively, we show that understanding the effects of multiple stressors and their effects on host and herbivores is critical for developing stress resilient crops.

Pilot evaluation of Bt sugarcane and the sterile insect technique for managing *Eldana saccharina* under shade-house conditions

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Caswell MUNYAI, Lawrence MALINGA

Abstract

The African sugarcane stalk borer, *Eldana saccharina* Walker (Lepidoptera: Pyralidae), remains a major constraint to sugarcane production in South Africa, and reliance on chemical control is increasingly unsustainable. This study evaluated the performance of genetically modified (GM) Bt sugarcane expressing Cry1A (GM CRY1A) alone and in combination with the sterile insect technique (SIT) under shade-house conditions. A non-Bt cultivar (88H0019) and GM CRY1A were grown in two shade houses, with one receiving regular releases of sterile *E. saccharina* moths and the other serving as a non-release control. Stalk damage was assessed at harvest using percentage stalk bored length (%SBL), percentage internodes bored (%INB), stalk red length (%SRL), and larval infestation per 100 stalks (e/100).

Overall infestation levels were low across the trial (mean 1.2 e/100 stalks), reflecting limited pest pressure. Nevertheless, GM CRY1A consistently exhibited significantly lower damage and infestation than 88H0019 across both shade houses. In the SIT release environment, non-Bt sugarcane showed the highest damage (%SBL 0.28; %INB 0.35; %SRL 0.81) and infestation (3.7 e/100), whereas GM CRY1A maintained minimal damage (%SBL 0.02; %INB 0.03; %SRL 0.03) and very low infestation (0.16 e/100). The release of sterile moths alone did not significantly reduce stalk damage or larval abundance in non-Bt sugarcane, and no synergistic interaction between SIT and Bt sugarcane was detected under the conditions of this study.

These findings demonstrate that GM CRY1A sugarcane is highly effective in suppressing *E. saccharina* damage and reproduction, while SIT showed limited impact under low-infestation, early-crop conditions. Although SIT did not contribute measurably to suppression in this trial, its integration with Bt sugarcane remains theoretically promising. Future studies should incorporate higher initial pest densities, increased release rates, and older sugarcane or field-based trials to better evaluate potential additive or synergistic effects within area-wide integrated pest management programmes.

#11488

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Development of non-chemical management approaches for serpentine leafminer (*Liriomyza huidobrensis*) in protected cropping

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Anu JAYAWEERA, Soo Jean PARK, Lok Nath ARYAL, Md Sahadat HOSSAIN, Sanjana AKTER, Fazila YOUSUF

Abstract

The Serpentine Leafminer, *Liriomyza huidobrensis* Blanchard, is an invasive pest that poses a serious threat to Australia's vegetable and ornamental industries, particularly within protected cropping systems. This study examines a suite of behavioural and biological management approaches aimed at developing integrated, non-chemical control strategies for serpentine leafminer. The study developed a model trap combining colour, shape, and plant-derived lures to improve monitoring and suppression. It also investigated plant volatiles for potential lure-and-repel applications, assessed substrate-borne vibrational signals (vibrometry) as a tool for mating disruption, and evaluated the effectiveness of the parasitoid *Neochrysocharis formosa* as a biological control agent. Collectively, these approaches provide a framework for reducing reliance on chemical insecticides and enhancing the resilience of protected cropping systems against serpentine leafminer infestations.

Optimising Inherited Sterility in *Eldana saccharina*: Biological and Reproductive Responses to X-ray and Gamma Irradiation for Sterile Insect Technique Application

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Nelisiwe HLATSHWAYO, Givemore MUNHENGGA, Jarishma GOKUL

Abstract

The African sugarcane stalk borer, *Eldana saccharina* Walker (Lepidoptera: Pyralidae), a major lepidopteran pest of sugarcane in southern Africa, poses a significant threat to crop productivity, highlighting the need for sustainable and environmentally compatible control strategies such as the sterile insect technique (SIT). This study assessed the comparative effects of X-ray and gamma irradiation on the biological and reproductive performance of the F1 generation of *E. saccharina* for the development of an effective inherited sterility (F1 sterility) programme. Parental crosses were exposed to 150, 180 and 200 Gy to generate F1 offspring, from which key biological parameters (pupation, emergence, survival, and pupal weight) and reproductive outputs (sex ratio, fecundity, fertility, and egg hatch) were measured. Across both irradiation types, higher doses generally reduced pupation, emergence, survival, and reproductive performance. Dose-dependent declines were observed in pupation, emergence, and overall F1 survival, with pupation and survival at 150 Gy being significantly higher than at 180 and 200 Gy for most crosses, while 200 Gy produced the lowest pupation ($\leq 35\%$ in several gamma treatments) and survival proportions. Emergence also declined at higher doses, with some crosses at 180 Gy showing reductions exceeding 50%. Reproductive parameters indicated strong sterility induction, with significant reductions in fertility and egg hatch at 180 and 200 Gy, where egg hatch typically fell below 30%. Sex ratio remained largely unaffected in X-ray treatments but displayed dose-dependent shifts under gamma irradiation. X-ray and gamma treatments exhibited comparable trends, demonstrating similar efficiency in inducing inherited sterility. These results confirm that X-ray irradiation can achieve F1 sterility levels equivalent to gamma irradiation and represent a viable alternative for SIT development against *E. saccharina*, provided that dose optimisation is carefully maintained.

Entomopathogenic Fungi from Omani Soils: Evaluation of Plant Growth Promotion and Insecticidal Activity on Maize (*Zea mays* L.)

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Ainas Suliman ALALAWI, Husam AL HINAI

Abstract

Entomopathogenic fungi represent a sustainable alternative to chemical insecticides due to their dual capacity to control insect pests and promote plant growth through endophytic colonization. This study aimed to isolate EPFs from Omani soils using the wax moth (*Galleria mellonella*) baiting method and to evaluate their effects on maize (*Zea mays* L.) development and aphid mortality under glasshouse conditions. Five fungal isolates were identified through ITS-based molecular analysis. The two isolates *Trichoderma sp.* and *Aspergillus aflatoxiformans*, were tested for maize production. Maize plants were inoculated using root dipping, foliar spray, and combined root dipping plus foliar spray methods. The results revealed significant impacts on maize plants. *Trichoderma sp.* significantly enhanced maize growth compared with *A. aflatoxiformans* and the control, as evidenced by increased morphological and physiological parameters, particularly under the combined application method. In addition, *Trichoderma sp.*-treated plants exhibited significantly higher chlorophyll a (7.92), chlorophyll b (5.30), and total chlorophyll content (4.67) than the control, while *A. aflatoxiformans* showed slightly lower pigment values (chlorophyll a: 7.34; chlorophyll b: 4.88; total chlorophyll: 4.30), indicating a weaker but positive physiological effect; chlorophyll fluorescence (Fv/Fm) values were significant in fungal treated plants (0.68–0.69) than in the control (0.63), with no significant difference between the two fungal species, reflecting improved photosynthetic efficiency and reduced physiological stress. In contrast, *A. aflatoxiformans* exhibited comparatively weaker growth-promoting effects but demonstrated stronger and faster insecticidal activity against aphids, achieving significantly corrected mortality of 58.84% after 48 h at 10^8 conidia mL⁻¹, with mortality increasing further after 96 h and showing a clear concentration- and time-dependent response. Both fungi successfully colonized maize tissues endophytically without causing disease, highlighting the strong potential of locally isolated entomopathogenic fungi as sustainable plant growth promoters and biological control agents for environmentally friendly agricultural practices in Oman.

Termite Damage to Economic trees in Benue State, Nigeria: Termite Diversity and Nature of Attacks, Economic Cost of control and plantation owners' knowledge and perception.

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Stephanie AVAR-TSUE

Abstract

This study was therefore designed to identify farming practices that create ideal conditions for termite proliferation, evaluate the species diversity and abundance of termites affecting economic trees, determine the financial cost of termite infestation on economic trees in order to develop an integrated strategies for their management. A total of 120 orchards were selected and trees were randomly inspected for physical evidence of termites' infestation. A structured questionnaire to investigate plantation owners' knowledge, attitudes, and practices in relation to termite infestation was administered to 402 plantation owners and farmers. Focus Group Discussions, direct field observations, were also conducted in each community and termite samples were collected from infested trees. A total of 2,458 economic trees were inspected across the four study locations, 572 (23.7%) showed visible signs of termite infestation. Cashew trees had highest infestation rate with 37.1 % showing evidence of termite infestation. The Genus *Macrotermes* were the most predominant termites infesting trees with *M. bellicosus* and *M. malaccensis*. Orange and mango were predominantly cultivated in Kwande and Ushongo, palm trees were the major economic trees in Ogbadibo. There was a significant association between location of study and types of economic trees ($\chi^2 = 218.323$; $p = 0.000$). There was no significant association between signs of termite infestation and location of plantations ($\chi^2 = 30.107$; $p = 0.090$). There was a significant difference in pesticide application compared to other control methods ($\chi^2 = 33.565$; $p = 0.014$). Farmers termite-related perceptions are significantly influenced by local experience and indigenous knowledge resulting to ineffective control efforts. Our finding justifies the need to build the capacity of farmers and deploy more effective integration of termite control options to mitigate the impact of termite-related fruit production losses in Benue State, Nigeria.

From forest edge to meadow centre: spatial patterns of beetle assemblages after mechanical control of invasive goldenrod

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Abstract

Mechanical control of invasive goldenrods (*Solidago* spp.) by deep rotary mulching had been proposed as a conservation tool, but its effects on ground-dwelling invertebrates and the spatial reach of disturbance away from forest-edge refugia were poorly known.

We used a single meadow originally dominated by goldenrod divided into a mulched and an untreated invasive half. On each half, we deployed a grid of pitfall traps in five parallel lines from forest ecotones towards the meadow centre and sampled carabid and staphylinid beetles over two post-mulching seasons. Rather than treating the halves as independent replicates, we focused on edge–centre gradients within each half and their contrast between halves.

We analysed abundance, richness and community composition, modelling the interaction between treatment and position along the gradient and its change between years. Using published bioindication schemes for carabids and staphylinids, we derived community-weighted indices to test whether the meadow centre of the mulched half was selectively depleted of poorly dispersing, disturbance-sensitive species compared to edges and to the invasive half. Trait-based gradients between halves and years constrained the relative importance of immigration versus local reproduction and yielded estimates of disturbance reach and persistence to guide the width of mechanically treated strips.

Influence of soil-conserving strip cropping on ground beetle communities

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Abstract

Agricultural intensification represents one of the main causes of the global threat to species diversity. A significant component of intensification is land consolidation into large monocultural and thus homogeneous areas. A further negative consequence of intensification is soil degradation through accelerated water erosion. In the Czech Republic, approximately 50% of arable land is threatened by water erosion, highlighting the need for effective anti-erosion measures. Currently, soil-conserving strip cropping (SC) is being implemented as an anti-erosion management on sloping fields.

We aimed to assess the influence of soil-conserving SC on ground beetle communities associated with sloped arable fields. This practice may enhance biodiversity by reducing erosion-driven disturbance of soil fauna habitats while increasing spatial heterogeneity through alternating strips of different crops, thereby providing a wider range of resources, microhabitats, and in some cases also refugia.

To evaluate these effects, we monitored ground beetles (Coleoptera: Carabidae) using pitfall traps over a three-year period (2023–2025) in Bošovice, Czech Republic, comparing strip-cropped fields with conventionally managed monocultures.

Our results demonstrate that soil-conserving SC significantly enhances ground beetle abundance. Depending on the season, an enhancement in species diversity was also recorded. While conventional fields showed reduced species richness in the erosion-prone upper parts of the slope, SC maintained high richness across the entire topographic gradient. Notably, our data demonstrate that one type of crop strip can serve as a refuge for beetles while the adjacent strip remains unvegetated or is recently disturbed. Crucially, we observed a clear preference of the red-listed species *Poecilus sericeus* for SC fields, indicating that this management could directly benefit endangered species potentially sensitive to erosion. These findings suggest that SC promotes resilient agroecosystems and may enhance ecosystem services such as natural pest control.

Scaling up Integrated Pest Management for *Phthorimaea absoluta*: from experimental greenhouse trials to commercial tomato production

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Marianna STAVRAKAKI, Konstantina ALIPRANTI, Terpsichori STEFANAKI, Archontissa DERMITZAKI, Elena TROULI, Nikolaos TZAGKARAKIS

Abstract

Managing the tomato leafminer *Phthorimaea absoluta* remains challenging due to its high adaptive capacity and rapid resistance development. This study evaluated control strategies through a stepwise experimental approach, from small-scale greenhouse trials to commercial applications. Initially, a small-scale greenhouse experiment was conducted to assess four management schemes against *P. absoluta*: an untreated control, a chemical-based scheme, a biological scheme of moderate efficacy (BIO A), and a biological scheme of high efficacy (BIO B). The results revealed clear differences among the four schemes, with BIO B achieving the greatest reduction in infestation levels, followed by BIO A, while the chemical scheme showed reduced effectiveness over time. These findings were used to design an improved Integrated Pest Management (IPM) protocol. The improved IPM protocol was implemented in a commercial hydroponic tomato greenhouse in Ierapetra (southern Greece) under working production conditions. Green approaches allowed early establishment of the predator *Nesidiocoris tenuis* contributing to effective pest suppression. The protocol maintained *P. absoluta* infestation levels below 1/ mine per leaf for most of the cropping period, despite continuous external pest pressure that allowed limited chemical interventions (only 18% of total applications). In addition, the IPM protocol was pilot-tested in commercial open-field tomato crop. Despite higher population fluctuations, consistent implementation of the protocol based mainly on biopesticides (80% of total applications) maintained *P. absoluta* infestation below damage thresholds. This approach sustained the presence of *N. tenuis* acted as a key regulatory factor of pest populations. Both results highlight the importance of systematic pest monitoring, as early detection enables timely and targeted plant protection strategies. Overall, the results demonstrate that scaling up from small-scale greenhouse experiments to commercial crop level supported the development of reliable and sustainable IPM strategies, significantly reducing reliance on chemical insecticides and improving the long-term management of *P. absoluta*.

Screening of RNAi target genes for management of *Ceutorhynchus obstrictus*

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Triin KALLAVUS, Éricmar AVILA DOS SANTOS, Liina SOONVALD, Riina KAASIK, Silva VILUMETS, Kristof DE SCHUTTER, Eve VEROMANN

Abstract

RNA interference (RNAi) is gaining recognition as a highly selective and environmentally sustainable approach for insect pest control, which offers a promising alternative to conventional chemical insecticides. In oilseed rape production, the cabbage seedpod weevil (CSW), *Ceutorhynchus obstrictus* (Marsham), continues to pose a serious challenge due to its ability to cause significant damage to the crop, which results in substantial yield reduction. To explore RNAi as a targeted management option for this pest, we conducted a systematic assessment of gene silencing efficiency across a set of candidate genes.

Seven genes with essential physiological roles and known RNAi sensitivity in related coleopteran species were selected for evaluation. Double-stranded RNA (dsRNA) was synthesized for each gene and introduced directly into the hemolymph of adult CSW through microinjection to ensure reliable uptake and reduce variability that can occur with oral delivery. After treatment, insects were monitored for mortality, and transcript levels were quantified using RT qPCR to measure the extent of gene downregulation.

The combined analysis of mortality and transcript reduction enabled the identification of the most effective gene targets, particularly those that produced consistent gene knockdown with the elevated mortality. These results demonstrate the potential of RNAi as a sustainable approach for CSW control. Furthermore, the identification of responsive gene targets provides a foundation for the future development of RNAi-based pest control products for CSW.

Effects of a Mixed Crop of Wheat with Spice Plants on Arthropod Diversity and Biological Pest Control

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Christine BECKER, Annete REINEKE

Abstract

The project "Transformative Intercropping Systems for One Health" (TRIO) investigates the integration of perennial spice crops, particularly umbelliferous species, into wheat (*Triticum aestivum* L.) cultivation in order to promote sustainable, biodiverse, and climate-friendly agricultural practices within the One Health framework. The use of umbelliferous species in intercropping systems, especially in Europe, has rarely been tested and little is known about their effect on biological pest control. Umbelliferous species can enhance the abundance of natural enemies by providing nectar, pollen, shelter, and – in case of perennial crops – overwintering habitats.

