SYMPOSIUM 00 · Open Symposium
ORAL · Mon 17 Aug · 15:45 · Halle 4 · Session 7 · presented in Symposium 27 · Abstract ID 148377

Immune Priming in a Clonal Ant

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Although insects lack the adaptive immune system characteristic of vertebrates, they can nonetheless mount specific and lasting immune responses against pathogens, a phenomenon known as immune priming. Here, we investigate immune priming in the clonal raider ant Ooceraea biroi, a system allowing us to create colonies of genetically identical, age-matched individuals, and even multiple generations within a short time. We show that bacteria-primed O. biroi exhibit increased survival upon subsequent bacterial challenge, and that this protection is specific to the priming bacteria. To uncover the molecular mechanisms underlying this phenomenon, we analyze transcript isoform diversity and alternative splicing patterns of immune-related genes. We also show that immune protection can extend beyond the initially exposed individual: healthy nestmates of bacteria-primed ants also showed enhanced survival following bacterial challenge, suggesting that immune protection spreads through social interactions within the colony. Together, these results highlight both the individual and social dimensions of immune priming in O. biroi, offering insights into how collective immunity may arise in eusocial insects.

SYMPOSIUM 00 · Open Symposium
ORAL · Mon 17 Aug · 16:00 · K8 · Session 10 · presented in Symposium 04 · Abstract ID 149717

The evolution of inbreeding in haplodiploids

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While inbreeding is often thought to be unconditionally maladaptive, theory indicates that a preference for inbreeding should commonly be favoured by selection. This result can be understood through the lens of inclusive fitness: in systems where males can mate multiply, females can provide their male relatives with an additional mating opportunity, that would not exist if inbreeding was avoided. Both sexes pass on alleles to offspring, and with probability r, the male transmits allele copies also present in the female. Thus, while females may lose offspring to inbreeding depression, the loss can be overwhelmed by the inclusive fitness benefit she gains through increased related male fertilisations. However, while this problem has been well-studied in diplo-diploid organisms, no expectations exist for the evolution of inbreeding preference / avoidance in haplo-diploids, where intriguingly, inbreeding is particularly common, especially amongst the social insects. In this talk I will present a theoretical model showing that the inclusive fitness benefit bestowed by inbreeding is at best equivalent between haplo-diploids and diplo-diploids. Indeed, in many populations, the model shows that inbreeding preferences are harder to evolve in haplo-diploids. I will finish by discussing the discrepancy with this result and what we observe empirically, emphasising the effect of haploid males on inbreeding depression and the peculiar ecology displayed by social insects.

SYMPOSIUM 00 · Open Symposium
ORAL · Tue 18 Aug · 10:15 · K7 · Session 15 · presented in Symposium 23 · Abstract ID 149468

From North to South: How Does Temperature Affect Ant Communities in the Western Palearctic, and to What Extent?

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We have been investigating the ecological significance of thermophily in ant communities over 30 years ago. During this period, our research group have accumulated extensive empirical data, which we would like to summarize. Despite ongoing debate, ant communities in the Western Palearctic are widely considered to be primarily structured by dominance hierarchies, with species broadly categorized as dominant or subordinate. Dominant species are typically behaviorally aggressive and competitively exclude subordinate species from shared resources, whereas subordinate species tend to minimize direct encounters with dominants. Thermophilous species are consistently subordinate within these hierarchies, and thermophily may therefore act as a compensatory ecological strategy facilitating their coexistence with dominant competitors.

Using standardized bait observations conducted across diurnal thermal gradients, we quantified species abundance (thermophilous versus non-thermophilous) and evaluated the outcomes of interspecific competitive interactions under contrasting thermal conditions. This experimental framework was applied across a broad latitudinal and climatic gradient, extending from boreal sites in northern Europe (Jöskar Island, Tvärminne Archipelago, Finland) to arid desert environments in North Africa (Erg Chebbi, Merzouga, Morocco) and Middle East (Negev Desert, Israel), as well as Mediterranean ecosystems in Spain, Israel, and Morocco.

We hypothesized that thermophily would confer a selective advantage under thermally extreme conditions, particularly in desert ecosystems, whereas its ecological benefits would be reduced or potentially absent in temperate and boreal habitats

SYMPOSIUM 00 · Open Symposium
ORAL · Tue 18 Aug · 12:00 · K8 · Session 16 · presented in Symposium 04 · Abstract ID 146000

The African termite raiding ant Megaponera analis: Behaviour and functional ecology

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Ants and termites play important roles in tropical ecosystems, leading to an evolutionary arms race that led to the development of diverse foraging, predation, and counter-predation strategies. This resulted in the emergence of specialized termite predators, such as the African termite raiding ant Megaponera analis, which organizes coordinated raids on termites of agricultural importance belonging to the subfamily Macrotermitinae. Decades of field and laboratory studies have examined the natural history of M. analis describing its distribution, raiding behavior, chemical ecology, task allocation, rescue, helping behavior, and nursing of wounds. However, its potential for the management of termites is yet to be explored. This review, synthesizes the literature on M. analis, outlining recent progress, identifying knowledge gaps, proposes directions for future research, and possible applications of the knowledge in different fields.

SYMPOSIUM 00 · Open Symposium
ORAL · Tue 18 Aug · 12:00 · K9 · Session 17 · presented in Symposium 20 · Abstract ID 146363

Phylogenomics and quantitative morphometrics of Vanuatuan Strumigenys trap-jaw ants reveal numerous new species and signals of an endemic adaptive radiation

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The South Pacific region harbors thousands of tropical islands and endemic species, making it one of the most geologically complex and biologically unique regions on the planet. In ecology, ants serve as important biodiversity indicators because they are highly abundant, diverse, and ecologically dominant insects in terrestrial habitats. Recent advances in biodiversity research in the South Pacific region have revealed the Vanuatuan archipelago as a novel ant biodiversity hotspot, with numerous newly discovered endemic species which includes the miniature trap-jaw ant genus Strumigenys Smith, 1860. Here, we employ an integrative taxonomic framework that combines phylogenomics using ultraconserved elements (UCEs), biogeography, and quantitative morphometrics to delimit species, infer the evolutionary history, and explore the morphological diversity of Strumigenys ants in Vanuatu. Our results reveal the presence of at least fourteen Strumigenys species, several of which are newly discovered and endemic to the archipelago, making Strumigenys the most species-rich ant genus in Vanuatu. Moreover, the UCE phylogeny revealed a clade of high elevation endemics that exhibit substantial morphological variation and whose evolutionary history indicates the first potential case of an endemic adaptive radiation in Vanuatuan ants.