As part of the TRIO project, we explore intercropping systems in wheat as a viable alternative to applying pesticides by enhancing biological pest control through the promotion of natural enemies. Key research questions include: a) Can strip intercropping of wheat with umbelliferous spice plants effectively promote biological control of pest populations? b) Are natural enemies capable of dispersing between plant partners in intercropping systems? c) Does the inclusion of umbelliferous species increase the attractiveness of these systems to beneficial insects?

Field trials are established from 2024 to 2026 at four sites in Hesse, Germany, assessing summer wheat, caraway (*Carum carvi* L.), coriander (*Coriandrum sativum* L.), as well as perennial wheat, caraway, and fennel (*Foeniculum vulgare* Mill.), grown in a randomized block design. Among the different crop types, we assess arthropod diversity, predation and parasitization rates, and the movements of beneficial insects. Additionally, we collect volatile plant substances of umbelliferous spice plants to evaluate their attractiveness to beneficial insects and pests.

Through a comparative analysis of arthropod diversity and their ecosystem functions in a strip intercropping system of perennial spice plants with wheat, we aim to contribute to a more comprehensive understanding of the significance and role of insects and their ecosystem services in agricultural systems.

Hyperspectral Remote Sensing as a Tool for Aphid Detection in Winter Wheat

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Abstract

Aphids (Hemiptera, Aphididae) are major cereal pests causing yield losses through sap feeding and virus transmission. Their high reproductive capacity and climate-driven dynamics make them a persistent challenge for winter wheat. Integrated pest management (IPM) relies on intervention only when pest populations exceed stage-specific economic thresholds, but field scouting is time-consuming and spatially limited.

This study evaluates a remote sensing approach based on canopy-level hyperspectral reflectance (350–2500 nm), combined with supervised machine learning (ML), to classify wheat canopies with aphid populations above or below economic thresholds. Reflectance was measured at three phenological stages: stem elongation to heading, flowering, and milky grain development. For each observation, aphid pressure was assigned relative to the stage-specific threshold. Spectral data, including vegetation indices (VIs), were used to train ML classifiers to separate “treatment required” from “no treatment required.” Classification performance was consistently high ($F1 = 0.88\text{--}0.99$), with the best results at flowering ($F1 = 0.98$). Models using the full spectrum achieved the highest accuracy, while VI-based models also performed strongly, suggesting that selected indices could be applied to sensors with fewer bands. Among VIs, the Modified Triangular Vegetation Index (MTVI; $r_{pb} = -0.77$ to -0.82) and Triangular Vegetation Index (TVI; $r_{pb} = -0.66$ to -0.75) were most strongly correlated with canopy changes caused by aphid infestation.

The study identifies spectral regions and indices most sensitive to aphid-induced stress, providing a basis for application in imaging systems such as drone- or satellite-based monitoring. Linking hyperspectral reflectance and ML classification to economic thresholds offers a pathway towards threshold-aware, site-specific pest management. This supports IPM by enabling more precise insecticide application, reducing unnecessary treatments, and improving pest control efficiency. More broadly, the findings demonstrate how remote sensing can be integrated with IPM to advance sustainable crop protection under increasing pest pressure and climatic variability.

Assessment of insecticidal activity of non-thermal plasma against *Tribolium castaneum* and *T. confusum* (Coleoptera: Tenebrionidae)

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Florin BILEA, Monica MAGUREANU, Constantina CHIRECEANU

Abstract

Tribolium castaneum and *T. confusum* (Coleoptera: Tenebrionidae) are two of the major insect pests of stored grains causing qualitative and quantitative losses. The widespread use of synthetic insecticides to eliminate pest infestations in stored grains has caused the pests to become resistant. Therefore, there is a great need to discover alternative methods for their control. Plasma is an environmentally-friendly technique; it does not require any chemicals as it uses only air and electrical energy and it does not produce any waste as the species generated during the treatment are transient in nature. The lab-scale experiment described in this paper aimed to evaluate the effect of plasma treatment on adults of *Tribolium castaneum* and *T. confusum*. A dielectric barrier discharge in coaxial geometry was used and the insects were either directly exposed to plasma or indirectly treated by the plasma effluent gas. The results showed complete elimination of insects treated with plasma for 5 min, and considerably accelerated mortality with increasing exposure time. For only 2 min of plasma treatment, mortality at two weeks was over 80%. Indirect treatment, with the insects placed after the plasma reactor and exposed to the plasma effluent gas, was less effective compared to direct treatment. The substantial difference compared to direct treatment demonstrates the essential contribution of short-lived species produced in the plasma and possibly of the radiation emitted by the plasma or the electric field. Longer follow-up of survivors showed that plasma treatment does not completely eliminate, but substantially reduces the insect's procreative capacity.

Acknowledgements: This work was performed within the framework of ADER 2.1.7 project financially supported by Agriculture and Rural Development Ministry of Romania

Pollen sources in the epicuticle of insects: foraging in perennial monoculture and weeds in the Andean highlands

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Abstract

Pollen grains present in a given area allow us to reconstruct the historical or current vegetation of that place. Insect habits can change over time due to food availability. There is little information on the abundance, distribution, and food preferences of insects associated with *Persea americana* Mill. and its weeds. A field study was conducted in Ecuador at the end of the rainy season in monoculture avocado plantations at 2,475 meters above sea level, with the voluntary presence of insects. The middle stratum of the monoculture canopy height showed greater diversity and abundance for most insect orders, especially Diptera and Hymenoptera. In the weeds, the lower strata showed greater abundance of Hemiptera, Diptera, and Coleoptera. The highest foraging activity of insects, regardless of order, was recorded between 10:00 a.m. and 11:00 a.m., in the SE and SW orientations. Acetolysis determined that there is a significant correlation between the feeding of each order and pollen intake. In the principal component analysis (PCA), there is a separation between the groups associated with the presence and absence of pollen, which explains 93.4% of the variation produced. Diptera with the highest presence of pollen in the epicuticle were frequent pollen consumers, especially flies of the Syrphidae family. Hemiptera, Neuroptera, and Coleoptera were associated with the botanical families Poaceae, Asteraceae, and Plantaginaceae. Diptera, Lepidoptera, and Hymenoptera were associated with Lauraceae, Brassicaceae, and Amaranthaceae. There is selective pollen impregnation in insects, influenced by pollen morphology, insect characteristics, and floral availability in the environment.

ASSESSMENT OF YIELD RELATED TRAITS OF RICE CULTIVARS AND EFFICACY OF DIFFERENT PESTICIDES AGAINST SCIRPOPHAGA INCERTULAS WALKER (LEPIDOPTERA: PYRALIDAE)

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Abstract

Rice (*Oryza sativa* L.) is a major staple crop globally, yet its productivity is significantly constrained by the yellow stem borer (YSB), *Scirpophaga incertulas* (Walker), one of the most destructive pests in rice-growing regions. The present field study evaluated the yield-contributing traits of seven rice cultivars—Chenab Basmati, PK-386, KSK-133, KSK-434, Super Basmati, KSK-282, and Kissan Basmati—to identify high-performing varieties against natural YSB pressure. Additionally, the performance of eco-friendly and conventional control strategies, including neem extract (30 mL/L), *Metarhizium anisopliae* (2 mL/L), and chlorpyrifos (1 mL/L), was assessed on PK 1121 Aromatic rice under field conditions during the 2020 season.

Yield parameters such as tillers per plant, grains per panicle, 100-grain weight, and spike length varied significantly among cultivars, with Kissan Basmati exhibiting the highest yield potential. Among the management treatments, chlorpyrifos showed the highest suppression of YSB, recording the lowest percentages of dead hearts (20.00%, 13.33%, 13.30%) and white heads (23.66%, 20.33%, 19.00%) across three applications. Neem extract and *M. anisopliae* demonstrated moderate yet promising reductions in infestation, offering viable sustainable alternatives to chemical insecticides. In contrast, untreated plots exhibited the highest levels of dead hearts (40.33%, 39.54%, 42.11%) and white heads (37.12%, 38.23%, 40.14%).

The findings highlight the importance of host plant selection and integrated pest management (IPM) in combating YSB. Botanical and microbial agents, particularly neem extract and *M. anisopliae*, show strong potential for incorporation into environmentally sound rice pest management strategies, reducing reliance on chemical pesticides and supporting sustainable rice production.

Enhancing urban arthropod biodiversity through the establishment of sown wildflower strips

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Helga SIMON, Anna NAGY, Attila TORMA

Abstract

Urbanization is a global phenomenon that can adversely affect biodiversity through a range of interacting processes, with potential consequences for arthropod assemblages as well. These processes include the habitat fragmentation and degradation, the presence of various pollutants, and the urban heat island (UHI) effect. Furthermore, the high proportion of built-up areas may restrict arthropod movement among remaining habitat patches, thereby influencing dispersal and biotic interactions. One potential approach to mitigating these impacts –particularly on pollinators - is the establishment of sown wildflower strips. However, such strips may offer resources for other arthropods in urban environments by providing food, shelter, overwintering sites, and potentially favorable microclimatic conditions through shading, while also contributing to habitat connectivity. In this study, we examined the extent to which urban arthropod communities are associated with small-scale sown wildflower strips. Twenty flower strips were established across the city of Szeged using a commercial seed mixture, and their arthropod assemblages were compared with those of urban green areas used as controls. Preliminary analyses indicate differences in species richness and abundance of pollinators and phytophagous insects between flower strips and control areas. These results suggest that sown wildflower strips may play a role in supporting arthropod diversity in urban environments, although further investigation is required to assess their long-term and broader ecological effects.

Local rather than landscape-scale factors shape arthropod diversity in greened schoolyards

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Abstract

The greening of urban spaces is increasingly resorted to as an adaptation to climate change, both to cool urban heat islands and to improve soil permeability, and many local authorities have thus initiated some degree of renaturation programs. Such initiatives also have the potential to improve biodiversity conservation by providing new habitats for local species, particularly insects. However, in densely built and populated urban environments, space available for renaturation is scarce. Most renatured spaces are thus limited in surface and habitat complexity, and data is still lacking to evaluate the actual habitat quality and contribution to biodiversity of these urban micro-ecosystems.

The BugToSchool project is focusing on the arthropod communities that have colonised 18 recently greened schoolyards within the city of Nice (South of France). Because these schoolyards were unsealed over a short period of 3 years and revegetated by the same city service using a common plant palette, they can be considered as independent replicates of newly created habitats exposed to the same species pool, and as such can be used to isolate the effects of different ecological factors on their colonisation by arthropod communities.

Over the year 2024, we conducted four inventory sessions of arthropod diversity using a combination of sampling methods. We analysed the influence of two categories of ecological factors on three different diversity metrics (abundance, taxonomic richness, functional richness) : (i) local factors related to the green space itself like area or plant richness ; (ii) landscape-scale factors related to the greenness of the environment around the schoolyard, like the quantity and fragmentation of green cover.

We found that all three diversity metrics were positively influenced by weed richness and flower abundance and origin (local vs exotic ones), and that local factors were better predictors of arthropod diversity than landscape-scale ones.

Apoidea Communities and Pollen Residues Reveal Environmental Pressures in the Alpine City of Trento (Italy)

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Maria Vittoria ZUCCHELLI, Sergio ANGELI

Abstract

Pollinators are essential for plant reproduction, biodiversity maintenance, ecosystems health and most crop plants rely on them. However, pollinators face many threats due to habitat loss and fragmentation, climate change and increasing pesticides exposure. The project aligns with the objectives of the EU Biodiversity Strategy for 2030 and the EU Pollinators Initiative, addressing the urgent need to reverse pollinator decline. This study investigates the correlation between the presence of the key pollinators Apoidea (Hymenoptera) and environmental health conditions in the Trento area (Italian Alps). In Trento around 1000 Apoidea individuals, representing six families (Apidae, Halictidae, Andrenidae, Megachilidae, Colletidae and Melittidae) and genera including *Ceratina*, *Halictus*, *Lasioglossum*, *Osmia*, *Megachile*, *Rhodanthidium*, *Anthidium*, *Anthophora*, and *Bombus* (e.g. *B. pascuorum*, *B. terrestris*, *B. argillaceus*, *B. vestalis*), have been collected so far using pan traps and net transects. Furthermore, visual transects allowed the observation of 1,306 individuals, which were classified into size-based categories defined in this study: 45% small bees, 14% large bees, and 18% bumblebees (*Bombus spp.*). Additionally, pollen samples from local bees were collected and analysed to detect agrochemicals and heavy metal residues. A total of 32 agrochemical active ingredients were screened, including 5 insecticides (chlorantraniliprole, acetamiprid, carbaryl, etofenprox, pirimicarb), 24 fungicides (e.g. folpet, captan, dithiocarbamates, tolylfluanid, fludioxonil), and 3 herbicides (glyphosate, metamitron, pendimethalin). This research contributes to a deeper understanding of environmental health conditions and assess exposure to agrochemicals and other pollutants.

The effects of Cow Manure Treated by Fruit Beetle Larvae, Waxworms and Tiger Worms on Plant Growth in Relation to its Use as Potting Compost

WALEED ALWANEEN (King Abdulaziz City for Science and Technology, Waleed478@hotmail.com)

Abstract

Dairy industry is flourishing in world to provide milk and milk products to local population. Besides milk products, dairy industries also generate a substantial amount of cow manure that significantly affects the environment. Moreover, heat produces during the decomposition of the cow manure adversely affect the crop germination. Different companies are producing Vermicompost using different species of worms/ larvae to overcome the harmful effects using fresh manure. Tiger worm treatment generally improved plant growth parameters, especially in the compost-manure ratio (75% compost, 25% cow manure), followed by a ratio of 50% compost, 50% cow manure, Plant growth in Waxworm treated manure was weak compared with plant growth in compost treated by Fruit Beetle (FB), Waxworms (WW), Control (C) notably in the compost (25% compost, 75% cow manure) and 100% cow manure where there was no growth at all. Fresh plant weight, fresh leaf weight and fresh root weight were significantly higher in the compost treated with Tiger worms in (75% compost, 25% cow manure); no evidence was seen for any significant differences in the dry root weight measurement between Fruit Beetle (FB), Tiger worms (TW), Waxworms (WW), Control (C) in all composts. Tiger worms produced the best product, especially at the compost ratio of 75% compost, 25% cow manure followed by 50% compost, 50% cow manure.

Shaping Soil Ecosystem Services Providers: Agroecological Practices Drive Mite Communities in Mediterranean Vineyards

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Lucas L. GODOY, Lucas DUCROS, Halima RAJOUL, Maud HUCHOT, Anne MEROT, Carlos BARRETO, Gilberto José DE MORAES, Raphael de Campos CASTILHO, Léo GARCIA, Alice CHARALABIDIS, Elena KAZAKOU, Marie-Sthephane TIXIER, Denise NAVIA

Abstract

Soil harbors a substantial proportion of terrestrial biodiversity, underpinning soil health, and providing ecosystem services for sustainable agriculture. Vineyards are a major crop in Europe, yet conventional practices can disrupt belowground communities. Agroecological approaches may help maintain and restore soil health, in part through soil mesofauna, sensitive bioindicators of management intensity. We investigated the effect of management practices in French Mediterranean vineyards, across a gradient of agroecological intensity (management system, plant diversification and ground cover) on soil predatory (Mesostigmata) and detritivorous (Oribatida) mite communities; and bioindicators species of management intensity, with adjacent garrigue as reference. Surveys were conducted in 2023 (24 commercial plots) and in 2024 (9 experimental plots). Mites dominated the soil mesofauna across plots (71–79%). Oribatida was the most abundant with 49–59.5% (56 morphospecies across 37 families). Mesostigmata accounted for 9% and showed high diversity (58 species across 15 families). Overall, 11 Oribatida taxa and 14 Mesostigmata taxa were identified as bioindicators of vineyard management. Oribatida responded strongly to management: garrigue and vineyards with permanent cover supported the highest abundance and diversity, whereas these metrics were consistently lower in conventional management and temporary cover or bare soil. Organic vineyards achieved diversity levels comparable to garrigue. Mesostigmata abundance was relatively stable across systems, but diversity was lower under conventional and temporary cover, while organic-managed and permanent-covered plots maintained values close to those observed in garrigue. On experimental plots, the pattern was confirmed: Plant diversification helped sustain both abundance and diversity of predatory mites over time, while bare soil resulted in significantly lower predatory mite abundance. Agroecological practices, particularly organic farming and plant diversification, support richer and more diverse soil mite communities in Mediterranean vineyards, underscoring their value as sensitive indicators of management-driven changes in belowground biodiversity. Further studies should link these findings with ecosystem services provision.