SYMPOSIUM 00 · Open Symposium
ORAL · Tue 18 Aug · 16:45 · K10 · Session 30 · Abstract ID 146417

Persistent behavioral variation among termite soldiers confronted with an intruder

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Termites, like other social insects, exhibit a division of labor characterized by morphologically distinct castes. While variation in behavior between termite castes is expected, behavioral variation within castes is less understood. Most termite species possess a soldier caste, which is morphologically specialized for colony defense. Previous studies examining pairs of termite soldiers suggest that soldiers within the same colony vary in aggression level, although it is unknown if this variation is persistent and if it remains in a larger context. In this study, we exposed groups of workers and soldiers of the dampwood termite Zootermopsis nevadensis to a hypothetical intruder, the carpenter ant Camponotus obscuripes. Termites were placed in a circular arena with an exit hole simulating a nest with a defensible position, and an ant was placed outside the exit. Then, the behavioral response of the termite group was recorded and later analyzed using tracking software. This trial was repeated daily for two weeks using the same groups of soldiers each time. Soldiers varied in their response to the intruder, with some taking a more active or less active role in defense relative to their groupmates. This variation in aggression was persistent across trial days and was also correlated with variation in behavior when an ant was not present, though the specific factors that contribute to this variation are unclear. Overall, these results contribute to a wider understanding of within-caste variation in termites, as well as how this variation may influence vital tasks such as colony defense.

SYMPOSIUM 00 · Open Symposium
ORAL · Tue 18 Aug · 17:00 · K10 · Session 30 · Abstract ID 146457

Species-specific behavioral consistency suggests a phylogenetic component to personality in ants

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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.

SYMPOSIUM 00 · Open Symposium
ORAL · Tue 18 Aug · 17:15 · K10 · Session 30 · Abstract ID 147185

Blade-running: An efficient yet simple behavior to potentially combat summit disease in ants

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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.

The follow-up experiment was supported by a grant of the Romanian Ministry of Research, Innovation and Digitization (CNCS/CCCDI–UEFISCDI; project no. 25/2024 COFUND-BIODIVMON-MonitAnt, PNCDI IV) to B.M. and Á.Sz.

SYMPOSIUM 00 · Open Symposium
ORAL · Tue 18 Aug · 17:15 · Halle 4 · Session 25 · presented in Symposium 27 · Abstract ID 149473

Symbiont fidelity in two fungus-growing ant genera and their fungal cultivars

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Fungus-farming "attine" ants are a model system for exploring symbiotic evolution. While all attine ants are obligate symbionts, lower-attine fungal cultivars are facultative symbionts and higher-attine fungal cultivars (including leaf-cutter cultivars) are obligate symbionts. Genome-level studies have revealed that the ancestor of higher-attine fungi underwent major genetic remodeling, presumably as the result of an episode of strict (i.e., species-to-species) coevolution. Strict coevolution is incompatible with the current paradigm of diffuse coevolution in both lower- and higher-attine agriculture, but a recent study demonstrated high levels of symbiont fidelity in the Cyphomyrmex wheeleri group, in which ants have been associated with particular fungal cultivars for millions of years and rare switches to new cultivars were consistently associated with ant speciation events. The conclusions of this study were weakened, however, from the inability of the genetic markers employed to adequately distinguish species boundaries. With the advent of phylogenomic methods, we can now properly delimit species boundaries for both symbionts. Preliminary results based on recently developed UCE markers for both ants and ant-associated fungi strongly corroborate the previous finding of ancient associations of ant species with particular fungal species in the C. wheeleri as well as in other lower-attine groups, including groups belonging to the higher-attine ants, providing support for the hypothesis that strong symbiont fidelity may have provided the opportunity for the strict species-to-species coevolution that presumably produced higher ant agriculture.

SYMPOSIUM 00 · Open Symposium
ORAL · Tue 18 Aug · 17:30 · K10 · Session 30 · Abstract ID 148689

Temporal and Spatial Variation in Granivory by Pogonomyrmex rugosus

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Harvester ants (Pogonomyrmex spp.) are dominant granivores in arid ecosystems, where their foraging behavior influences seed fate, plant recruitment, and community structure. Although often viewed as impediments to rangeland restoration due to seed removal, harvester ants are keystone species whose behavioral responses to resource distribution and seasonality remain insufficiently integrated into restoration ecology. We examined seed selection and temporal foraging dynamics of Pogonomyrmex rugosus across two contrasting New Mexico ecosystems: Chihuahuan Desert shrubland (Las Cruces) and grassland–juniper woodland (Corona). Ant community composition was also documented at each site. Seed removal experiments were conducted using biased (near-colony) and unbiased (landscape-scale grid) designs to assess how spatial proximity to nests influences foraging decisions. Seed cafeterias containing four native plant species: Bouteloua eriopoda, Oryzopsis hymenoides, Ratibida columnifera, and Sporobolus airoides, were deployed for 24 hours and repeated monthly from July to October 2024. Pogonomyrmex rugosus did not preferentially choose any seed species. Seed removal was consistently higher near colonies than across the landscape and peaked in late summer, indicating spatial and seasonal modulation of foraging activity. These findings emphasize the role of harvester ant foraging behavior in seed availability and underscore the importance of incorporating ant behavioral ecology into restoration strategies rather than treating ants solely as restoration constraints.

SYMPOSIUM 00 · Open Symposium
ORAL · Tue 18 Aug · 17:45 · K10 · Session 30 · Abstract ID 146247

From soil to canopy: ecology and evolution of nesting in ants

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Ant colonies are superorganisms in which the nest plays a central role by providing protection from external conditions, structuring the spatial organization of the colony, and concentrating most social interactions. Ants exhibit a remarkable diversity of nesting types, ranging from subterranean tunnels to very complex arboreal carton and silk constructions. Despite its ubiquity across ant species and its important role in colony functioning, nesting type has rarely been examined from an interspecific perspective. Here, we present a global macroecological and macroevolutionary analysis of nest types across more than 4,400 ant species.

By integrating phylogenetic, biogeographic, and environmental data, we investigate how major nest types are distributed globally and how they have changed through the evolutionary history of ants. Specifically, we examine how nesting types are shaped by environmental conditions. Transitions toward arboreal nesting are associated with increased forest cover, suggesting that forested environments promote shifts away from ground nesting. Conversely, high environmental seasonality is associated with a lower occurrence of arboreal nesting, indicating that strong seasonal fluctuations may constrain shifts toward arboreality. Across ant lineages, we observe that similar nesting strategies recur in comparable ecological conditions, indicating convergent shifts in nesting type.

Overall, our work highlights nesting type as a functional component of the superorganism with an important role in linking colony organization to the external environment and in shaping the diversification of social insect societies.

SYMPOSIUM 00 · Open Symposium
ORAL · Tue 18 Aug · 18:00 · K10 · Session 30 · Abstract ID 149966

Do driver ants function as keystone predators in African rainforests?

Max Tercel; Luke Powell
CIBIO-InBIO

Driver ants (Dorylus (Anomma)) are extraordinary social insects that form some of the largest animal colonies on Earth, conducting spectacular daily raids across vast areas of African rainforests. Although frequently proposed as keystone species, their ecological effects remain poorly quantified. We present an ongoing, multifaceted field study from lowland tropical rainforest in Equatorial Guinea examining trophic interactions, prey transport biomechanics, ecological impacts of raids, and movement ecology of Dorylus wilverthi and D. sjostedti. Our project is beginning to reveal the ecology of driver ants, with multiple lines of evidence suggesting they may be highly influential keystone predators in African rainforests. This presentation outlines the first results arising from the project. Driver ants are highly generalist predators, collectively exploiting prey from more than 25 animal orders. Demographic structure differs between D. wilverthi and D. sjostedti, with the former exhibiting an additional super-major size class absent in D. sjostedti, allowing D. wilverthi to carry prey items approximately 15% heavier on average. Ongoing analyses quantify how raids impose strong but transient predation pressure on local arthropod assemblages, reducing diversity immediately after raids while increasing beta diversity across broader spatial scales. Preliminary behavioural observations paired with litter sampling suggest that driver ants capture prey over areas of approximately 3000 m^2 per raid. Our analyses also allow extrapolation of prey biomass removed during raids. Finally, we present taxon-specific susceptibility to predation and discuss how these effects scale up to community-level patterns, clarifying the keystone role of driver ants in Afrotropical forests.

SYMPOSIUM 00 · Open Symposium
ORAL · Tue 18 Aug · 18:15 · K10 · Session 30 · Abstract ID 149597

Population structure of an ecosystem engineer, the mound building termite Macrotermes bellicosus

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The fungus-cultivating termite, Macrotermes bellicosus, is a major ecosystem engineer within West Africa’s Comoé National Park (CNP), one of the region's largest and most diverse savannahs.

Typically, M. bellicosus mounds are a frequent sight with a patchy distribution across the landscape, with individual patches and colonies often lasting for several decades.

Recent years have shown a steady decline in live M. bellicosus colonies across the CNP, with many of the previously long-lasting patches dying out completely.

We investigate the local population structure of M. bellicosus, combining spatial, temporal and genetic methods to unravel patterns and driving forces behind the recent decline in live colonies.

To this end we utilize next generation sequencing to infer population genetic parameters, via the SNP analyses of long-term monitored colonies, and integrate these insights with other ecological colony variables, to establish a comprehensive baseline for future long-term investigations of regional M. bellicosus population dynamics.

Results reveal a striking genetic complexity, with high levels of inbreeding and low genetic diversity within local patches on one hand, and colonies with polyamorous parentage on the other.

This suggests low rates of gene flow and genetic isolation between local M. bellicosus patches, even at a short distance.

Given the rapid decline of entire patches which previously existed for decades, this isolation indicates that once a local patch died off, it is unlikely to be recolonized by colonies from neighbouring patches, suggesting a significant threat to the persistence of the regional population.

SYMPOSIUM 00 · Open Symposium
ORAL · Wed 19 Aug · 11:15 · K9 · Session 35 · Abstract ID 149186

Geographic variation of wing shape allometry in honey bees (Apis mellifera)

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The shape of body parts can depend on their size. This relationship is often called allometry. Some suggest that allometries are evolutionary constraints that remain stable over time and space. However, there is also evidence that, in some species, allometries can differ between populations and change under selective pressure.

This study investigated fore wing allometry in honey bee (Apis mellifera) workers. A publicly available dataset of 1,832 wings representing four main evolutionary lineages from Africa, Europe, and the Middle East was used. The wing shape was described using the coordinates of 19 landmarks, which were analyzed using the methodology of geometric morphometrics. The allometric relationship was analyzed using a Procrustes multivariate linear model, in which shape (landmark coordinates) was modelled as a function of wing size (log-transformed centroid size), lineage (categorical factor), and their interaction.

The Procrustes ANOVA revealed a strong effect of wing size on shape, indicating pronounced allometry. Lineage explained an even larger proportion of shape variation, demonstrating substantial shape differentiation among lineages independent of size. Importantly, the interaction between wing size and lineage was also significant, which shows that lineages differ in their allometric trajectories, indicating that evolution has acted not only on shape itself but also on the underlying scaling relationships.

SYMPOSIUM 00 · Open Symposium
ORAL · Wed 19 Aug · 11:15 · K8 · Session 34 · presented in Symposium 19 · Abstract ID 152891

Neural coding of pathology-related odorants in the honeybee brain

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For honeybees, hygienic behaviour is key to reducing the spread of diseases, thus helping the colony to cope with the pathology or the infestation. Hygienic behaviour includes the detection, uncapping and removal of diseased brood and is primarily mediated by olfactory cues. Odorants could either be produced by the brood or by the pathogenic agent and can be detected by hygienic bees inside the hive. Hygienic behaviour is elusive, with only a small percentage of the middle-aged nurse bees displaying it, before they transition to foragers.

In my poster, I will present preliminary results and future directions of my PhD project, outlining the main objectives, methodological approaches, and expected contributions of the work. My central question is: how are pathology-related odorants processed in the honeybee brain?

We focus on the antennal lobe, the primary olfactory centre in the brain. Worker bees from a strain that has been selected for strong hygienic behaviour are age-marked and selected according to task displayed (e.g., foragers returning to the hive with full pollen baskets, nurses patrolling brood cells, workers uncapping sealed brood cells, workers removing affected brood). Then we perform calcium imaging of the antennal lobe, while test and control odorants at different concentrations are delivered to the antennae through an automated and computer-controlled olfactometer.

The study of the neural mechanisms of hygienic behaviour provides a fundamental understanding of how neural circuits encode and integrate sensory information to drive complex, socially relevant behaviours.

SYMPOSIUM 00 · Open Symposium
ORAL · Wed 19 Aug · 11:30 · K9 · Session 35 · Abstract ID 145678

RNAi-based Varroa destructor biopesticides inside the honey bee colony

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The parasitic mite Varroa destructor infests honey bee (Apis mellifera) colonies worldwide and causes rapid increases in colony mortality. Biopesticides using RNA interference (RNAi) technology are a novel tool to control V. destructor and improve honey bee health. We investigated the effects of vadescana dsRNA, a RNAi-based treatment which has been registered for varroa control in the United States, on individual worker bees and the pharmacokinetic pathway of the dsRNA across the bee colony and into its target organism V. destructor. Vadescana is applied in a sucrose solution distributed by worker bees into honey bee brood where the mites will get into contact with the treatment. Distribution pattern and concentrations inside honey bee brood and corresponding brood cells were quantified using qPCR. Absorption into the mite via oral ingestion and cuticular exposure was experimentally tested utilizing fluorescently labelled dsRNA sequences. The presence of the treatment inside the mite was confirmed by confocal microscopy. To detect off-target effects on worker bees present in the colony during treatment, we monitored individual workers with RFID technology. Honey bee lifespan was found to be significantly longer compared to untreated bees and an increase in foraging trips was observed. These findings not only contribute towards more efficient varroa control in the future but also further our understanding of the pharmacokinetics of dsRNA inside the honey bee colony.