Evaluation of insect frass as a biofertilizer in field trials with lupins in Greece

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Nikos PAPADIMITRIOU, Christos RUMBOS, Georgios THALASSINOS, Vasileios CHALKIDIS, Efi LEVIZOU, Vasileios ANTONIADIS, Christos ATHANASSIOU

Abstract

Insect frass from edible species, a nutrient-rich organic fertilizer, has been shown to enhance soil fertility by providing macronutrients, as well as beneficial microorganisms, which help crop growth. In a series of field tests in Greece with lupins that were carried out in 2024 and 2025, we evaluated frass from the yellow mealworm, *Tenebrio molitor* L. (Coleoptera: Tenebrionidae), through a series of parameters that quantified plant growth and soil characteristics. Initially, the applied frass was analyzed for its nutrient content, i.e., macronutrients (N, P, K, and Ca) and micronutrients (Fe, Cu, Zn, and B). The trials were carried out in two different soil types, i.e., acidic and alkaline, on two lupin varieties. The total treatments were ten i.e., control, treatment with a conventional fertilizer, 0.1%, 0.5%, and 1.0% frass, applied to each of the two lupin varieties, with the percentage of frass corresponding to the amount of frass that was added in the upper 10-cm soil layer. Based on our results, the application of 0.5% frass, corresponding to approx. 5 tn/ha, noticeably increased the yield in both varieties, as compared with the control. In contrast, we found that 1.0% was phytotoxic in some of the treatments, which resulted to yield levels that were similar or even lower than those in the control. Our findings clearly demonstrate the potential to use insect frass as a biofertilizer in lupin cultivation, especially in the case of acidic soils.

Financial support for this research has been provided by PRIMA, a program supported by the European Union, under grant agreement No 2231, project CIPROMED (PRIMA Call 2022 Section 1 Agri-food IA).

Typology of Continental Microhabitats: Principles and Perspectives for Insect Studies

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Abstract

Within the political framework of the French National Plan in favour of pollinators, a pollinators traits database has been created, led by the French NGO Arthropologia in collaboration with the French National Museum of Natural History. This database is part of the French Taxonomical Reference program (TaxRef) and relies on cooperation with multiple organisations, NGOs and research centres (e.g. French National Reserves, CNRS, Oreina, Gretia).

The database's objective is to provide a formalised architecture which can be used and applied to all pollinators, in order to centralise knowledge on the different taxa involved in pollination services.

To render possible the implementation of different traits -such as larval development or nesting habitat- in the database, a microhabitat typology has been created. The aim of this typology is to encompass the vast majority of continental microhabitats (terrestrial and aquatic) used by different taxa to complete their life cycle, by taking into account their ecological and behavioral diversity, as well as the various levels of specialisation that exist.

Initially developed in order to address pollinator-related needs, this work has the vocation to be transversal and to include every taxonomic group of continental fauna.

In terms of perspectives, this microhabitat typology is primarily designed to be operative and coherent with field study requirements, as it integrates existing databases and typology developed for specific taxonomic group (e.g. Syrph the Net for Syrphid studies, dendromicrohabitat typology for saproxylic beetles). It also serves as a tool for academic research by centralising ecological traits across very different taxa, with a nested architecture allowing statistical analysis at different levels of precision. This work has been carried out thanks to the contribution of numerous experts.

Diversity of bees (Hymenoptera, Apoidae) and hoverflies (Diptera, Syrphidae) along differently managed forest roadsides in Latvia

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Dagmāra ČAKSTIŅA, Līga PENTJUŠA, Zane LĪBIETE, Linda GERRA-INOHOSA

Abstract

The flowering plant species along forest roads can serve as an important feeding and development setting for pollinators. In Latvia, new forest roads are constructed and existing ones reconstructed annually, but their impact on the diversity of pollinators remains underexplored.

The aim of this study was to determine the diversity of bees and hoverflies on differently managed forest roadsides. Three different types of forest roads were selected: two managed road types with different width of verges and one closer-to-natural road type. Bees and hoverflies were collected in 2024 thrice per summer in May, June and July using white, blue, and yellow pan traps.

In total, more than 80 species of hoverflies and 19 bee genera were identified. The dominant hoverfly species were *Helophilus pendulus*, *Xylota segnis*, and *Neocnemodon pubescens*. The dominant bee genera were *Bombus*, *Lassioglossum* and *Hyaleus*. The largest number of hoverfly species was observed in June, while the largest number of bee genera was observed in July. More species of hoverflies were found along managed forest road verges. Minor differences in the composition of both hoverfly/bee species/genera were also observed between the three forest road types. Preliminary results point towards the potential of managed road verges in promoting higher bee and hoverfly species diversity than natural forest roads and their value in pollinator conservation.

The study was conducted within the framework of a project "Forest Roads as Multifunctional Ecosystems: Biodiversity, Ecosystem Services, and Disservices" (grant No. LZP-2023/1-0558) funded by the Latvian Council of Science.

#11022

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Flower preferences and network roles of wild bees in semi-natural habitats

Izabela KOT (Department of Plant Protection, Subdepartment of Entomology, University of Life Sciences in Lublin, Leszczyńskiego 7, 20-069 Lublin, Poland, Izabela.kot@up.edu.pl)

Katarzyna KMIEĆ, Weronika GORAJ, Edyta GÓRSKA-DRABIK, Cezary SEMPRUCH

Abstract

Wild bees (Hymenoptera, Anthophila) provide a crucial roles in ecological systems, including pollination of crops and wild plants. However, ongoing decline of their diversity and abundance is observed in many areas due to urbanization, agricultural practices, impoverishment of flora, natural habitats loss or their fragmentation, and other changes occurring in the natural environment. Wild bees exhibit varying degrees of host plant specificity. Some species are polylectic and visit a diverse array of plants across many families, while others are oligolectic, meaning they specialize in collecting pollen from a narrow range of plant species (a few members of a botanical family or a genus or a few related genera). In turn, monolectic bee species collect pollen only from one plant species or one genus. Food plant spectrum of wild bees, and thus the structure of plant pollinator networks, may result from the bees' proboscis length, floral cues such as odour, colour and corolla length as well as pollen size. In this study, based on literature data from Central Europe, we analysed plant–pollinator networks from semi-natural habitats to identify the floral resources of wild bee species. The analysis of biodiversity and network structure (including modularity, nestedness and species centrality) between more than 350 wild bee species and over 330 herbaceous plant species from 30 botanical families were carried out. The obtained results revealed a complex organization of plant-pollinator interactions, which may support the development of conservation strategies and attempts to increase their populations in natural habitats by improving the availability and diversity of their food resources.

Assessment of wild pollinator biodiversity in Côte d'Ivoire and the impact of practices on their communities

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Abstract

The biodiversity of pollinators has declined significantly in recent decades, following the trend of more than 40% of invertebrate species now threatened with extinction. This is due to several factors, including intensive agricultural activities, excessive pesticide use, habitat loss and climate change. Côte d'Ivoire is no exception to these challenges. The country is facing considerable losses in yields and a decline in the quality of market garden production. Producers are therefore finding it increasingly difficult to respond effectively to market needs, which is compromising the balance between supply and demand. In view of this situation, it is therefore essential to reconsider agricultural practices and notably, reduce the use of chemical inputs. This study aims to assess pollinator biodiversity in peri-urban vegetable farms and to take stock of agricultural practices. The goal is to raise awareness among producers to adopt more responsible and environmentally friendly attitudes. We therefore conducted a study at 23 sites in nine locations, bringing together conventional, organic and agroecological transition farmers. A total of 2,057 specimens were collected. Of the 801 already identified, 18% are pollinators, mainly represented by beetles and hymenopteran. This percentage could increase once other groups have been identified. Field surveys indicate that 61% of market gardeners regularly use pesticides. This could impact pollination activity and thus partly explain the yield losses observed on farms. More in-depth analyses will be carried out to assess the real impact of agricultural practices on the overall wildlife biodiversity in these localities. The results will be used to propose areas for improvement, guidelines and guides to good agricultural practices tailored to each locality in order to support and strengthen pollinator biodiversity.

#12806

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Exploring margin composition across European landscapes to conserve pollinators in agroecosystems

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Hanna CHOLÉ, Benoît GESLIN, Joan VAN BAAREN, Ute FRICKE, Sarah REDLICH, Pavel SASKA, Jiří SKUHROVEC, Ronan MARREC, Kévin TOUGERON, Anne-Laure JACQUEMART, Fernando P. GAONA, Thierry HANCE

Abstract

Pollinators are essential for crop production, but their numbers are declining largely due to anthropogenic factors. This may result in pollination deficits, threatening food security through production losses. The implementation of agroecological infrastructures in field margins can help conserve pollinators and their pollination service in agroecosystems. However, the benefits of such local management practices depend on the quality, quantity, and availability of their resources through time. Also, landscape resources may favour or hamper the benefits of local margin resources, an interaction that may be dynamic through time and space.

To better understand how local margin and landscape composition interactions dynamically affect pollinators in temperate cereal agroecosystems, we observed flower-visiting insects in 40 winter wheat field borders from four European countries (Belgium, Czech Republic, France, Germany). Each field had four different margin compositions: a grass margin, a hedge margin, a grass and flower margin, and a hedge and flower margin. Richness and abundance of flower-visiting insects were recorded along observation transects in these margins at two different dates (early spring 2024 and late spring 2024). Flower richness and density in each margin was also recorded. Landscape composition and proportion of different surface classes (annual crop cover, seminatural open and closed habitats, small woody features cover) at five buffer scales (250-2000m) around pollinator transect were compiled from rasterized satellite imagery.

Results underline the value of flower richness to support pollinators independently of the margin composition. Pollinator responses to margin compositions differ depending on taxa and the surrounding landscape composition. Scale effects further highlight differences in local and landscape requirements between pollinator taxa. These results are discussed regarding pollination service conservation in agricultural landscapes, and some practical recommendations for margin management are proposed.

Comparative sensitivity of flower-visiting Diptera to insecticide exposure

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Fabio SGOLASTRA, M^a Isabel ARNALDOS SANABRIA, M^a Dolores GARCÍA GARCÍA, Ana Isabel MUÑOZ COSTA, María Luisa MORENILLA FERNÁNDEZ, Angel PÉREZ RUZAFÁ

Abstract

In recent years a decline in the abundance and diversity of pollinating insects has been observed. The factors involved in this decline include changes in land use, the introduction of exotic species, climate change and the increasing use of pesticides associated with the intensification of agriculture. However, significant knowledge gaps and methodological limitations persist in the current risk assessment of pesticides. It should be noted that, to date, the study of the impact of pesticides on pollinators has focused mainly on honeybees and bumblebees, and only recently on some species of solitary bees (e.g., *Osmia* spp.), while other groups have received less attention. Diptera (Order Diptera) are one of the most diverse groups of insects, found in virtually all habitats except the open sea and glaciers. Within this order, family Calliphoridae are a prominent group of flies of forensic, health and veterinary importance, as well as being pollinators, parasitoids and ecological indicators. Here, we hypothesise that exposure to sublethal doses of pesticides increases the sensitivity of pollinating Diptera to other stress factors (i.e., flooding due to torrential rains), affecting their development and survival. In this study, an assessment was conducted to determine the sensitivity of two Diptera species, *Calliphora vicina* and *Lucilia sericata*, to an insecticide. The standardised methodology of oral exposure in honeybees and syrphids was adapted to construct dose–response curves and calculate median lethal doses (LD50) for the two species. Differences between both species were observed and results were compared with those available in the literature for other pollinator species. The cross-cutting nature of this work ranges from its agroecological and ecological application in the broad sense of the trophic role that these dipterans play in their ecosystems, to the advancement in knowledge of forensic entomology in agricultural settings that it may imply.

Foraging behaviour of floral visitors as an indicator of pollination potential in sweet cherry orchards

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Abstract

Sweet cherry production relies heavily on managed and wild insect pollinators. Pollination success depends not only on the presence of flower visitors but also on their behaviour and traits. Although Chile is among the world's leading cherry producers, information on the diversity and pollination roles of insect visitors in its orchards remains scarce. In this study, we used video monitoring to assess the foraging behaviour of floral visitors in 16 conventional orchards in central Chile. In 2023, we recorded 3,012 insect visits. Bees comprised 65% of visits, with honey bees (*Apis mellifera*) alone accounting for 64% and fewer than 1% for wild bees. Besides, 33% of the visits were attributed to flies—mainly *Dilophus* sp. (Bibionidae) and several syrphid species— and 2% to beetles. Bees spent the shortest time per flower, exhibited greater inter-floral movement, and contacted the stigma most frequently, behaviours associated with high pollination potential. In contrast, flies and beetles typically remained longer on flowers, moved little between them, and often consumed floral resources without making contact with the stigma. These behavioural patterns suggest that hymenopterans are the most effective pollinators in these systems. Nevertheless, the high abundance of flies in the orchards may partly compensate for their limited pollination efficiency. Additionally, we found a significant positive relationship between body size and the likelihood of stigma contact, highlighting a key morphological trait associated with pollination effectiveness. The overall low diversity and small size of floral visitors in these conventional cherry orchards may explain why few of the species present have the potential to be effective pollinators. Promoting practices that enhance bee floral visitor diversity could increase the presence of alternative pollinators, reduce reliance on managed honeybees, and contribute to more stable cherry yields.

Mapping pollinator richness: a multi-species approach applied to Northern Italy

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Raffaele REPOLI, Valerio BALOCCO, Simone TOSI

Abstract

Faced with growing concerns for the decline of pollinators, policymakers and local administrators are seeking new tools for territorial planning. While a great amount of data about pollinating insects is publicly accessible on online databases, the willingness to implement conservation measures is often critically hampered by the lack of integrated information on pollinator richness, their diversity, and their dependency on spatial variability.

Here, we identified richness maps as crucial tools to transfer key information on pollinators to technicians and policymakers. Our maps integrate faunistic, land use, elevation, and bioclimatic data from Northern Italy. We used faunistic data from online, open-access data repositories, accounting for more than 50000 individual observations. We focused on bees, butterflies, and hoverflies, representing the main groups of pollinators addressed by European monitoring schemes. At first, the species presence was modelled in maxent according to publicly available thematic maps on land use, elevation, and bioclimatic indices. We then combined the maxent models for more than 300 bee, 200 butterfly, and 80 hoverfly species to obtain multi-species richness maps for each of the three pollinator groups.

Our spatial analyses display that all three pollinator groups were influenced by land use and elevation. Bee species richness was high in the open natural habitats of the Pre-Alps and Apennines mountains. Butterfly diversity followed a similar trend, but showed higher richness in the Alps, as compared to bees. Hoverflies displayed an opposite trend with good richness in lowland agricultural areas.

Our research frames pollinators distribution at the regional level, guiding interventions for the environmental protection and recovery. Next, we will use empirical field monitoring data to validate and fine-tune the developed distribution models, and quantify the effect of environmental variables on pollinator richness.