SYMPOSIUM 00 · Open Symposium
ORAL · Wed 19 Aug · 11:45 · K9 · Session 35 · Abstract ID 146908

Towards a Taxonomic Resolution in Stenammini Ants: Whole-Genome Sequencing Reveals Social Hybridogenesis Candidates and Phylogenetic Incongruences

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Becoming queen in social insects is generally environmentally acquired rather than genetically determined. However, this is not the case in an exceptional reproductive system, known as social hybridogenesis. Here, two distinct lineages of ants can only produce queens on their own while they need to hybridize to produce workers. Convergent evolution toward such an unusual reproductive strategy appears common in harvester ant species, in particular in three species of Messor, an ant genus belonging to the taxonomically chaotic tribe of Stenammini. To better understand the evolution of this reproductive system and its taxonomic impact on established species, we sequenced the whole genome of 115 species of Stenammini (including 100 Messor). By reconstructing robust phylogenies of the Messor genus and its tribe, we reveal incongruence between morphological identifications, nuclear and mitochondrial signal, which suggests that a comprehensive revision of the genus is necessary. We also reveal several Messor species that appear hybrids, suggesting that many unusual reproductive systems are yet to be discovered in harvester ants.

SYMPOSIUM 00 · Open Symposium
ORAL · Wed 19 Aug · 12:00 · K8 · Session 34 · presented in Symposium 19 · Abstract ID 144604

Phylogenomics reveal the evolution of social parasitism in vespid wasps (Hymenoptera: Vespidae)

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Social parasitism, where individuals or species exploit the social organization of a host, represents one of the most paradoxical outcomes of social evolution. It blurs the boundary between cooperation and conflict, and reveals how fragile and dynamic social evolution can be. In wasps (Vespidae), social parasites infiltrate and manipulate colonies of their (often) close relatives, but despite their highly derived social parasitic lifestyles, the evolutionary origins and frequency of these life history transitions from free-living, social to socially parasitic behavior remain unresolved.

To address this open question, we reconstructed a comprehensive phylogeny of the wasp family Vespidae using ultraconserved elements (UCEs) as molecular makers. We placed our taxonomic emphasis on the subfamilies Polistinae and Vespinae, where social parasitism occurs. Our dataset included representatives of five vespid subfamilies and we were able to include the majority of the known socially parasitic wasp species, along with their hosts, yielding a robust phylogenetic framework that allows for testing competing hypotheses.

Our findings reveal the origins and evolutionary pathways of social parasitism in wasps, suggesting a more complex evolutionary history than previously supposed. Our analyses also reveal how a combination of phylogenetic constraints and behavioral adaptations shaped the repeated transitions to social parasitism and therefore provides novel information for understanding the traits associated with a switch from cooperation to conflict.

SYMPOSIUM 00 · Open Symposium
ORAL · Wed 19 Aug · 15:00 · K9 · Session 41 · presented in Symposium 15 · Abstract ID 146459

Gut-microbiome, genomic, and transcriptomic factors promote aggression in an ant

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Animals frequently display aggressive behaviour, for example, when fighting for food or mates. If aggression results in access to higher-quality food, it can lead to increased fitness and thus be adaptive. Aggression intensity can be influenced by various extrinsic and intrinsic factors. However, we currently lack understanding what factors cause an animal to start aggression. Here, we analysed an ant species to test if chemical, microbiome, genomic, transcriptomic, or environmental traits are linked with the start of aggression and the reactions to it, that is, reacting aggressively or peacefully. We found eight gut bacterial operational taxonomic units, mutations in two genes, and eight differentially-expressed genes, which were positively or negatively associated with the start of aggression or reactions to it. These traits are partly associated with hormone signalling as well as neurological and synaptic functions. Our results suggest that the traits are possibly interconnected and may act in concert to influence the start of aggression and the reactions to it. We speculate that these traits likely play an important role for the evolution and maintenance of aggression in this ant and beyond and possibly represent an evolutionary-conserved pathway to aggression.

SYMPOSIUM 00 · Open Symposium
ORAL · Wed 19 Aug · 15:15 · K7 · Session 39 · presented in Symposium 10 · Abstract ID 146456

Macroevolutionary consequences of nutritional symbioses in Formicinae ants

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Symbiotic associations among different kinds of organisms can profoundly influence the nature and tempo of their evolution. There is increasing evidence that microbial endosymbionts have played important roles in the diversification of some insects, including ants. The subfamily Formicinae contains presently around 3,300 described species, of which approximately 1,900 alone are contained in the tribe Camponotini. Within the Formicinae, all Camponotini (11 genera), along with the two more distantly related genera Formica and Plagiolepis, have specialized bacteriocytes that house bacterial symbionts involved in nutrition, raising the question of whether these symbionts are associated with enhanced diversification and evolutionary success of their ant hosts. We used a macroevolutionary approach to investigate this hypothesis by generating an updated phylogenomic dataset for formicine ants, sampling as far as possible across the root node of each genus and including ca. 400 species. Maximum likelihood analyses produce a robustly supported phylogeny that resolves remaining uncertainties about intergeneric relationships and serves as the basis for divergence time estimation on a reduced taxon set. We estimate diversification dynamics across this dated phylogeny and test whether shifts in diversification rate are correlated with the evolution of nutritional symbioses involving bacteriocytes in the Formicinae. Our results provide important insights into the diversification of some of the most species-rich clades of ants and their bacterial partners.

SYMPOSIUM 00 · Open Symposium
ORAL · Wed 19 Aug · 16:15 · K7 · Session 39 · presented in Symposium 10 · Abstract ID 149478

Discovery of spontaneous raiding in an army ant relative sheds light on the evolution of mass raiding behavior

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Sophisticated collective behavior of group-living animals is often difficult to intuitively understand what evolutionary processes gave rise to such behavior. The spontaneous mass raids performed by doryline army ants are an iconic example of a complex collective behavior. Recent studies on a phylogenetically related model species, Ooceraea biroi, have found that artificially increasing colony size can stimulate a transition from scout-initiated raids to army ant-like spontaneous raids. Therefore, it has been hypothesized that the group size expansion drives the evolution of sophisticated collective behavior. Here we report natural history observations on a raid of Cerapachys sulcinodis. The authors already reported that this species has life-history traits resembling the army ant syndrome, characterized by larger colony size (up to 1,850 workers/colony) than that of other non-army ant dorylines. The raid of Cerapachys was initiated spontaneously without a single scouting ant, as in army ants, but the number of workers that joined the raid was small, as up to a few hundred, and the furthest range of foraging was 9.2m from their nest. They preyed on the brood of the other ants, like the other doryline ants, and many other general soil arthropods. This finding filled a knowledge gap in the biology of rare non-army doryline ants, an important key to understanding the evolutionary trajectory toward army ants. In addition, supports the hypothesis that swarm behavior emerges from an interaction of intrinsic tendencies and increased colony sizes, providing insight into the evolution of army ants' complex group behavior.

SYMPOSIUM 00 · Open Symposium
ORAL · Wed 19 Aug · 17:15 · K8 · Session 46 · presented in Symposium 05 · Abstract ID 149882

Effect of a selfish genetic element on mate preference in a socially polymorphic ant

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Gene-centered natural selection generates both cooperation and conflicts across levels of biological organization. Hence, investigating how evolutionary conflicts shape social behaviour is key to better understand the evolution of sociality. In the alpine silver ant Formica selysi, a supergene with two haplotypes, M and P, determines whether colonies are monogyne (one queen) or polygyne (multiple queens). The P haplotype promotes polygyny but also behaves as a selfish genetic element: it favours its own transmission through a lethal maternal effect that prevents P-carrying mothers from producing non-P-carrying offspring. Moreover, P has deleterious effects on several fitness-related traits. Because of these genetic costs, mating preferences should depend on supergene genotype of each partner, with cases where the interests of females and males align or diverge, leading to cooperation or conflict over mate choice. To investigate this, we filmed mating interactions between pairs of queens and males originating from two populations and representing all possible supergene combinations. We assessed the willingness of each partner to mate. Mating patterns depended strongly on the queens' origin: queens from the low-altitude population exhibited assortative mating with respect to social form, while queens from the high-altitude population mated randomly, although monogyne queens mated more than polygyne queens. This suggests that choosiness and/or partner power varies between populations. Our findings will help understanding how genetic conflicts driven by selfish transmission and genetic load shape mating behaviour in a socially polymorphic species.

SYMPOSIUM 00 · Open Symposium
ORAL · Wed 19 Aug · 17:30 · K6 · Session 44 · presented in Symposium 02 · Abstract ID 149980

Inactive leaf-cutter ants mediate task allocation through workload-dependent activation

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Social insect colonies are self-organized groups of related individuals that work together to maintain key biological functions. Balancing their metabolic energy expenditure to grow and reproduce involves appropriate task allocation among workers in naturally variable environments. Workers can switch among tasks when demand changes; however, this flexibility is limited and task-specific and task switching can represent a large cost to colony productivity. Do colonies generally meet productivity demands by significant work reallocations among tasks with different priorities, or instead by engaging those individuals who are inactive? Most studies addressing this question focus on narrow sets of tasks, such as nest maintenance and foraging, and experimentally remove workers to elicit task switching. Here we present an experimental study of work allocation among a comprehensive set of tasks in the desert leaf-cutter ant Acromyrmex versicolor. The size of their fungus garden, the source of food for the colony, was increased or decreased and individual workers were marked and followed prior to and after these manipulations. We found that colony activity was increased by the activation of inactive workers when fungus garden size doubled, and active workers inactivated when the fungus garden size was halved. While there were widespread task shifts among active workers, the recruitment of inactive workers to tasks in demand was significant and responded more to the colony workload changes. Leaf-cutter ant colony work performance changes hinges on a combination of strategies, but relies heavily on the worker reserve pool.

SYMPOSIUM 00 · Open Symposium
ORAL · Thu 20 Aug · 15:30 · K7 · Session 57 · Abstract ID 146489

Using ants in Vanuatu for case-based teaching of integrative taxonomy

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There is a dwindling number of taxonomists across the globe, which is part of the “taxonomic impediment” to biodiversity conservation. Therefore, we need to train more students in taxonomy as well as to make the taxonomic process more robust to reduce the misidentification of species that lead to flawed conclusions about biogeographic and evolutionary processes. This is where “integrative taxonomy” is useful because it combines traditional comparative morphology approaches with molecular approaches such as COI barcoding and phylogenomics as well as ecology and biogeography to resolve species boundaries more accurately. However, these tools and methods do not directly transfer taxonomic expertise and knowledge to the next generation of taxonomists and biodiversity scientists, thus leaving the “taxonomic impediment” to biodiversity conservation partially unattended. Here, we present a teaching framework of integrative taxonomy utilizing collaborative and case-based learning to provide integrative taxonomic training to university students. Specifically, we provide case studies based on our own ongoing research of ant biodiversity in Vanuatu and the broader South Pacific region. So far, this integrative taxonomic training course has resulted in the delimitation and descriptions of new ant species in the genera Myrmecina, Pheidole, and Vollenhovia from Vanuatu as well as provided foundations for future, broader revisions of these groups. Based on student surveys, this teaching approach of integrative taxonomy gives them a deeper understanding and appreciation for the mechanisms generating biodiversity, provides a sense of community, and enhances their scientific self-efficacy by increasing their confidence in taking on their own taxonomic projects.

SYMPOSIUM 00 · Open Symposium
ORAL · Thu 20 Aug · 15:45 · K7 · Session 57 · Abstract ID 148806

Acrobat ants across the Mediterranean: Population structure of the Crematogaster scutellaris complex

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Ants of the Crematogaster scutellaris complex are ecologically dominant and behaviorally diverse members of Mediterranean ecosystems, where they play key roles in structuring arthropod communities and influencing ecosystem dynamics. Although global phylogeographic studies have provided initial insights into the diversification of Crematogaster, species boundaries within the C. scutellaris complex remain poorly resolved. Limited morphological differentiation, particularly in the eastern Mediterranean, characterized by exceptional ant diversity, has hindered taxonomic resolution and remains understudied. Here, we conducted a population-level genomic study across the Mediterranean distribution of the C. scutellaris complex to assess genomic differentiation and uncover previously unrecognized diversity. We generated low-coverage whole-genome sequencing (lcWGS) data and used genome-wide single nucleotide polymorphisms (SNPs) to infer phylogenetic relationships and assess population structure. Genome-wide analyses revealed deep divergences across the complex, including a pronounced east–west genetic split, a pattern commonly observed in Mediterranean taxa. Beyond this broad-scale structure, we identified distinct and divergent lineages restricted to large Mediterranean islands such as Crete, suggesting long-term isolation and potential endemic diversification. In contrast, populations from less remote islands, including the central Aegean archipelago, exhibited complex patterns of genetic structure indicative of historical connectivity, recurrent gene flow, and secondary contact. Our results highlight the Mediterranean basin as a mosaic of evolutionary processes shaping diversification within this ecologically important group. This study demonstrates how population-level genomic approaches can effectively disentangle cryptic species complexes, refine species boundaries, and provide insights into the evolutionary mechanisms driving speciation in Mediterranean ants.