#11316

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Assessing the impact of the oriental hornet (*Vespa orientalis*) on honeybee colonies using semi-automated video monitoring

Joan AMENGUAL (University of the Balearic Islands, Palma, Spain, Joan.amengual@uib.cat)

Gabriel ARBONA, Cayetano HERRERA, Mar LEZA, Francisco PERALES LÓPEZ, Gabriel MOYÀ ALCOVER

Abstract

The invasive oriental hornet (*Vespa orientalis*) is becoming a rapidly expanding threat to pollinators and beekeeping across southern Europe. While the impacts of the yellow-legged hornet (*Vespa velutina nigrithorax*) on managed honeybee colonies are well documented, information on the ecological and apicultural effects of *V. orientalis* remains scarce.

In this study, we assessed the predation pressure exerted by *V. orientalis* on honeybee (*Apis mellifera*) colonies in 25 hives from 5 apiaries located in Málaga province (southern Spain). Sampling was conducted during September and October 2025. Approximately 450 hours of automated, non-invasive video monitoring were used to record hornet activity and honeybee traffic at hive entrances, allowing the characterization of predation patterns. An Artificial Intelligence model was trained to detect invasive hornets and to quantify honeybee traffic entering and leaving colonies. Additional behavioral parameters, including the number of successful and unsuccessful capture attempts and the time spent ambushing, were analyzed using the semi-automated tracking software BORIS.

We expect to observe that foraging *V. orientalis* workers frequently attempted to prey upon *A. mellifera* workers at colony entrances, reducing honeybee activity. This study represents an initial step toward the implementation of automated, field-scale monitoring of honeybee colonies and contributes to improving our understanding of *V. orientalis* impacts on managed *A. mellifera* hives.

Can direct sequencing of honeys help us better track honey bee health?

Thibault LEROY (GenPhySE, Université de Toulouse, INRAE, ENVT, 31326, Castanet Tolosan, France, Thibault.leroy@inrae.fr)

Julie BIRGEL, Emilien ROTTIER, Kamila CANALE-TABET, Claire HOEDE, Benjamin BASSO

Abstract

Recently, our BeeGEES team (GenPhySE, Toulouse) has made significant progress in sequencing DNAs present in honey, capturing information from bees, plants, and associated microbiota. This strategy offers several advantages, including being non-lethal, reducing the carbon footprint associated with sampling, and providing access to broader environmental information. After confirming that extraction and direct shotgun sequencing of honey samples was feasible, we first validated that the proportion of honey bee DNA is large enough to allow whole-genome analysis of nuclear DNA, while also enabling the study of the rest of the species coming from the surrounding environment (eDNA). This approach can address important issues in the beekeeping sector, particularly with regard to product traceability (e.g. combating frauds), by analyzing plant DNA from nectar and pollen, as well as other DNA that can be used as biomarkers of their origins.

For this poster, we will focus on another important potential application, the possibility to identify bee parasites and pathogens through honey sequencing, in order to directly assess colony health. Using an experimental design performed at INRAE Avignon (France), we collected honeys from migratory hives at specific time points throughout the season. As a proof of concept, we questioned whether the mite infestation can be tracked by analysing the varroa reads. Indeed, our goal was to determine whether the abundance of DNA reads from the parasite can be used to accurately track the exponential phase of its infestation dynamics. In this poster, we will present the conceptual framework, methodological workflow, and early results from this pilot study, highlighting how direct honey sequencing can be used to monitor parasites and pathogens (including the early detection of emerging ones), while also providing insights into additional agroecological dimensions.

Study on target site resistance to acaricides in Italian population of *Varroa destructor*

Emanuele MAZZONI (Università Cattolica del Sacro Cuore , Emanuele.mazzoni@unicatt.it)

Filippo COMINELLI, Maria Cristina REGUZZI, Eleonora CALDI, Mohamad MOKHLES, Luana BATAGLIA

Abstract

The ectoparasitic mite *Varroa destructor* Anderson and Trueman (Acari: Varroidae) remains one of the most critical challenges for beekeeping, representing a major driver of colony loss worldwide. Current control strategies rely on acaricides that may be either “soft” (organic acids and essential oils) or “hard” (synthetic). In Italy, the two main classes of registered synthetic acaricides are pyrethroids (IRAC MOA 3A) and octopamine receptor agonists (IRAC MOA 19). Resistant populations are spread worldwide due to the overexpression of detoxification enzymes or point mutations that structurally alter the molecular targets of acaricides. Effective management therefore requires continuous monitoring to detect early signs of resistance within local *V. destructor* populations. Pyrethroid resistance has been linked to four mutations in the voltage-gated sodium channel gene (L925V, L925I, L925M, and M918L), while resistance to octopamine receptor agonists is associated with five mutations (N87S, T115N, Y215H, F290L, and Y337F). To date, the prevalence and geographic distribution of these mutations in Italian *V. destructor* populations, excluding Lombardy and the Piacenza province and only for pyrethroids, remain largely undocumented. This study focus on conducting a molecular screening for the aforementioned resistance markers in mites collected across multiple Italian regions. Mites were sampled using sticky boards with the collaboration of beekeepers and regional beekeeping associations. Targeted gene fragments corresponding to the two resistance-related loci were amplified via PCR using specific primers and subsequently sequenced using the Sanger method. The resulting genotypic data provide insight into the distribution and frequency of resistance mutations, contributing to a broader understanding of the population structure of *V. destructor* in Italy and supporting the development of more effective and regionally tailored control strategies.

Volatile chemical profile of the Asian hornet *Vespa orientalis* (Hymenoptera: Vespidae) and its electroantennographic activity.

Antonio ORTIZ (University of Jaen, Aortiz@ujaen.es)

Lucía RUIZ-MARTOS

Abstract

The new invasive species, *Vespa orientalis* (Hymenoptera: Vespidae) is spreading in Europe, moving north and west from its native Mediterranean Middle East range. Since its first detection in Spain (Valencia, 2012 and Cadiz, 2018) and have rapidly expanded throughout Malta, Italy, Greece, France and Romania.

The Oriental hornet poses a significant threat to various sectors. Its populations severely affect apiculture by preying on honeybees (*Apis mellifera*), often invading hives and generating intense predatory pressure causing the colony collapse. Beyond apiculture, the hornet endangers biodiversity by preying on other vital pollinators, thus affecting agriculture and urban ecosystems. The increasing spread of this species, facilitated by favorable climatic conditions, necessitates urgent and coordinated control measures.

Monitoring the spread and early detection of this *V. orientalis* is essential to develop effective monitoring strategies to curb its expansion but to date; a wide range of food attractants has shown very low selectivity and efficacy.

In order to identify semiochemical compounds that could ultimately help optimize and/or replace these trophic mixtures with more selective attractants, this study was initiated. Using ultrasound-assisted extraction and solid-phase microextraction (SPME), the chemical profiles of workers, gynes, and males of *V. orientalis* were isolated and analyzed by GC-MS spectrometry. The first results indicate the presence of C6-C10 n-oxo-acids in the volatiles released by queens, but not in extracts from males or workers. Additionally, short-chain esters, 2-alkyl ketones, and aldehydes were detected in the volatiles emitted by workers.

To confirm the biological activity of these compounds and mixtures, we evaluated the electroantennography (EAG) responses of oriental hornets to volatile components released by conspecifics. Regarding the EAG response, workers showed a significant response to short-chain aldehydes and alkyl ketones, while males responded significantly to n-oxo-carboxylic acid and esters.

These preliminary results are crucial for developing effective control methods for this invasive species.

Tracking pesticide exposure through bee-collected pollen

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Abstract

The honeybee (*Apis mellifera*) is a key managed pollinator, essential for crop fertilization. Declines in colony health have been linked to multiple stressors, including pesticide exposure and habitat changes. This study assessed pesticide residues in pollen collected by honeybees and examine the influence of seasonality and landscape composition. Pollen samples were collected from six Latvian apiaries during the 2024 flowering season. Analysis of 41 samples detected 47 pesticide residues above the LOQ, predominantly fungicides. The compounds most frequently detected were glyphosate, clopyralid, boscalid and acetamiprid, while the highest concentrations were detected for glyphosate (0.84 mg kg^{-1}), fluazifop-P-butyl (0.66 mg kg^{-1}), boscalid (0.61 mg kg^{-1}) azoxystrobin (0.48 mg kg^{-1}) and acetamiprid (0.35 mg kg^{-1}). Pollen Hazard Quotient (PHQ) were calculated for all samples (residue concentration in pollen (mg kg^{-1}) were transformed to ppb and divided by the oral/contact acute LD_{50} for bees ($\mu\text{g bee}^{-1}$), with none exceeding the critical threshold of 50, indicating low acute risk to honeybees. However, in one case, the PHQ was near the threshold. Pesticide concentrations peaked in late May and early June and decreased thereafter, with occasional smaller peaks observed in late July. Further analysis are required to determine whether landscape composition significantly affects pesticide contamination. Initial, unpublished data from 2024 at the same sites show comparable seasonal trends. These results provide insight into temporal patterns of pesticide exposure in social insects and reveal peak-risk periods during the flowering season. Understanding these dynamics is essential for developing management strategies that minimize pesticide impacts on pollinators and support the sustainability on pollination services provided by honeybees.

Visualizing Winter Cluster Dynamics in Honey Bee Colonies Using a High-Density Temperature Sensor Network

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Minwoong SON, Heeji KIM, DongHee LEE, Kyeong Yong LEE

Abstract

Understanding the spatial dynamics of winter clustering is critical for assessing honey bee colony survival under cold conditions, yet direct observation of cluster movement inside hives remains technically challenging. In this study, we present a novel monitoring framework that enables indirect visualization and tracking of winter cluster dynamics using a high-density temperature sensor network. A total of 64 temperature sensors were embedded within standard hive frames to form a fixed three-dimensional sensing grid inside the colony. Continuous temperature data were collected at high temporal resolution and converted into spatial temperature fields through interpolation-based visualization methods. Rather than focusing on absolute thermal conditions, this approach emphasizes relative temperature gradients and spatio-temporal shifts, allowing the inferred movement, expansion, and contraction of the winter cluster to be visualized over time. The system enables the reconstruction of cluster-level dynamics, including vertical and horizontal displacement patterns and responses to external temperature fluctuations, without physically disturbing the colony. Preliminary observations demonstrate that the method can capture fine-scale structural changes in the winter cluster that are not detectable using conventional single-point or low-density sensing approaches. This methodology provides a scalable and non-invasive tool for studying overwintering behavior in honey bees and offers a foundation for future applications in colony health assessment, comparative studies of overwintering strategies, and data-driven decision-making in smart apiculture systems.

Assessment of honeybee-associated viruses in honeybees and wild pollinators in nature protected zones in Luxembourg

Matteo RIPAMONTI (Luxembourg Institute of Science and Technology, Matteo.ripamonti@list.lu)

Imen KHARRAT-JARBOUI, Marine PALLEZ, Lisette CANTU-SALAZAR, Andreas REICHART, Alexander WEIGAND, Michael EICKERMANN

Abstract

Wild pollinator communities are increasingly threatened by habitat loss, agricultural intensification, and other anthropogenic pressures. In parallel, the potential impact of commercial honeybees on wild pollinators through pathogen spillover remains debated. To date, no data are available on how honeybee-associated viruses may affect wild pollinator health within species-rich nature protection zones in Luxembourg.

The DESPOT project aims to fill these gaps. In particular, the project is assessing the abundance and virulence of Deformed Wing Virus (DWV) types A and B, and Sacbrood Virus (SBV), in selected indicator species of wild pollinators, including solitary bees, bumblebees, and hoverflies, across six protected areas in Luxembourg. Viral prevalence and loads in wild pollinators are compared with those detected in managed honeybees (*Apis mellifera*) from apiaries surrounding these zones.

Virus detection and quantification are performed using droplet digital PCR (ddPCR), enabling sensitive and accurate quantification of viral targets, including cases of very low viral load. By addressing key actions of the national pollinator protection plan, this study provides evidence-based insights into pathogen circulation at the interface of apiculture and nature conservation. The results will support stakeholders in developing guidelines to promote a balanced coexistence between commercial beekeeping and wild pollinator conservation in protected landscapes.

Integrative morphometric and molecular approaches reveal cryptic speciation within the *Eriophyes* spp. (Acari: Eriophyoidea) complex on rosaceous hosts

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Krzysztof Tomasz KOLATAJ, Tobiasz DRUCIAREK, Mariusz LEWANDOWSKI

Abstract

Eriophyoid mites (Acari: Eriophyoidea) are among the smallest arthropods, typically measuring less than 200 μm , and include many species of considerable agricultural importance. They feed exclusively on plants and cause a variety of injuries such as galls, blisters, leaf deformation, and russetting, while also serving as vectors of plant viruses. Most eriophyoid mites exhibit high host specificity, often restricted to a single or closely related host species, making them valuable models for studying host-associated genetic differentiation and ecological speciation. The pear leaf blister mite, *Eriophyes pyri* (syn. *Phytoptus pyri*), and morphologically similar forms such as *E. mali* on apple (*Malus domestica*) and *E. sorbi* on rowan (*Sorbus aucuparia*) have long been debated regarding their species status, whether they represent a single polyphagous species or a complex of host-associated cryptic species. In this study, we combined morphometric and molecular approaches to investigate host-associated genetic divergence in populations of blister mites (genus *Eriophyes*) collected from pear (*Pyrus* spp.), apple, and rowan. Two molecular markers were analyzed: the mitochondrial cytochrome c oxidase subunit I (COI) and the nuclear 28S rDNA D2 region. Phylogenetic analysis was conducted using the Bayesian inference method to assess cryptic speciation and evolutionary relationships among populations. Our study revealed host-associated genetic divergence among *Eriophyes* populations from apple, pear, and rowan, including the occurrence of two distinct species on apple. Moreover, the substantial genetic variability within the pear- and rowan-associated populations, combined with the absence of morphometric differentiation, indicates the presence of cryptic lineages. This study provides the first integrative molecular and morphometric assessment of blister mites on multiple rosaceous hosts, addressing long-standing taxonomic and epidemiological ambiguities within the *Eriophyes* spp. complex.

Mitogenomics of an orphan South Pacific leaf beetle lineage: resources to find a missing link

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Jesús GÓMEZ-ZURITA

Abstract

Phylomitogenomics has great potential for resolving phylogenetic relationships in a cost-effective way. However, mitogenomic data remain scarce for many animal groups. This is particularly true for insects, which account for about one third of available mitogenomes but represent only about 0.5% of described insect diversity. This gap is also evident in our group of interest, the Eumolpinae, a leaf beetle subfamily of ~7,000 described species, for which mitogenomic data exist for only 11 species. Our phylogenetic studies on this subfamily have revealed an enigmatic, independently evolved lineage endemic to the South Pacific that lacks clear affinity with other eumolpine groups and appears to have originated around the Cretaceous–Paleogene transition. Our ability to incorporate homologous data from the remaining subfamily diversity to identify the evolutionary placement of this lineage is currently limited. Nonetheless, the growing availability and taxonomic diversity of mitogenomic data and their demonstrated phylogenetic utility motivated us to generate high-quality mitogenomes for this lineage, in the hopes of eventually finding, even with indirect efforts, the evolutionary links of South Pacific Eumolpinae.

Here, we present three complete, fully annotated mitochondrial genomes of *Taophila* Heller species endemic to New Caledonia, representing this South Pacific lineage. Mitogenomes assembled from Illumina libraries are compact and largely retain the ancestral insect gene order, except for a trnA–trnR rearrangement. Nucleotide composition, codon usage, and other genomic features conform to typical insect patterns. Mitophylogenomic analyses recover a well-supported topology consistent with previous studies, including the separation of major Eumolpini lineages and the placement of *Taophila* within one of them, and were used to infer relationships among Eumolpinae and their closest relatives. These data contribute to expanding mitogenomic resources, improve their representation in the Tree-of-Life, and increase the likelihood of resolving the evolutionary connections between *Taophila* and other Eumolpinae worldwide.