SYMPOSIUM 00 · Open Symposium
ORAL · Thu 20 Aug · 16:00 · K7 · Session 57 · Abstract ID 146798

Functional and phylogenetic responses of ant assemblages to experimental fire regimes in a tropical savanna

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Fire is a globally important disturbance and a powerful tool for conservation management in fire-prone habitats such as savannas. How fire affects the taxonomic diversity of ants is well documented across savannas of the world. However, much less is known about the effects of fire on the phylogenetic and functional diversity of ants. This is problematic, because different facets of diversity have unique responses to disturbance. Here, we assess changes in the phylogenetic and functional (i.e., variations in size, shape and color) diversity of ant assemblages in response to three fire-related predictors: fire frequency, fire activity and vegetation cover. We simultaneously assess assemblages of four vertical strata – hypogaeic, epigaeic, leaf litter and arboreal. As previously shown with taxonomic diversity, we find that co-occurring ant assemblages of different strata form distinct phylogenetic and functional entities. Furthermore, we find that functional and phylogenetic diversity show marked differences in response to fire, and these in turn differ among strata. The most pronounced changes occurred in above-ground assemblages, whereas the weakest changes occurred in below-ground assemblages. Our results provide novel insights into trait-based adaptations to fire disturbance and has important implications for fire management for biodiversity conservation.

SYMPOSIUM 00 · Open Symposium
ORAL · Thu 20 Aug · 16:15 · K9 · Session 59 · presented in Symposium 13 · Abstract ID 146013

To save my sister or not: Understanding the evolution of rescue and wound-care behaviors in a termite hunting ant

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In many termite species, a pugnacious soldier caste mediates colony defense at their foraging sites by inflicting lethal injuries to their predators. To reduce these injury-induced mortality risks, termite hunting ants rescue their injured nestmates from the hunting site by carrying them back to the nest. Thus saving them from opportunistic predators that prey upon the injured. The second mortality risk comes in the form of infections when their open wounds are exposed to soil pathogens, fostering the need for wound care by their nestmates inside the nest. These two adaptations together reduce combat mortality significantly. Rescue and wound care behaviours have so far only been studied in West African populations (Côte d'Ivoire) of Megaponera analis. Here we extend our study to Mozambique and South Africa, to examine if these behavioural adaptations vary across M. analis populations and to identify possible evolutionary drivers underlying their emergence. We show that the Mozambican population does not perform rescue behaviour due to a naturally low injury rate of 1%, compared to 19% in the Ivorian and 7% in the South African populations. These injury rates strongly correlated with the pugnaciousness of the hunted prey in the three populations. Despite these differences, all three M. analis populations performed wound care. Our study highlights that rescue behaviour seems to be a plastic trait potentially dependent on injury rates and the pugnaciousness of the prey, while wound care behaviour is highly conserved across different populations of the same species.

SYMPOSIUM 00 · Open Symposium
ORAL · Thu 20 Aug · 16:15 · K7 · Session 57 · Abstract ID 146493

Fire-driven changes in trophic resource use and diel activity of ant communities

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Wildfires are an increasingly frequent component of global change and constitute a major disturbance to terrestrial ecosystems, affecting community structure and ecosystem functioning. These effects are often mediated not only by changes in species composition, but also by shifts in functional organization and temporal patterns of activity. Ants are widely recognized as ecosystem engineers and play a key role in ecosystem processes through their consumption of resources, (predation, granivory, nectarivory, and scavenging/detritivory). Because patterns of resource use reflect the functional structure of communities, assessing how fire alters ant trophic responses is essential to understand how ant assemblages respond to wildfire disturbance and how their ecological roles may be reorganized under ongoing global change. Here, we present preliminary results from a field experiment conducted in Mediterranean pine forests four years after wildfire. We assessed how fire influences ant trophic preferences and patterns of resource use in burned and unburned areas, and whether these responses vary across the daily activity cycle. Using a baiting experiment across three wildfire sites, we exposed ant communities to seven resource types representing distinct trophic functions at different times of day. Our preliminary results indicate that bait occupancy in burned areas is reduced during midday and shifts toward the afternoon, and that ant assemblages in burned sites exhibit a stronger relative preference for sugar-based resources compared to unburned areas. Together, these findings suggest that wildfire amplifies diel differences in ant activity and trophic ecology, with potential implications for the functional organization of ant communities in fire-prone landscapes.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 144313

Occurrence and diversity of Edible Termites (Isoptera: Termitidae) Archived in the Natural History Collections of the National Museums of Kenya

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National Museums of Kenya

Edible termites constitute a vital source of animal protein, micronutrients, traditional medicine, and household income across many African communities. Despite the ecological and socio-economic importance of termites, their diversity and distribution remain inadequately documented in scientific repositories. This study intends to document and analyze archived specimens of edible termites housed in the Invertebrate Zoology department of the National Museums of Kenya (NMK) to assess their occurrence, diversity, and collection patterns and trends across Kenya. Data were extracted from the NMK termite collection database, covering specimens collected between 1950 and the present. Information included species identity, collection locality, and year. A total of 329 specimens were recorded, representing four genera and ten species. The most represented taxa were Macrotermes jeanneli, Macrotermes herus, Macrotermes subhyalinus, and Odontotermes kibarensis. These findings enhance understanding of Kenya's edible termite diversity and highlight the potential to promote them for food security and sustainable livelihoods. At the same time, it provides baseline data for present and future ecological, nutritional, and sustainable harvesting studies of edible termites in Kenya. Moreover, the study underscores the critical role of museum collections as repositories of indigenous biological knowledge, supporting future research as these collections are living data that provide tangible evidence of the past and present. Therefore, strengthening the documentation and accessibility of such collections can advance biodiversity conservation, support insect food initiative research, and foster the integration of indigenous and scientific knowledge for sustainable resource management.

Keywords: Edible termites, Macrotermes, Odontotermes, Museum collections, Food security.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 144997

The enigmatic Hawaiian harvester ant (ok, not really), Pogonomyrmex owyheei

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They “Owyhee” region of southern Idaho is named for Hawaiian explorers/traders and is home to a harvester ant with a complex taxonomic history. At one point it was a subspecies of Pogonomyrmex occidentalis, then was raised to species status, as P. owyheei, and then later demoted to a subspecies of P. salinus, where it currently sits. For simplicity, I will refer to it as P. owyheei in this abstract. It is difficult to discern the range of the P. owyheei owing to its three name changes in one century; truthfully, though, it is quite difficult to discern anything about this ‘species’ other than the general region where it occurs (the Owyhee River and Owyhee Mountains). In order to provide some order to the situation, we sampled Pogonomyrmex harvester ants from the intermountain west, including from Arizona, Idaho, Nevada, Utah, and Wyoming, sequenced a portion of the COI gene and characterized the angle of their basal tooth (the current character used to distinguish P. occidentalis and P. salinus). Interestingly, populations historically called P. owyheei are sister to the P. occidentalis/P. salinus clade, and do group with P. salinus based on mandible morphology. Furthermore, and as suspected, some of the historic populations of P. owyheei showed characteristics of hybridization with P. salinus. Hybridization was investigated using microsatellite markers. Currently we are working to ascertain whether the hybridization has any effect on caste determination in this system.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 145644

Morphometric Diversity of Varroa destructor Infesting Apis mellifera intermissa in Algeria: Implications for Regional Adaptation and Sustainable Management