Species Delimitation and Evolutionary History of Cryptic *Angelabella* Micromoths (Lepidoptera: Gracillariidae) in Xerophytic Environments of the Neotropics

Jose CERDEÑA (Universidad Nacional Mayor de San Marcos, Jose.cerdena@unmsm.edu.pe)

Gerardo LAMAS, Hector VARGAS, Jackie FARFAN, Andres LAGOS

Abstract

Xerophytic environments on the western slopes of the Andes harbor a unique diversity of insects that remains poorly studied at the genetic level, particularly in Peru, limiting our understanding of the processes that led to their diversification. This study focuses on the monotypic genus *Angelabella* (Gracillariidae, Lepidoptera), whose distribution is restricted to xerophytic areas of Peru and Chile, and whose populations on the western slopes of southern Peru had not been previously delimited. Using molecular phylogenetic and morphometric analyses, nine species are delimited within the genus, extending its distribution northward to Mexico. Genetic diversity within each species was assessed using the mitochondrial COI gene, revealing moderate levels of diversity and haplotype networks that reflect genetic variability. Additionally, the genetic structure of populations from southern Peru was analyzed using single nucleotide polymorphisms (SNPs) obtained through ddRAD-seq, revealing discordance with the COI results. While COI identifies distinct phylogeographic groups, SNP data indicate that populations are currently connected, suggesting recent gene flow despite historical isolation. These findings highlight the importance of integrating mitochondrial and nuclear markers to reconstruct evolutionary history and to understand population structure in insects from xerophytic environments of southern Peru. This study provides new insights into the diversity and distribution of *Angelabella* and demonstrates how population genetics can uncover historical and contemporary processes that would not be detected using a single genetic marker.

An integrative taxonomic approach to parasitic wasps: assessing the prevalence of cryptic species

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Antonia-Elena BEREȘ, Florina-Georgiana CABA, Maria-Magdalena DASCĂLU, Lucian HĂNCEANU, Andrada JAUGARIU-VICOLEANU J, Marius MIHĂȘAN, Mircea-Dan MITROIU, Ovidiu-Alin POPOVICI

Abstract

Parasitoid hymenopterans comprise a group of small insects responsible for managing populations of other arthropods. They are important in maintaining many agricultural pest species below levels that would cause significant economic damage. To effectively implement these insects in biological control efforts, it is important to understand species boundaries and identify any hidden species groups. What may seem like generalist species are often collections of closely related species with distinct host preferences and therefore distinct economic potential and ecological effects. We are focusing on the molecular taxonomy of a few genera (Chalcidoidea: Eupelmidae and Pteromalidae and Proctotrupoidea: Scelionidae) and its integration into an interdisciplinary approach (integrative taxonomy). We are using techniques such as DNA barcoding using standard molecular markers, second- and third-generation sequencing, reduced genome representation, phylogenomics and coalescent-based modelling to delimit cryptic species in the target groups. Molecular data will be combined with morphology to give a biological dimension to the delimited species. Our hypothesis is that cryptic species represent a significant proportion of the currently known biodiversity. Financial support provided by the Romanian Agency UEFISCDI through the grant PARACRYS (PN-IV-P1-PCE-2023-1971).

Integrative analysis of obscure lineages elaborates generic taxonomy of Polyommata blue butterflies (Lepidoptera, Lycaenidae)

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Nazar SHAPOVAL, Galina SHAPOVAL, Zsolt BÁLINT, Hao HUANG, Ilya LEONTIEV, Vladimir LUKHTANOV

Abstract

The subtribe Polyommata is one of the most diverse and taxonomically complicated groups of butterflies comprising about 500 species. For decades, its generic taxonomy remained controversial and was a matter of debates between splitters and lumpers. A number of studies have recognized all the diversity of the Palaearctic Polyommata in only several huge genera while other authors described numerous genus-group taxa comprising a few or even single species. Important studies presenting robust phylogeny of Polyommata widely accepted nowadays were published by Talavera et al. (2013, 2022). On a base of dated phylogeny, these authors suggested a minimal age interval 4–5 Myr to define genera. Despite previous efforts, some genus-level taxa of Polyommata still lack phylogenetic hypothesis, which may be crucial for elaborating a rigid taxonomic scheme.

In the present study, on a base of dated multilocus analysis covering nine genes we incorporated genus-level taxa of the subtribe Polyommata previously uncovered by phylogenetic analyses into the existing phylogenetic framework to revise genus-level taxonomy of the group.

Our study revealed the monophyly of the genus *Agriades* and presence of several monophyletic morphologically distinct lineages within it. Some taxa previously associated with *Agriades* were recovered within the genus *Albulina*. The genus *Bozanonia* was reconstructed as the sister lineage of the genus *Afarsia*. The genus *Grumiana* was recovered within *Plebejus* sensu lato as the sister lineage of the genus *Arianna*.

Most of the revealed genera fit into the age interval 4–5 Myr suggested by Talavera et al. (2013) except members of the *Plebejus* clade, which diversified 2.5–4 Mya. Treatment of these taxa within the genus *Plebejus* would lead to morphologically undiagnosable taxonomic entity, thus we recognize *Plebejus*, *Lycaeides*, *Arianna* and *Grumiana* as separate genera. Our study demonstrates that application of age limits defining higher taxa must be verified by morphology and biogeography.

Importance of I instar larvae in understanding of phylogenetic relationships within the family Neanuridae (Collembola: Poduromorpha)

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Adrian SMOLIS

Abstract

Neanuridae is the largest and most diverse subfamily within Collembola, comprising over 1,600 described species and representing a wide range of ecological adaptations and morphological diversity. Despite the substantial number of known taxa and a relatively comprehensive understanding of adult morphology, data concerning juvenile stages remain insufficient. The limited availability of such data significantly constrains our understanding of developmental patterns and their taxonomic and phylogenetic implications within the group. Larval morphology has been described for only a single species belonging to the Caputanurinae subfamily, approximately a dozen species within the Neanurinae subfamily, and two species representing the Pseudachorutinae subfamily. Knowledge of early ontogenetic stages remains highly uneven across Neanuridae lineages.

Studies on other Collembola families, including Onychiurinae and Hypogastruidae, have demonstrated that ontogenetic development is often accompanied by an increase in the number of setae on various body segments, reflecting progressive chaetotactic differentiation during growth. In contrast, available data suggest that most Neanuridae species do not exhibit pronounced differences in chaetotaxy between juvenile and adult stages. However, *Pseudachorutella intricata*, one of the firsts representative of the Pseudachorutinae subfamily for which the morphology of the first instar larva has been described, represents a notable exception. In this species, clear differences in chaetotaxy between juvenile and mature individuals have been documented, indicating a more complex ontogenetic pattern than previously assumed for the family.

These findings highlight the need for further studies to determine whether such developmental changes are characteristic of Pseudachorutinae as a whole or represent an isolated case. Additionally, it remains unclear whether similar ontogenetic patterns may occur in other, as yet unstudied, representatives of Neanuridae. A detailed understanding of first instar larval morphology not only contributes to a more complete characterization of individual species but may also provide valuable characters for phylogenetic analyses at both the family and subfamily levels.

Thousands of Wasps, Hundreds of BINs: Are Barcode Clusters Real Species?

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Marko MUTANEN, Maria KHAN

Abstract

Species delimitation remains a major challenge in hyperdiverse and understudied insect groups, particularly within “dark taxa” where morphological identification is difficult and taxonomic expertise is limited. DNA barcoding and the resulting Barcode Index Numbers (BINs) are increasingly used as proxies for species boundaries, yet their biological validity remains insufficiently tested in many parasitoid wasp lineages, including Braconidae. Here, we present results from a large-scale DNA barcoding survey of Finnish Braconidae based on Malaise trap samples collected across the country. A total of 9,120 specimens were processed, of which 8,923 yielded high-quality COI barcode sequences. Neighbor-Joining analysis and BIN clustering recovered 906 BINs in the dataset. When compared to the currently documented Finnish Braconidae fauna (1,454 described species), our results reveal substantial undocumented diversity. Notably, 303 BINs are represented by singletons, indicating a high proportion of rare or previously unsampled lineages. These findings demonstrate that intensive Malaise trap sampling combined with DNA barcoding is highly effective for uncovering hidden diversity and advancing the documentation of dark taxa in Braconidae. However, the observed barcode diversity also raises a critical question: do BINs reliably correspond to true species boundaries in this group? To address this, our ongoing work aims to sequence 3–5 independent nuclear markers for a representative subset of taxa. By comparing nuclear marker-based species delimitation with COI-derived BIN assignments, we will directly assess the congruence between barcode clusters and multilocus species boundaries. This integrative framework will provide empirical evidence for evaluating the robustness of BINs as species proxies and contribute to improved taxonomic resolution in hyperdiverse parasitoid wasps.

What history can a fossil reveal? Sclerites, glands and more in a Baltic amber Pselaphinae (Coleoptera: Staphylinidae)

Viviane NUNES (University of Tübingen, Vivianenunesbio@gmail.com)

Mario SCHÄDEL, Margarita YAVORSKAYA

Abstract

Despite the remarkable extant diversity, ecological breadth, and global distribution of Pselaphinae, their fossil record remains fragmentary and temporally discontinuous. In the past decade, the description of several Cretaceous taxa from Spanish and Burmese ambers has advanced our understanding of early pselaphine evolution, revealing an unexpectedly rich fossil diversity. Nevertheless, the deepest phylogenetic split within the subfamily - between Faronitae and the remaining taxa, collectively referred to as the “higher Pselaphinae” - has been inferred mainly from extant taxa and putative Cretaceous stem-lineage fossils. This highlights the need for fossil representatives from multiple geological periods to resolve this early divergence, which is crucial for tracing back morphological evolution in a clade characterized by exceptional morphological disparity. Here, we report a member of Faronitae preserved in Baltic amber (Eocene) and provide a morphological characterization based on micro-CT data. This discovery fills a temporal gap between mid-Cretaceous fossils and the modern fauna and represents a time calibration point. The specimen exhibits a mosaic of plesiomorphic traits, such as a discal elytral fovea, and derived features otherwise known only from higher Pselaphinae (e.g., nearly clubbed antennae), offering insights into early morphological transformations. Micro-CT data revealed external and internal structures rarely preserved in fossils, including lateral glandular openings on the head connected to large cephalic glandular reservoirs, remnants of which are recognizable. This feature, known in extant Faronitae, suggests evolutionary significance, and may be related to chemical defense. In addition, partially preserved musculature and inner sclerites across all body tagmata provide insights into functional morphology. The specimen shows an interrupted tentorium, an apomorphy of Pselaphinae. The tentorial bridge remnants extend anteromedially further than in extant species, reflecting a plesiomorphic condition. Overall, our data illustrate how micro-CT-derived morphological information can be combined with existing phylogenetic hypotheses to track key innovations in diverse beetle groups.

A new dragonfly relative from the Upper Triassic of southern Germany

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Abstract

The last common ancestor of dragonflies (Anisoptera) and damselflies (Zygoptera) most likely lived either in the Permian or the Triassic, making these periods particularly interesting for research on fossil (stem-) odonatan remains. This particularly holds true because sediments of that age yield a plethora of fossil wings from various extinct lineages. One of these lineages leads to Triadophlebiomorpha – an important group of dragonfly relatives. The group, as the name suggests, mainly, but not exclusively, includes fossils from the Triassic. The systematic affinity of Triadophlebiomorpha is still unresolved. However, from the lack of characteristic wing venation features it is apparent that it is not an ingroup of either of the two extant Odonata clades (Zygoptera and Anisoptera). Wings in species attributed to Triadophlebiomorpha share a relatively plesiomorphic basal complex and a conspicuously widened area between the veins RP3+4 and MA.

Here, a new fossil specimen of a not yet formally described species from the Upper Triassic of southern Germany is presented. The fossil was excavated in a quarry in northern Bavaria and stems from the Coburger Sandstein (Keuper) and is Carnian in age. The left and right wing fragments are morphologically consistent with other species attributed to Triadophlebiomorpha. However, the fossil stands out from its closest relatives by featuring a large CuA-CuP wing area with several CuA branches and intercalaries. The newly discovered fossil morphology represents a valuable source of information for phylogenetic analyses aiming to test the assumption of monophyly for Triadophlebiomorpha and, if it is reinforced, the position of the fossil within the Triadophlebiomorpha tree of life.

Mustard to the rescue: Modulating tachykinin-related peptides, allatotropins, and immune responses via allyl isothiocyanate in the pest species *Tenebrio molitor* L.

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Radosław GMYREK, Natalia KONOPÍŃSKA, Arkadiusz URBĄŃSKI

Abstract

Insects are the most numerous group of animals in the world. Although many species play a vital role as pollinators, some of them contribute to serious economic losses, e.g., the *Tenebrio molitor* beetle, which can cause losses of up to 15% of the global production of stored grains. This highlights the need for novel, biosafe, and species-specific insecticides. There are two promising groups of molecules with the potential to complement current biological methods of insect pest species control: neuropeptides – key regulators of insect physiology, including immune system activity – and transient receptor potential (TRP) channels, a conserved family of cation channels involved in cell signaling. Although interactions between these two groups have been described in vertebrates, their relationship in insects remains poorly understood. Therefore, the main aim of this study was to investigate the interaction between Painless channels (one of the best-known insect TRP channels) and two immunomodulatory neuropeptides, namely, tachykinin-related peptides (TKRP) and allatotropins (AT), in *T. molitor*. We analysed the effect of Painless channels activation via allyl isothiocyanate (AITC) on the expression levels of selected neuropeptide genes in neuroendocrine tissues. To investigate the immunomodulatory role of TRP channels, we also examined the expression levels of immune-related genes in the fat body. The obtained results showed changes in TKRP and AT precursor and receptor gene expression in the brain and ventral nerve cord, as well as alterations in the expression of immune-related genes in the fat body.

This study provides new insight into TRP channel-neuropeptide associations in invertebrates and enhances the understanding of the immunomodulatory role of TRP channels and the potential crosstalk between neuroendocrine and immune systems. It is also a crucial step toward designing selective and targeted methods of insect pest species control.

This research was partially supported by project OPUS 2021/41/B/NZ9/01054 (National Science Centre, Poland).

The effect of insulin-like peptides on immune system of *Tenebrio molitor* L.

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Abstract

Effective methods for large-scale insect rearing and biological pest control require a comprehensive understanding of the molecular mechanisms regulating insect metabolism, growth, immunity, and survival. Insulin-like peptides (ILPs) play a key role in these processes by activating the conserved insulin/insulin-like signaling (IIS) pathway, which is evolutionarily maintained from insects to mammals. Through this pathway, ILPs control the balance between growth, reproduction, and immune responses. Despite numerous studies on the influence of ILPs on major immune-related signaling pathways, there has been a lack of research addressing their direct impact on hemocytes — the main immune cells involved in both cellular and humoral responses in insects.

Our study demonstrated that ILPs activity in *Tenebrio molitor* is dose- and time-dependent. Short-term exposure (2 hours after application) led to an increase in phagocytic activity, suggesting that ILPs may initially stimulate cellular defense mechanisms and activate hemocytes for pathogen elimination. However, 24 hours after treatment, a marked decrease was observed in both phenoloxidase activity and hemocyte phagocytic capacity, which may indicate a secondary suppression of cellular immune responses in the later phase of the reaction. At the same time, an increase in lysozyme activity was recorded, suggesting a shift in immune balance toward the activation of humoral mechanisms. Obtained results were supported by transcriptomic data.

These findings highlight the role of ILPs as regulators of hemocyte function in *T. molitor*, a species of significant importance both for edible insect production as well as in the context of crop and stored product pest management. Understanding the molecular basis of such interactions may contribute to the development of new, targeted strategies for insect population control and optimization of mass-rearing systems in industrial applications.