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Varroa destructor is the most destructive ectoparasitic mite of honey bees, severely affecting colony health, productivity, and pathogen transmission. Despite the wide ecological diversity of Algerian beekeeping systems, information on intraspecific morphological variation of Varroa populations remains scarce. This study assessed the morphometric variability of phoretic female V. destructor collected from three contrasting Algerian agro-ecological zones: Boumerdès (Mediterranean coastal), Blida (sub-humid piedmont), and Mila (semi-arid interior plateau). Mites were sampled from colonies of Apis mellifera intermissa (four colonies per region) and analyzed using detailed morphometric measurements, including body length (BL), body width (BW), genital shield length and width (GSL, GSW), anal plate dimensions (APL, APW), lateral plate width (LPW), and derived shape ratios. Statistical analyses included ANOVA, post-hoc tests, correlation analysis, and multivariate approaches. Overall morphology was relatively homogeneous across regions; however, significant differences were detected for several traits. Body width differed significantly among regions (Blida: 1.62 ± 0.05 mm; Boumerdès: 1.69 ± 0.06 mm; Mila: 1.71 ± 0.07 mm; $p < 0.05$), as did lateral plate width (Blida: 0.42 ± 0.03 mm vs. Boumerdès and Mila: 0.46–0.47 ± 0.04 mm; $p < 0.01$). Shape ratios (BL/BW and GSL/GSW) also showed significant regional variation ($p < 0.05$). Correlation analysis revealed strong and consistent relationships between BW and GSW ($r = 0.71$) and between anal plate length and shape ratio ($r = 0.78$), while region-specific correlations suggested localized morphological covariation. Morphometric monitoring represents a valuable, low-cost tool for detecting early adaptive changes and supporting region-specific, sustainable varroa management strategies

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 146269

Integrative Taxonomic Revision of the Genus Leptogenys Roger (Hymenoptera: Formicidae) in Taiwan

Fu-Ya Chung; Mamoru Terayama; Katsuyuki Eguchi; Wendy Y. Wang; Feng-Chuan Hsu; Chung-Chi Lin

Leptogenys Roger (1861) is the largest genus within the ant subfamily Ponerinae, comprising 334 described species distributed across tropical and subtropical regions. This genus is characterized by linear mandibles, pectinate tarsal claws, and reproductive ergatoid (wingless) queens. In Taiwan, four Leptogenys species — L. chinensis, L. confucii, L. diminuta and L. kitteli — have been recorded. However, this genus has not been revised for over three decades, and recent collections suggest the existence of new or previously unrecorded species. In this study, we combined molecular (COI, 28S, and Wg) and morphological approaches to reassess the diversity of Leptogenys in Taiwan. The results identified two new species and one newly recorded species, L. peuqueti, which previously known from Southeast Asia and China. The molecular data strongly support the morphological distinctiveness of these lineages. The two new species can be distinguished from congeners by body size, mesosomal sculpture and the shape of petiole and subpetiolar process. Furthermore, the morphology of ergatoid queens and males is described. These findings indicate that the diversity of Leptogenys in Taiwan has been significantly underestimated and underscore the importance of modern integrative methods in regional faunal surveys.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 146340

Effects of serotonin on behavioral activities in males of honey bees (Apis mellifera L.)

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Serotonin is one of the biogenic amines that function as neuroactive substances across a wide range of organisms including insects, and regulates diverse behavioral and physiological processes. Males of honey bees (Apis mellifera L.) complete sexual maturation after about one week from adult emergence and departs from the mother colony for mating flight with a virgin queen. The locomotor and flight activities increase with age during sexual maturation. In previous studies, dopamine and octopamine, these are also biogenic amines, increase with age in the brains of males, and injection of these amines enhanced the behavioral activities. Thus, biogenic amines involved in regulation of behavioral activities in honey bee males. However, the behavioral role of serotonin remains poorly understood. We investigated age-related changes of serotonin levels, the expression levels of its receptor genes in the brain during sexual maturation, and effects of serotonin injection on the behavioral activities. The brain serotonin levels were significantly higher in 4- and 8-day-old than in 0-day-old. Relative expression levels of serotonin receptor genes did not significantly different between these ages. Serotonin injection did not significantly affect the locomotor activity, but significantly enhanced the flight activity. These results suggest that serotonin signaling increases during sexual maturation and selectively enhanced the flight activity in males of honey bees, possibly via constitutively expressed serotonin receptors. In this presentation, we further discuss the behavioral roles of serotonin in males based on additional assays using a serotonin receptor antagonist. This research was supported by JSPS Grants (No. 25KJ0379 and JP20K06077).

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 146424

Pollination requirements, wild bee diversity, abundance, and pollen affinity in almond agroecosystems

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Insect-mediated pollination is a fundamental ecosystem service supporting global food production. The rising demand for entomophilous crops, combined with the limited capacity of managed honey bees (Apis mellifera L.) to meet pollination requirements, has increased the reliance of agricultural systems on wild pollinators. In Morocco, almond cultivation constitutes an economically strategic sector; however, both cultivar-specific pollination requirements and the diversity and functional roles of pollinator assemblages remain poorly documented. This study aimed to (i) quantify the dependence of three almond cultivars (Espoir, Largueta and Planeta) on insect pollination and assess pollination deficits, and (ii) characterize the diversity, abundance, and pollen-use patterns of wild bee communities associated with almond orchards. Pollination dependency was evaluated using insect-exclusion netting to compare fruit set and yield among insect-isolated, open-pollinated, and open plus hand-pollinated treatments. In parallel, wild bees were sampled using a combination of sweep netting and colored pan traps methods, complemented by palynological analyses. Our results demonstrated that all three almond cultivars are obligatorily dependent on insect pollination, with significantly higher fruit set and yield under insect-pollinated conditions compared with exclusion treatments. A total of 813 bee specimens were recorded, representing 104 species, 17 genera, and five families, with Andrena, Eucera, and Lasioglossum emerging as the most species-rich and abundant genera. Integrated field and pollen analyses identified 26 species as effective almond floral visitors and eight species as almond pollen vectors particularly in Andrena flavipes, which appears to play a key

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 146468

Characterization of Moroccan Honeys: Antioxidant Potential, Mineral Composition, Antibacterial Activity, and Health Risk Assessment

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Twenty-four Moroccan honey samples were analyzed to evaluate total phenolic content (TPC), antioxidant capacity, elemental composition, antibacterial activity, and potential health risks. TPC showed marked variability, ranging from 47.83 to 316.69 mg GAE/100 g, while antioxidant activity (DPPH) ranged from 5.59 to 43.31 mg AAE/100 g, with a strong positive correlation between both parameters. Moringa and Acacia honeys exhibited the highest phenolic content and antioxidant capacity. Elemental analysis identified magnesium as the predominant essential element (6.51-187.04 mg kg^{-1}), followed by iron (0.57-28.58 mg kg^{-1}) and zinc (0.23-1.61 mg kg^{-1}), whereas toxic elements (Pb, As, and Co) were below detection limits in all samples. Antibacterial assays revealed concentration-dependent activity against gram-negative bacteria, with inhibition zones against Salmonella Typhimurium reaching 31.7 ± 0.1 mm at 50% honey concentration, while no inhibitory effects were observed against gram-positive strains. Principal component analysis explained 46% of the total variance, highlighting associations between mineral composition, phenolic content, antioxidant activity, and honey color. Health risk assessment showed that estimated daily intakes and hazard quotients for all elements were below established safety thresholds, indicating the absence of carcinogenic and non-carcinogenic risks. Collectively, these findings characterize Moroccan honeys as chemically diverse matrices with high antioxidant potential and a favorable safety profile. Future studies involving larger-scale sampling, elemental speciation, and in vivo investigations are recommended to further elucidate honey bioactivity and safety.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 146485

Do honey bees use propolis to fortify weak nest structures?