This research is supported by grant from the national budget of Poland, the program of the Ministry of National Education, Pearls of Science, PN/01/0084/2022

Decoding Neuroendocrine Responses to Low Temperature in *Tenebrio molitor* via Transcriptomics and Metabolomics

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Abstract

Cold stress imposes severe physiological challenges on insects, disrupting ion homeostasis, energy metabolism, and signaling pathways. The neuroendocrine system plays a pivotal role in coordinating these responses, yet its tissue-specific molecular and metabolic dynamics under low-temperature conditions remain poorly understood. In this study, we investigated transcriptomic and metabolomic alterations in the neuroendocrine system – brain and ventral nerve cord (VNC) – of *Tenebrio molitor* exposed to acute cold stress (-5 °C for 1 h).

Both tissues modulate fatty-acid desaturation/elongation and phospholipid headgroup metabolism; brain displays coordinated increases in inositol/ethanolamine and IMPase expression, pointing to PI-cycle remodeling that may support synaptic function at low temperature. This points to phospholipid turnover and fatty acid desaturation for membrane fluidity control. Induction of Hsp70/Hsp83 and ER-stress/ubiquitin pathways indicates a proteostasis-first program in VNC, prioritizing folding and clearance of cold-labile proteins. Both tissues accumulate polyols and trehalose/maltose. Brain couples this pool with trehalase induction (supporting dynamic mobilization in recovery) whereas VNC shows down-regulation of trehalase and polyol-catabolic enzymes, favoring conservation over turnover. Brain up-regulates Toll/AMPs (attacins/serpins), reflecting innate activation intertwined with stress signaling; VNC suppresses the same immune modules, consistent with resource reallocation toward structural and proteostatic priorities. Across tissues, ionotropic glutamate receptors are reduced (dampening excitatory drive); brain additionally shows dopamine pathway activation and GABA increase, while VNC shifts vesicle-trafficking machinery (synaptotagmins/complexin/clathrin) toward local recycling under curtailed long-range microtubule transport. Additionally in brain, endocrine reprogramming was evident: juvenile hormone biosynthesis genes (JH-III synthase, Jhbp) were strongly up-regulated, while insulin-like peptide Ilp7 was down-regulated, indicates a brain-centric switch from growth to resilience—stabilizing membranes and neural function while easing insulin-driven anabolism.

These findings provide novel insights into the molecular and metabolic architecture of cold tolerance in *T. molitor*, with implications for understanding insect stress tolerance strategies and improving thermal resilience in mass-rearing systems

Effects of insect PVK-2 and mammalian NMU-25 neuropeptides on the neuroendocrine system of *Zophobas atratus* beetles

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Martyna KWIATKOWSKA, Gracjan DUDEK, Szymon CHOWAŃSKI, Karolina WALKOWIAK-NOWICKA

Abstract

The neuro-endocrine system of mammals and insects shows a number of functional similarities. Structural and functional similarities are also observed among the signaling molecules used by this system - neurohormones. In recent years, research has mainly focused on demonstrating the effects of insect neuropeptides on mammalian cells. However, there is limited information in the literature regarding the effects of mammalian peptides on insects.

Here, we investigate the effect of an insect neuropeptide from the CAPA peptide family – periviscerokinin 2 (PVK2) and its mammalian counterpart neuromedin U-25 (NMU-25) on the morphology and functioning of the nervous system of *Zophobas atratus*, a model insect species.

We examined insect survival after peptide injection, morphological changes in the insect equivalent of the pituitary gland — the retrocerebral complex (RCC) — and alterations in the acetylcholinesterase activity in various parts of the nervous system following administration of the studied neurohormones. All tests were performed on 30-day-old adults.

We showed that injections of both peptides did not increase insect mortality. Injections of PVK and NMU25 caused dose- and time dependent atrophy of RCC in *Z. atratus*.

Study was supported by NCN 2021/41/B/NZ3/00221 project.

Endocrine-Disrupting Effects of Bisphenol Analogues on the Ecdysone Pathway in *Nasonia vitripennis*

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Javier CARRILLO, Mónica AQUILINO, Óscar HERRERO, Charlotte LÉCUREUIL

Abstract

The accelerated pace of global social and economic development has intensified the presence of chemical pollutants in the environment, many of which have adverse health impacts. Among them, bisphenols are of particular concern due to their endocrine-disrupting properties and their potential to provoke severe developmental consequences in exposed biota. This study aimed to investigate the effects of Bisphenol A (BPA) and its alternative, Bisphenol S (BPS), on the expression of key genes involved in the ecdysone signaling pathway in *Nasonia vitripennis*, a model hymenopteran widely used in developmental and environmental toxicology.

Gene expression was assessed following pupal exposure to 5, 50 and 500 µg/L of BPA or BPS, for 48 hours. Our findings indicate that both BPA and BPS alter gene expression in *N. vitripennis* in a dose- and sex-dependent manner. BPA exposure elicited a significant dose-dependent transcriptional repression in female pupae, with several target genes showing reductions of up to 50% at 500 µg/L; whereas males displayed comparatively opposite and attenuated responses. Conversely, BPS induced a contrasting regulatory pattern: female pupae exhibited strong transcriptional upregulation, particularly at 50 and 500 µg/L, while male pupae showed broad gene repression. Given the widespread use of bisphenol analogues as “safer” substitutes for BPA, these results underscore the need of mechanistic ecotoxicological evaluations to determine their potential developmental impacts. A deeper understanding of how bisphenols modulate hormonal signalling pathways is essential for assessing long-term ecological risks and informing public-health and regulatory strategies.

Molecular Responses of *Drosophila melanogaster* to Glyphosate, 4-Nonylphenol and Bisphenol: A Toxicity Assessment Study

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Abstract

Environmental contamination by endocrine disruptors and herbicides poses a major threat to global biodiversity. This study evaluates the toxicological effects of three high-priority pollutants –Glyphosate, 4-Nonylphenol (4-NP), and Bisphenol A (BPA)– using the model organism *Drosophila melanogaster*. Due to its genetic tractability and the conservation of key physiological pathways, the fruit fly offers a robust system for investigating the molecular mechanisms underlying xenobiotic stress.

In our experimental design, *D. melanogaster* was exposed to sub-lethal concentrations of each compound from the egg stage to adulthood, analyzing males and females separately. Transcriptional responses were assessed by RT-qPCR using a battery of biomarkers involved in: 1) hormonal regulation (primarily ecdysone and juvenile hormone pathways), 2) immune function, 3) oxidative stress response, and 4) cellular stress response. Stable housekeeping genes were identified and used for normalization.

Our results demonstrate that all three compounds induce significant transcriptional alterations even at sub-lethal exposure levels. Glyphosate exposure notably upregulated oxidative stress-related genes, consistent with enhanced cellular stress. 4-NP and BPA, both recognised endocrine disruptors, altered the expression of genes associated with ecdysone signalling and reproduction. These molecular effects correlated with a dose-dependent decrease in adult fertility and developmental delays. Statistical analysis confirmed that these shifts occur at concentrations relevant to environmental wastewater standards.

In conclusion, this research highlights the sensitivity of *D. melanogaster* as a multi-level screening tool for environmental toxicants. Our findings underscore the importance of investigating diverse molecular biomarkers and considering sex-dependent differences in the evaluation of endocrine disruptors. Furthermore, this study opens the door to future research to clarify the physiological implications of pollutant-driven transcriptional disruption in the context of environmental health.

Cotton Reproductive Structures Drive Diet-Dependent Trade-Offs Between Reproduction and Survival in the Boll Weevil

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Abstract

The biological conditions that enable the cotton boll weevil, *Anthonomus grandis grandis*, to survive and sustain itself during the tropical off-season remain poorly known. This study investigated the use of cotton flower buds, bolls, and pollen by boll weevils, as well as the physiological mechanisms that link food consumption to reproduction. In cotton bolls, larvae took longer to develop, resulting in larger adult insects. These adults had larger fat reserves and survived longer, particularly when given pollen. Conversely, females that matured in bolls exhibited markedly reduced reproductive success compared to those that developed in flower buds. Individuals fed flower buds, on the other hand, demonstrated improved ovariole growth, greater protein levels, and a considerable increase in daily egg production. Molecular investigations showed a dramatic reduction in vitellogenin (Vg) expression in females that consumed bolls or cotyledons, suggesting that their diet hindered their reproductive potential. Females fed buds had approximately 2.5 times more Vg expression than those fed bolls. However, food had no effect on FOXO expression. These findings, considered together, indicate a trade-off between reproduction and lifespan, which is dependent on nutritional quality. Flower buds encouraged reproduction, whereas bolls promoted fat storage and boosted survival rates. These findings, considered together, indicate a trade-off between reproduction and lifespan, which is dependent on nutrition quality. Flower buds encouraged reproduction, whereas bolls preferred fat storage and boosted survival rates. Feeding on cotton flower buds helps boll weevil continue to reproduce. In contrast, boll-based diets decrease egg formation while increasing fat storage, hence enhancing survival. This diet modification provides a biological explanation for how tropical populations survive in the absence of hosts and then quickly resume reproduction when they can feed on flower buds. These findings emphasize the importance of stringent crop-free periods, providing a physiological foundation for more integrated boll weevil management tactics.

From plant residues to insect hormones: furfural affects juvenile hormone biosynthesis

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Abstract

Plant secondary metabolites (PSMs) are natural compounds with diverse biological activities, including insecticidal properties, making them promising candidates for sustainable pest management. Furfural, a furan aldehyde derived from agricultural biomass, has been studied for its pesticidal potential; however, its molecular effects on insect endocrinology remain largely unknown. One of the key hormones that can be target of pesticide activity of furfural is juvenile hormone (JH), a hormone synthesized by the *corpora allata*, which plays a crucial role in controlling metamorphosis, regulating oo- and vitellogenesis, and influencing reproductive behavior and pheromone production in adult insects.

This study investigates the impact of furfural on the expression of genes encoding enzymes involved in hormone biosynthesis, as well as on the JH level in haemolymph, and retrocerebral complex of the beetle *Tenebrio molitor*, a model organism and a common storage pest. Furfural was administered to female beetles at two concentrations (10^{-5} M and 10^{-7} M) via injection. We focused on three key genes encoding enzymes of the JH biosynthetic pathway: farnesal dehydrogenase (*DEH*), juvenile hormone acid methyltransferase (*MET*), and methyl farnesoate epoxidase (*EPO*), and assessed hormone levels in selected tissues.

Our results indicate that furfural selectively disrupts the JH biosynthetic pathway and modulates hormone levels in target tissues, leading to alterations in reproductive processes. These findings support the hypothesis that furfural interferes with hormonal regulation in insects and highlight its potential as a selective, environmentally friendly bioinsecticide targeting endocrine pathways in coleopteran pest species.

Effects of Different Waste Groups on the Development of *Hermetia illucens* (Diptera: Stratiomyidae) Larvae

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Abstract

The rapidly growing global population and the reduction in food resources have heightened the importance of *Hermetia illucens* (Black Soldier Fly-BSF) larvae as an alternative protein source due to their ability to convert organic waste into high-quality biomass. This study aimed to determine the effects of different types of organic waste groups on the growth performance of *H. illucens* larvae. The study was conducted on two main experimental groups under controlled laboratory conditions (24-30°C temperature, 60-80% humidity) and specific lighting periods. In the first experimental group, the effects of boiled animal (lamb head, fat) and boiled vegetable (broccoli, carrot) wastes were examined, while in the second group, the effects of raw animal (beef lung) and raw vegetable wastes on larval growth were examined. Larval length and weight were measured until pupation. According to the findings, although the egg hatching potential in the boiled animal food medium was lower than in the vegetable group, the growth rate was found to be approximately three times higher than the vegetable group. Similarly, it was observed that larvae fed with raw animal feed grew faster and more efficiently than those fed with raw vegetable feed; the raw vegetable diet significantly prolonged development. As a result, it has been determined that optimal production efficiency in industrial BSF production is achieved using decomposed but moisture-balanced waste and, in particular, animal-based feed supplements. Consequently, the present study demonstrates that the strategic use of animal and decomposed waste in larval biomass production is a feasible and economical model for both waste recycling and reducing alternative feed production costs.

Bilateral symmetry of epithelial tissue flows emerges from long-range mechanochemical feedback

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Abstract

Essential for organismal function, external bilateral symmetry is a striking and widespread feature of the animal kingdom. Research into the developmental mechanisms that promote symmetry has largely focused on organ size or position. However, bilateral symmetry must emerge from symmetric morphogenetic tissue flows that shape tissues and organs. Here, by combining optogenetics, quantitative image analysis, and mechanical perturbations, we investigated the emergence of robust and coordinated bilateral epithelial flows during metamorphosis of the *Drosophila* thorax epithelium. We show that a long-range mechanical coupling exists between the two contralateral tissue sides, specifically at the basal surface of the epithelium. This mechanical coupling is associated with mechanochemical feedback between the lateral and medial tissue domains, promoting the formation of a basal actomyosin network along the medial-lateral axis. Mechanistically, assembly of this network relies on the basal extracellular matrix (bECM) receptor Dystroglycan (Dg). In turn, Dg-dependent basal tissue tension ensures the symmetry of bilateral epithelial tissue flows as well as 3D cell geometry. Our work shows how the bECM and mechanochemical feedback enable coupling between contralateral tissue sides to fine-tune bilateral symmetry during tissue morphogenesis by coordinating 3D cell geometry.

Echoes of silence: dsRNA-induced effects on fertility and parental RNAi in a leafhopper vector of phytoplasmas

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Abstract

RNA interference (RNAi) has emerged as a powerful tool to investigate gene function in insects and to explore innovative pest control strategies. However, substantial gaps remain in our understanding of the mechanisms that enable efficient RNAi responses in insects, limiting our ability to fully exploit and understand the potential of this technology. In this work, we investigated the occurrence of a widespread infertile phenotype following dsRNA delivery in a leafhopper vector of phytoplasmas, *Euscelidius variegatus*, with the aim of gaining insights into its metabolic determinants and its capability to transmit silencing signals to the progeny. Seven different genes were targeted through abdominal microinjection of double-stranded RNAs (dsRNAs) in adult leafhoppers, and the resulting offspring were evaluated to assess treatment impacts on prolificity and transgenerational transmission of gene silencing (parental RNAi, pRNAi). Genes related to core cellular metabolism were found to negatively affect both prolificity and ovary morphology. Sex-crossing experiments confirmed that the detrimental phenotype was maternally driven. Interestingly, only dsRNAs showing limited or no impact on ovary morphology and prolificity were able to trigger transgenerational silencing, from parents to their progeny. During this study, we also gathered some hints on the molecular mechanisms underlying transgenerational signal transmission, a line of investigation that is expected to provide new insights into the nature and dynamics of RNA-based inheritance in this vector species. Taken together, these results will enhance our understanding of the reproductive biology of leafhoppers and address existing knowledge gaps regarding RNA-mediated transgenerational signalling.

Estimation of developmental thermal parameters of the Chilean leafroller, *Proeulia auraria* (Clarke) (Lepidoptera: Tortricidae), using non-linear models.

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Abstract

Proeulia auraria (Lepidoptera: Tortricidae) is a leafroller native to Chile, affecting both, fresh fruit orchards and vineyards. Besides, historically it has been the sixth species in terms of quarantine rejections during post-harvest inspections to our fruit for exports. Thus, our group has worked to develop a phenological model as a predictive tool for precise pest management under field conditions. *P. auraria* individuals were collected in severely infested vineyards, brought to the lab, and reared on artificial diet. Once adults emerged, couples were placed in courtship arenas where females laid eggs. Eggs recently laid (less than 12 h old) were taken to climatic chambers set at constant temperatures (between 8 and 34°C). Development was checked daily, for at least 50 individuals/stage or instar, in each temperature regime, determining the time when eggs hatched, and larvae and pupae molted. Most phenological models developed to date for insect species estimate the lower threshold and degree-days using linear models fitted to data (developmental rate vs. rearing temperatures, at several thermic regimes). However, the linear approach does not allow to estimate the upper threshold or the optimal temperature. On the other hand, the use of non-linear models has been reviewed most recently, having the advantage of estimating both, the upper threshold and optimum temperature, but not the respective degree-days. Our work estimated, for each stage, all thermal parameters with a new approach for calculation of degree-days, using several of these non-linear models, by computing the derivative of the development rate with respect to temperature, and obtaining the mean positive value between the lower and upper thresholds. These parameters will be later validated in field tests, and used to develop an early-warning electronic system to inform growers on the progress of *P. auraria* biology over the season, covering most of the Chilean fruit growing areas.

Fluctuating asymmetry as a reliable biomarker of nutritive stress: The rice weevil (*Sitophilus oryzae* L) case

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Abstract

Developmental stability (DS) represents the ability of an organism to develop a genetically determined phenotype despite environmental stress. Feeding on an unsuitable host can act as a stressor for insects, leading to slower population development, reduced progeny production, and disrupted stability, ultimately decreasing population size. Fluctuating asymmetry (FA), expressed as slight random deviations from bilateral symmetry is a widely used indicator of disturbed DS, since stress is expected to affect organismal symmetry.

In this study, we used the rice weevil (*Sitophilus oryzae* L.) as a model organism to test the reliability of FA as an indicator of disturbed DS in relation to progeny production (PP) and feeding intensity (% of consumed kernels, %CK). Weevils were reared on wheat and maize (favorable hosts) and sorghum (unfavorable host) in “no choice” feeding tests over four months. FA was quantified on the ventral body side using geometric morphometric analysis.

Highly significant differences in PP and %CK were observed between individuals feeding on favorable hosts (629–658 individuals, 88.7–98.7%) compared to those feeding on sorghum (150–167 individuals, 7.9–14.4%). Procrustes ANOVA revealed significant asymmetry among populations. Correlation between symmetric and asymmetric shape components was low and non-significant ($r = 0.228$, $P > 0.05$). All populations showed significant FA, with the highest FA observed in individuals feeding on sorghum and the lowest in those feeding on wheat. Discriminant function analysis confirmed significant differences in asymmetric components between wheat and sorghum ($T^2 = 36.3995$; $P < 0.05$) and maize and sorghum ($T^2 = 27.4233$; $P < 0.05$), but not between favorable hosts ($T^2 = 20.4120$; $P > 0.05$).

These results demonstrate that higher FA corresponds to reduced PP and lower feeding intensity on the unfavorable host. Thus, FA reliably reflects host-related nutritive stress and represents a useful biomarker of disturbed DS in *S. oryzae*.

Research was carried out within the SafeSeed project (#6691) funded by Science Fund of Republic of Serbia.

Toward understanding of sex determination pathway in the African malaria mosquito *Anopheles gambiae*.

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Abstract

In the African malaria mosquito *Anopheles gambiae*, the identified sex determination pathway components include the primary sex determiner Yob conferring maleness, female-specific splicing factor Fle, and two terminal transcription factors Dsx and Fru. In addition to sex, the pathway regulates dosage compensation (DC) through Fle blocking splicing of the 007/SOA gene, which encodes DC machinery component, rendering its female transcripts non-productive and DC inactive in females. Loss-of-function mutations in Yob, fle, and 007/SOA result in discrepant phenotypic manifestations, suggesting existence of yet unidentified molecules within the sex determination pathway.

In this study, we aim to identify novel *A. gambiae* sex determination pathway genes using a combination of functional genomics and molecular interaction analyses. Through analysis of the *A. gambiae* developmental transcriptome, we identified four candidate genes with sex-specific expression or alternative splicing patterns across developmental stages and now are investigating their roles in CRISPR/Cas9-mediated knockout experiments, followed by comprehensive phenotypic and molecular analyses. In parallel, we employ co-immunoprecipitation using known sex determination proteins as baits to isolate interacting partner molecules, and mass spectrometry analysis to elucidate their molecular identity. By integrating different experimental approaches, this work contributes to basic understanding of molecular developmental processes in *A. gambiae* and may uncover novel targets for mosquito control. Progress of the study and its results will be presented.

Identification of an orphan family involved in nymphose of *Nasonia vitripennis*

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Abstract

In this study, we present the first comprehensive proteome-wide analysis of tissue-specific and developmental protein dynamics during *Nasonia vitripennis* nymphal development, with particular emphasis on testis differentiation. Protein abundance was profiled in heads, legs, and testes across four successive pupal stages, identifying more than 2,500 proteins. While a large ubiquitous core proteome was shared among tissues, distinct signatures of tissue- and stage specific expression emerged. Testes displayed the earliest divergence in proteomic profiles, reflecting the progressive onset of spermatogenesis and revealing sequential molecular programs associated with cytoskeletal remodeling, meiosis, and terminal spermiogenesis.

Clustering of abundance trajectories highlighted both conserved spermatogenic pathways and lineage-specific features characteristic of *Nasonia*. Notably, a significant proportion of detected proteins remained uncharacterized, revealing an unexplored repertoire of potential regulators of cell differentiation. We focused on 175 proteins developmentally regulated in the testis, each showing at least a two-fold abundance change between successive pupal stages. Among these, 11 were classified as orphan proteins with dynamic expression patterns during testicular development.

Using AFDB/FSS tools, structural predictions and 3D similarity searches revealed that four of these uncharacterized proteins form a novel family of six-bladed β -propeller-like proteins, likely related to exo- α -sialidases. Remarkably, this protein family appears restricted to Hymenoptera, suggesting a lineage-specific molecular innovation with potential roles in organ differentiation, tissue remodeling, and reproductive biology.

Together, these findings establish the first proteomic framework for *Nasonia* nymphal differentiation, bridging conserved mechanisms of male germline development with cladespecific molecular novelties, and providing new avenues for investigating the evolution of tissue specialization in insects.

A Luciferin 4-Monooxygenase-Like Gene Links Cold Tolerance and Learning in *Spodoptera frugiperda*

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Sima MAJIDIANI

Abstract

Cold tolerance in insects relies on rapid metabolic and neuronal adjustments that stabilize cellular homeostasis during acute thermal stress. In fall armyworm, *Spodoptera frugiperda*, we identified and functionally characterized a luciferin 4-monooxygenase-like (Sf-LUC) gene belonging to the acyl-CoA synthetase superfamily. Bioinformatic analyses showed that Sf-LUC retains canonical AMP-binding and oxidative adenylation motifs characteristic of adenylyate-forming enzymes. The gene showed higher expression in late larval instars and was highly enriched in the neural tissues, suggesting roles in energy metabolism and redox-sensitive neuronal activity. RNA interference using chitosan-formulated dsRNA achieved ~95% knockdown at 48 h and resulted in increased mortality, developmental delay, elevated supercooling points (SCP), impaired rapid cold-hardening (RCH), and disrupted associative learning. Injection of dsSf-LUC caused paradoxical up-regulation of Glycerol Kinase 1 and 2 (GK1 and GK2) transcripts but sharply reduced hemolymph glycerol, indicating a block in redox-dependent cryoprotectant synthesis. Behavioral assays revealed that Sf-LUC-deficient larvae failed to form stable odor-reward associations, while RCH offered limited recovery. These results demonstrate that Sf-LUC functions as a redox-regulatory enzyme linking oxidative metabolism, glycerol production, and neuronal plasticity under cold stress. Therefore, Sf-LUC represents a mechanistic bridge between cold tolerance and learning in *S. frugiperda* and a promising upstream RNAi target for integrated pest management.

Sirtuins mRNAs analysis expression in *Apis mellifera* evidences differences among drone, queen and worker

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Abstract

Honey bee (*Apis mellifera*) is a keystone species for global crop production and forest pollination. Nevertheless, a sustained decline in lifespan has been reported over the last five decades. Members of the *Sirtuin* gene family, which regulate stress responses, mitophagy, lipid metabolism, and other cellular processes, are potential modulators of lifespan in *A. mellifera*. However, *Sirtuin* mRNAs remain annotated as predicted in the honey bee genome, underscoring the need for experimental validation.

The aim of this study was to characterize the expression of *Sirtuin* mRNAs in *A. mellifera* using an integrated transcriptomic, bioinformatic, and molecular approach. Individuals from the three social castes—queen, worker, and drone—were collected during the autumnal equinox in Málaga, Santander (Colombia), within a single daily cycle. *De novo* and genome-guided transcriptome assemblies, differential gene expression and pathway analyses focused on *Sirtuin*-associated functions, were performed. MicroRNA profiling was conducted *in silico* using both newly generated datasets and publicly available long-read PacBio transcriptomes from the NCBI Sequence Read Archive.

To experimentally validate *Sirtuin* mRNA variants, 3' RACE RT-PCR primers were designed based on sequences reported in the NCBI Gene database and applied to RNA isolated from head, thorax, and intestine of each caste. Transcriptomic analyses confirmed the expression of *Sirtuin* mRNAs and revealed pronounced caste-specific differences in gene expression, tRNAs, and microRNAs, particularly between queens and drones or workers, and between workers and drones. RT-PCR assays further demonstrated tissue-specific and temporally dependent expression patterns for individual *Sirtuin* mRNAs.

These results indicate that *Sirtuin* expression is tightly associated with caste-specific physiological roles and may contribute to the marked differences in lifespan observed within honey bee colonies. This study provides the first integrated experimental evidence supporting the expression and regulation of *Sirtuin* mRNAs in *A. mellifera* and offers novel insights into the molecular mechanisms underlying lifespan regulation and species conservation.

Muscarinic receptors — an eminence grise of insect metabolism?

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Karolina WALKOWIAK-NOWICKA, Paweł MARCINIAK, Arkadiusz URBĄŃSKI, Joanna PACHOLSKA-BOGALSKA

Abstract

Muscarinic receptors (mAChRs) are ubiquitously expressed proteins. In vertebrates, they are found in almost all types of cells, including cells engaged in metabolism, such as hepatocytes, adipocytes, enterocytes or cells of pancreatic islets. Thus, they are involved in the complex regulation of metabolism as well as food intake and digestion.

The presence and physiological role of mAChRs in insects are poorly understood. Thus, in our studies, we tried to answer the following question: whether and how they affect metabolism in insects. We carried out our research on *Tenebrio molitor* larvae — on the one hand, a popular pest, and on the other hand, one of the most important species in the edible insects industry.

Our analysis conducted on the fat body showed that activation or inactivation of mAChRs by different agonists/antagonists significantly changes the activity of enzymes of key metabolic pathways. Moreover, to answer the question of whether there are direct or indirect effects, we analysed changes in the expression levels of genes encoding insulin-like peptides (ILPs) and insulin-like peptide receptors (ILPR) in the fat body, gut and brain of larvae. We found that the application of mAChR agonists or antagonists modulated the expression of the tested genes in a tissue- and time-dependent manner.

#16321

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

Experimental model for evaluating rearing conditions and bioconversion by BSF

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Mathilde RADEK

Abstract

The MicroDEMi experimental model was designed to evaluate rearing conditions, feeding diets, and genetics of black soldier fly (BSF) using controlled experimental units. Experimental conditions, including ambient parameters and larval rearing duration, are predefined to align with industrial realities. The model allows for twenty-five replicates per experimental condition and up to 4 conditions + control per trial, enabling robust statistical evaluation. This framework provides a valuable tool for assessing raw materials, genetic performance, and optimizing growth time in BSF farming.

Effects of developmental diet on adult energy stores in *Drosophila*

Peter KLEPSATEL (Institute of Zoology Slovak Academy of Sciences, Peter.klepsatel@savba.sk)

Emanuel MAKWISA, Emanuel PROCHÁZKA, Martina GÁLIKOVÁ

Abstract

Early-life nutrition can have lasting consequences for adult physiology, but its effects on energy reserves in early adulthood remain insufficiently understood. We manipulated yeast and sugar concentrations in the developmental diet of *Drosophila melanogaster* and measured total energy reserves after 10 days of adulthood on a standardized diet. By comparing these values with reserves at eclosion, we also assessed net change during early adulthood. We further tested how these responses depended on sex, population, and reproductive status.

Developmental diet had clear effects on energy reserves in early adulthood. Flies reared on low-sugar larval diets, despite emerging with lower reserves, showed the greatest net increase in energy during early adulthood, whereas flies from high-sugar diets showed the smallest net change. These effects were influenced by sex and reproductive status. In males, adult energy reserves more closely reflected larval nutritional conditions, whereas in females this relationship was weaker, likely due to the energetic demands of reproduction. Mating was generally associated with lower energy reserves.

These results show that developmental diet influences not only energetic condition at adult emergence, but also the trajectory of energy reserves during early adulthood.

How to Process Samples for Metabolomics in Ecology: A Comparative Study of Preanalytical Storage Methods

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Axel BERINGUE, Johanna RIVAS, David RENAULT, Marion CHORIN, Hervé COLINET

Abstract

The technical progress of metabolomics—the analysis of metabolite composition of cells, tissues, and biofluids—and its ability to unravel phenotypical responses of organisms to their environment was accompanied by the democratization of their use in a wide range of scientific fields. While the reliability of analytical procedures was thoroughly assessed, the effects of preanalytical processing on sample metabolic profiles (i.e., conditioning, storage, transportation, etc.) remain quite unclear. This uncertainty is especially notable for samples collected in the frame of ecological studies, which often involve field sampling and remote sample production, leading to extended transportation durations and suboptimal storage conditions. In this study, we evaluated the impact of storage duration and temperature, along with the effects of freeze-drying (or lyophilization; the process of stabilization through dehydration by sublimation), on the metabolic profiles of samples relevant to ecological studies. Specifically, we focused on the lesser mealworm (*Alphitobius diaperinus*), and the fruit fly (*Drosophila melanogaster*). The levels of 60 different metabolites were quantitatively analyzed using targeted metabolomics through gas chromatography mass spectrometry (GC–MS). We report significant metabolic shifts associated with freeze-drying, resulting in both increases and decreases in the contents of more than half of the quantified metabolites across all assessed chemical families. Several amino acids exhibited more than a fourfold increase in all investigated matrices. Furthermore, while samples stored at -80°C exhibited profiles most similar to those of samples analyzed right after collection, the metabolic profiles of these samples gradually changed over the 6 months of storage. Interestingly, metabolic shifts related to sample preanalytical processing and storage were relatively consistent across the biological matrices studied, particularly between the two insect species. Based on these observations, we propose several recommendations for reliable preanalytical sample processing in ecological studies, considering logistical and economic constraints.

#12490

Poster Session 2 - Wine & cheese party

01/07/2026 at 16:00, Exhibition area

A novel amino acid transporter from *Anopheles gambiae*

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Catriona ANDERSON, David THWAITES

Abstract

Proteins in mosquito blood meals are effectively digested and absorbed in midgut. For this to occur, the midgut must contain both proteases (upregulated following ingestion) and a range of specific amino acid transporters. Here we identify a novel amino acid transporter from *Anopheles gambiae*. Putative members of the SLC36-related gene family (a division of the Amino Acid/Auxin Permease family) were identified. Substrate specificity was predicted using structural models (AlphaFold Server) and knowledge of distantly-related mammalian transporter structure-function. Functional characterisation of novel transporters was performed using the *Xenopus laevis* heterologous expression system and radiotracer flux measurements. This novel transporter mediates H⁺-coupled uptake of a broad range of small and medium length neutral amino acids. Kinetic analysis of proline transport gave a $K_m = 1.9\text{mM}$. An orthologue in *Aedes aegypti* has been previously identified as being expressed at the apical membrane of midgut epithelia and is upregulated after a blood meal.

Are phenolic compounds from oat seeds responsible for feeding intensity of the rice weevil (*Sitophilus oryzae* L.)

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Radenka KOLAROV, Milica ŠKORIĆ, Ljiljana BRBAKLIĆ, Sanja MIKIĆ, Sonja GVOZDENAC

Abstract

Cereals represent a vital component of human nutrition. However, these commodities are very susceptible to infestation with stored product insect species. These insects feed, develop, and reproduce on stored grains, producing significant economic losses. One of the most damaging insects to stored cereals is rice weevil (*Sitophilus oryzae* L.). Although it has a strong preference for wheat, it is capable of damaging oats grains as well. Adults feed mainly on endosperm, while larvae feed on germ, resulting in reduced germination and nutritional value of kernels. Understanding the feeding preference and of this pest is essential for effective postharvest management, as well as defining seed resistance traits. It is well-known that different phenolic compounds are powerful natural insect deterrents, acting as plant defenses by reducing insect feeding, slowing growth, lowering reproduction, and even killing pests, functioning as repellents, toxins, or by making tissues indigestible due to high amount of tannins.

This study aimed to evaluate the feeding intensity (% of consumed grains) of *S. oryzae* in 32 different oat genotypes and assess their resistance to infestation, in a "no-choice" assay. Phenolic compounds were extracted from seeds using 70% methanol. The total content of phenolic compounds, tannins and flavonoids was determined in obtained extracts. Additionally, the antioxidant capacity of the extracts was measured by three different assays (DPPH, ABTS and FRAP). *S. oryzae* caused 10.33-77.87% losses of oats seeds, which indicate a significant difference in genotypes suitability to this pest. The total phenolic content ranged between 1.93 and 2.23 mg of quercetin equivalents per gram of seed. However, no significant correlation between phenolic, tannin and flavonoid content and feeding intensity were observed.

This research was supported by the Science Fund of the Republic of Serbia, #6691, New biorational methods for stored seed pest control and protection: To serve and prevent - SafeSeed.

Transcriptome analysis reveals key genes implicated in the adaptive physiology and development, of the drywood termite *Incisitermes schwarzi* (Isoptera)

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Amit ROY

Abstract

Termites are eusocial keystone insect species that feed on wood matter and plants to obtain cellular energy in tropical, subtropical and warm temperate regions. Certain invasive wood-feeding isopteran termite pests such as *Coptotermes* (Rhinotermitidae), and *Macrotermes*, *Odontotermes* and *Microtermes* species (Termitidae) have caused immense damage to eucalyptus forests in Malaysia, Australia, and India, Africa, respectively, due to increased wood decomposition sensitivity to warming temperatures, leading to global economic losses. Traditional forest pest management strategies have failed to curb these termite infestations, thereby urgently calling for the deployment of novel methods. A detailed understanding of the termites' adaptation and physiology at the molecular level would aid in development of future management measures utilizing molecular tools such as RNA interference (RNAi) technology. In this study, we have selected the drywood termite, *Incisitermes schwarzi* (Isoptera: Kalotermitidae) to investigate how these specific termites survive during their voracious feeding on spruce and birch deadwood in a drywood habitat. To understand their wood digestion response and the detoxification behavior of the natural toxins present in deadwood, we have conducted gene expression analysis in different life stages and different tissues using RNA-seq data. Differential gene expression (DGE) analysis across developmental stages and tissue types, have revealed multiple gene families related to wood detoxification, wood digestion, development of the termites, their eusocial behavior, and adaptation to biotic/abiotic stressors. Further to understand the RNAi susceptibility/resistance of the termites, we have identified RNAi machinery genes and explored their expression dynamics across the different life stages in the drywood termites. We have identified suitable reference/housekeeping genes for validating the termite transcriptome data using RT-qPCR and enzymatic assays. The differentially expressed genes identified through this study could help in understanding of termite physiology and adaptation to their lignocellulosic habitats and serve as excellent putative gene targets for future RNAi-based termite management.

Metabolomic Profiling of *Tribolium castaneum*(Coleoptera Tenebrionidae) Following Carbonyl Sulfide Fumigation

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Keon Mook SEONG

Abstract

Tribolium castaneum, a major stored-grain pest, contributes to substantial global food losses and degrades product quality. Fumigants are currently the primary means of controlling stored-grain pests. However, ozone depletion caused by methyl bromide and the spread of phosphine resistance have increased the need to develop alternative fumigants. Carbonyl sulfide (COS) has drawn attention as a promising alternative fumigant due to its high insecticidal activity and broad efficacy. Prior work has shown that COS exposure impairs mitochondrial function in *T. castaneum*. Nevertheless, the metabolite-level changes induced by COS remain insufficiently characterized. In this study, we conducted comparative metabolomic profiling of *T. castaneum* following COS exposure to define metabolite-level changes and to elucidate the associated toxic mechanisms and physiological responses. LC-MS/MS analysis detected a total of 284 metabolites in positive-ion mode and 321 in negative-ion mode across COS-treated and control samples (raw union). Based on the detected metabolites, enrichment analysis revealed pronounced class-level shifts, particularly in carboxylic acids and derivatives, organonitrogen compounds, and keto acids and derivatives. Subsequently, pathway analysis indicated pronounced changes in alanine, aspartate and glutamate metabolism as well as glycerophospholipid metabolism, valine, leucine and isoleucine biosynthesis, and nicotinate and nicotinamide metabolism. Notably, metabolites associated with mitochondrial function, including 2-oxoglutaric acid and nicotinamide, showed significant changes in the COS-treated group relative to controls. These results suggest that COS may disrupt mitochondria-associated metabolic processes in *T. castaneum*. This study provides a metabolomic framework for understanding COS toxicity and supports its evaluation within integrated strategies for stored-grain pest control.

Effects of food quality on host exploitation by an endoparasitic wasp

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Mona KROESEN, Christa SCHAFELLNER

Abstract

Koinobiont endoparasitic braconid wasps, which develop within the hemocoel of their host larvae, require specific adaptations to match their metabolism to that of their hosts. The solitary *Glyptapanteles porthetriae* (Hymenoptera: Braconidae) is a key natural enemy of *Lymantria dispar* (Lepidoptera: Erebidae). Due to its high reproductive potential and strong host-location ability, the parasitic wasp may contribute significantly to the collapse of *L. dispar* outbreak populations. At high population densities, both the host and, consequently, the parasitoid larvae experience reduced food quantity and quality. The larvae of *G. porthetriae* feed exclusively on hemolymph, yet their specific nutritional requirements, interactions with host metabolism, and responses to nutrient deficiencies remain largely unknown. We provided parasitized and unparasitized *L. dispar* larvae with either a high-quality (HQ) wheat-germ diet or a low-quality (LQ) diet in which micro- and macronutrients were substantially reduced and replaced with indigestible cellulose. Larvae were reared individually, and nutritional indices (e.g., consumption rate, growth rate, metabolic efficiency) were recorded for each developmental stage. Immediately after egression of the wasp larvae, samples of host hemolymph, host carcass, and wasp prepupae were collected and analysed separately for selected metabolites (sugars, cyclitols, glycogen, proteins, lipids). Samples from unparasitized controls were collected at corresponding developmental stages. Endoparasitic development in LQ-fed individuals was prolonged by approximately 50 % on average; however, neither the fresh nor dry mass of cocooned *G. porthetriae* prepupae was affected by diet quality. Upcoming biochemical analyses will clarify which host nutrients are actually consumed by wasp larvae, how parasitization influences the accumulation of metabolic reserves in host larvae, and whether reduced food quality is compensated by prolonged endoparasitic development and increased consumption rates or instead results in nutrient deficiencies in wasp prepupae.

The Role of Hybridization in Altering Pathogen Transmission Risk in UK Mosquito Populations

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Jolanta HUGHES, Mustapha TOURAY, Marcus BLAGROVE

Abstract

Mosquito-borne diseases are on the rise globally, driven by factors like habitat change, invasive species, and climate shifts. These environmental changes can boost the spread of pathogens. Hybridization may occur when closely located mosquito species interbreed, producing genetically mixed offspring. *Culex pipiens* complex comprises of morphologically and physiological highly similar species which exhibit a broad host range, feeding on both birds and humans. This behavior makes them potential "bridge vectors" for zoonotic pathogens. In this study, we generated hybrid laboratory strains by crossing male and female individuals of two mosquito forms, *Culex pipiens pipiens* and *Culex pipiens molestus*, both maintained as laboratory colonies. The F_1 hybrids were confirmed using species-specific PCR to ensure accurate identification. Approximately 50 adult females from the first generation were transferred to a new cage and experimentally infected with Usutu virus (USUV). The parental strains (*Culex pipiens pipiens* and *Culex pipiens molestus*) were also infected with the virus in the same way. The infected mosquitoes were incubated at 27 °C for 14 days. At the end of the incubation period, saliva was collected by inserting the mosquito's proboscis into a capillary tube filled with mineral oil for 1 hour. Both salivas and bodies were then transferred into 500 µl of TRIzol™ reagent and stored at -80 °C. Mosquitoes at 0 days post-infection (dpi) served as positive controls. Experiments were replicated three different times. Quantitative reverse transcriptase PCR (RT-qPCR) was then used to quantify viral RNA genome copies in both mosquito saliva and bodies. Our results indicate that hybrid mosquitoes are more susceptible compared to parental strains, they potentially have enhanced pathogen transmission. This study is the first to assess the susceptibility and transmission of the laboratory-produced hybrid *Culex* mosquitoes, and this data will allow future risk models and early warning systems to better predict USUV transmission.

Parasite-induced zombie behavior in carpenter ants: Unraveling the role of fungal protein tyrosine phosphatases

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Mark ARENTSHORST, Dorothy VAN LEEUWEN, Jisca L. VAN DAM, Arthur F. J. RAM, Vera I. D. ROS, Charissa DE BEKKER

Abstract

Manipulation of host behavior is a common strategy among parasites to increase their fitness. Carpenter ants exhibit so-called “zombie behavior” when infected by the entomopathogenic fungus *Ophiocordyceps*. Infected ants become hyperactive, separate themselves from their nestmates and ascend nearby vegetation, where they latch on and ultimately die in locations providing optimal conditions for fungal growth and spore dispersal.

Recent studies suggest that fungus-adaptive changes in ant host behavior are induced by secreted fungal proteins. Multi-omics and machine-learning approaches have identified several candidate effectors from *Ophiocordyceps*, including protein tyrosine phosphatases (PTPs). These enzymes have been implicated in behavioral manipulation of baculovirus-infected caterpillars, where they induce hyperactivity. However, their role in ant zombie behavior remains untested.

To investigate the hypothesized role of PTPs in inducing zombie ant behavior, we compared behavior of healthy ants and those infected with a wild type non-manipulating fungal strain to the behavior of ants exposed to purified PTPs or genetically modified fungi that constitutively produce these proteins. Observing differential behavioral phenotypes would confirm the role of PTPs in manipulating ant behavior and provide a foundation for identifying downstream host targets.

To further assess the effects of fungal PTPs on insect hosts, we have also tested whether they can rescue the phenotypes of previously described PTP knock-outs in baculoviruses. To this end, we genetically modified baculovirus strains to express *Ophiocordyceps* PTPs and performed infection and behavioral assays in caterpillars. If these recombinant viruses restore hyperactive phenotypes as observed for wild-type viral infections, it would suggest that PTPs are a convergent mechanism of host manipulation across different parasite-host systems.

Our ongoing efforts aim to provide further insight into molecular mechanisms of behavior manipulation in insects, advancing our understanding of interactions and coevolution between insects and fungi, as well as the regulation of insect behavior.

Ant Behavior Manipulation by an Entomopathogenic Fungus: The Role of Enterotoxins

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Charissa DE BEKKER

Abstract

Parasites engage in an evolutionary arms race with their hosts, which can result in complex strategies to enhance their transmission and fitness. Among these strategies are various forms of host behavior manipulation. Despite its prevalence, we still know little about how parasites hijack host behavior for their own benefit.

To fill this knowledge gap, our lab studies the interaction between the entomopathogenic fungus *Ophiocordyceps camponoti-floridani* and its carpenter ant host *Camponotus floridanus*. Once infected, the ants show several behavioral changes, such as a disrupted circadian rhythm and hyperactivity. In the final stage, they climb up vegetation and die in an elevated position that enhances fungal spore dispersal. Previous research proposes *Ophiocordyceps* to secrete effector proteins to induce these behavioral changes. These proteins may interfere with host behavioral and physiological pathways by interacting with host target proteins. However, which host pathways are affected by putative fungal effectors, and how these are connected to changes in host behavior, remains unknown.

Insights from comparative genomics and transcriptomics studies suggest that putative fungal enterotoxins might be connected to host manipulation. However, to date, this has not been functionally tested. To investigate if *Ophiocordyceps* secreted enterotoxins can affect ant physiology and behavior we have conducted several functional behavioral assays in which we compared ant behavior across four groups: 1) sham-injected/-infected ants, 2) enterotoxin-injected ants, 3) ants infected with the non-manipulating fungus *Beauveria bassiana* and 4) ants infected with enterotoxin knock-in strains of *B. bassiana*. Based on phenotypic outcomes, we will follow these assays by transcriptomic analyses to identify which host pathways are affected by these fungal enterotoxins and how they might give rise to altered behavior.

State-of-the-Art: Insect sexing in applied entomology

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Astrid T. GROOT

Abstract

Insect sexing is a critical process in applied entomology, as it is the basis for selective breeding and sex-specific applications, such as the sterile insect technique (SIT) in pest management and large-scale insect rearing. In mass-rearing and breeding programs, accurate sexing enables controlled male–female pairing to maintain genetic diversity, which enhances productivity, and select for desirable traits, such as improved feed conversion efficiency and disease resistance. In crop protection, it supports the study of genetically determined traits such as pesticide resistance, while in SIT, precise sexing ensures that only sterile individuals—typically males—are released. In sericulture, male larvae are preferred to improve silk quality.

Current insect sexing approaches can be broadly categorized into three groups: classical methods, molecular and genetic tools, and artificial intelligence (AI)-based techniques. Classical approaches, based on sexually dimorphic morphological traits or behavioral cues, remain widely used but are labor-intensive, error-prone, and difficult to scale. Molecular and genetic methods enable accurate early-stage identification, but are often destructive and cost-prohibitive for large-scale applications.

Recent advances in AI, particularly convolutional neural network (CNN)-based deep learning, offer non-invasive and high-throughput alternatives. These approaches leverage visual, acoustic, and behavioral data—individually or in combination—to enable rapid and automated insect sexing. As a result, AI-driven methods are emerging as scalable solutions with the potential to transform insect production, monitoring, and management systems.

In this presentation, we will highlight the current state of insect sexing technologies and underscores the growing role of AI in enabling sustainable and scalable applications in applied entomology.

What if They Feel? Re-evaluating insect subjectivity and the frontiers of welfare science

SOLIMARY GARCIA HERNANDEZ (UNIVERSITY OF SAO PAULO, Solimarygarcia@gmail.com)

Abstract

Historically, insects have been viewed as simple biological automata governed by rigid, programmed reflexes. However, emerging neuroscientific and behavioral evidence is prompting a fundamental shift in our understanding of invertebrate cognition, forcing us to ask: what if we are overlooking the subjective experiences of 99% of the world's animals? This review examines the current state of arthropod welfare science using multidimensional frameworks, such as integrated neurobiological and behavioral criteria for sentience, to evaluate the probability of affective states. I highlight recent findings of cognitive flexibility that challenge purely mechanical explanations. For instance, honeybees exhibit pessimistic cognitive biases after predatory threats, and bumblebees display positive, emotion-like states following unexpected rewards. These responses, alongside evidence of motivational trade-offs and centralized information processing in structures like the mushroom bodies, demonstrate that a mammalian-like neocortex is not a strict prerequisite for conscious experience. As the insect farming industry rapidly scales to process over a trillion individuals annually for food and feed, addressing their welfare has moved from a philosophical curiosity to an urgent applied science. Yet, critical methodological frontiers remain unexplored. Current research is heavily biased toward a few model species, such as bees and fruit flies, making it essential to investigate a wider range of taxonomic orders across diverse life stages. Furthermore, research must expand beyond a traditional pain-centric focus to explore positive affective states like reward, agency, and exploration. We must also validate operational welfare indicators and standardize humane slaughter protocols for large-scale production. Recognizing the potential sentience of insects demands a profound shift in entomological practice. Ultimately, this presentation serves as an invitation to look at these diverse organisms with new eyes, challenging our long-held preconceptions and merging rigorous scientific inquiry with our evolving ethical responsibilities toward the planet's most abundant animals.