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Propolis, a honey bee product comprised of plant resins and beeswax, is found in a variety of nest locations. Most research on propolis has concerned its antimicrobial properties provided by phytochemical contents and benefits for colony health. However, little is understood about the physical functions of propolis as a nest construction material. Prior to this study, we observed propolis at the attachment points of several naturally built combs. To investigate whether propolis may be associated with strengthening comb attachment areas, we installed 8 simulated honey bee (Apis mellifera) swarms into hive boxes each containing 7 modified wooden frames. We weakened the frames by sawing several thin grooves into the top bars, leaving them thin and flexible. Each frame was photographed weekly as colonies built and utilized combs within them. We analyzed photographs using a machine learning pipeline to measure the location and size of combs and propolis applied to frames. Data indicate that colonies applied propolis to the grooves of weak frames directly above combs and the amount of propolis in grooves increased as combs grew. In natural contexts, honey bee swarms must quickly locate suitable cavities for long-term nesting. The best cavity may be compromised in certain ways, such as the structural integrity of comb attachment points. Our study demonstrates colonies' ability to build combs from weak structures and employ propolis in the process. This allows us to better understand the building capacities of honey bees and how they may adapt to a variety of nest cavities.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 147412

Integrative taxonomy of Vanuatuan doryline ants reveals four new endemic species in the South Pacific

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Island ecosystems harbor many endemic species that are increasingly threatened by biodiversity loss due to climate change and habitat destruction. The South Pacific consists of thousands of islands and while this region has been of much scientific interest, many archipelagos and their biota remain understudied. Recent advances have begun to address this knowledge gap, identifying the Vanuatu archipelago as a previously unrecognized ant biodiversity hotspot. Ants are among the most ubiquitous, diverse, and ecologically dominant insects on the planet and therefore serve as important biodiversity indicators. Our study builds on these initial results by using an integrative approach to delimit the Vanuatuan members of the ant subfamily Dorylinae, combining ultraconserved elements (UCEs) as phylogenomic markers, morphometrics and comparative morphology. Furthermore, we combined our UCE dataset with molecular data from regional doryline species to place the Vanuatuan species in a broader phylogenetic context. Our results support the presence of four new endemic ant species and indicate that the Vanuatuan endemics arose via multiple independent dispersal events from different source regions, as well as via in situ speciation within Vanuatu. This study also highlights the need for a comprehensive dataset to better understand the biogeographical history of Dorylinae ants in the South Pacific, which in turn can shed light on general evolutionary and dispersal patterns for ants in this region.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 147635

Are we occasional colleagues? Exploring relationship between Eciton burchellii parvispinus and Azteca velox beyond the role of predator-prey.

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Univerersity of Southern Mississippi

Army ants are remarkable predators in the tropics and are considered keystone species because the success of many other species depends on their survival. Interactions between army ants of genus Eciton and non-Dorylinae ants (NDA) has been mostly studied from a predator – prey perspective. Army ants are nomadic and discard their trash in ephemeral piles known as middens, which vary in composition depending on the bivouac phase (nomadic or statary). Around 98% of prey items found in Eciton middens are NDA. However, recent studies suggest that exists non-predation interactions between Eciton and a variety of other tropical ant species, whose natural history remains poorly known.

In Santa Rosa National Park, a low elevation dry forest of Costa Rica, we observed Azteca ants – obligate arboreal species, highly responsive to nest disturbance – foraging in middens of Eciton burchellii parvispinum, particularly targeting pupal cases. These observations lead us to investigate the nature of the relationship between Azteca spp. and Eciton spp. beyond predation. Specifically, we tested whether Azteca velox can locate Eciton middens and which midden phase they prefer. Our findings address a significant gap in tropical myrmecology, where non –predatory interactions between Eciton and NDA remain largely undocumented. Understanding these will broaden our knowledge of interspecific relationships in tropical ecosystems. Given that army ants are sensitive to anthropogenic disturbance and are predicted to experience range shifts in response to climate change, our results highlight the ecological importance of conserving this keystone species and the communities that depend on them.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 148152

West Africa’s blind spot: Ant Diversity and Habitat Patterns in Guinea-Bissau

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In this project we conducted the first comprehensive survey of the ant fauna in Guinea-Bissau. Our sampling was carried out in the southeastern region of the country within Boé National Park, encompassing riparian forests, secondary forests, cashew plantations, savannahs, and villages. To assess ant abundance and species richness, our sampling employed both passive methods (deep traps, pitfall traps, Winkler extraction, and baiting) and active methods (vegetation sweeping, vegetation beating, and hand collecting). A total of 272 samples have been processed to date, yielding 15,729 individuals corresponding to 130 morphospecies. Of these, 121 represent new records for Guinea-Bissau, and 12 are potentially undescribed species, including species belonging to taxonomically depauperate and rarely sampled genera such as Loboponera and Calyptomyrmex. The northern and western distribution limits of several afrotropical species were also extended. Our preliminary results suggest that the degradation of native habitats negatively affects ant abundance and species richness, thereby placing the ecological roles performed by ants at risk. Overall, this study will provide a comprehensive checklist of ant species of Guinea-Bissau, assess the presence of exotic and potentially invasive ant species in the country, establish a genetic reference database using DNA barcoding, and compare species composition across different habitat types representing varying degrees of human influence in the Boé region. It is expected that the results of this study will fill an important knowledge gap regarding ant diversity in West Africa, while supporting conservation planning and establishing a baseline for understanding ant diversity in Guinea-Bissau.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 148675

Seasonal effects on tissue-specific immunity-related gene expression in honeybee queens exposed to different pathogen types

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Immune priming is a crucial process that enables insects to protect themselves against recurrent pathogen exposure. In addition, it can help to protect offspring from diseases. Utilizing oral exposure to dead bacteria and trans-generational immune priming, it has been demonstrated that we can “vaccinate” honeybees against the diseases. At the same time, we do not entirely understand the molecular underpinnings of this phenomenon. Here, we aim to study the seasonal effects of oral priming on tissue-specific immune gene expression in queens. This approach provides a step-by-step understanding of how oral priming functions and influences queen bee immunity at different times in the summer season. We use RT-qPCR approach with number of central immune genes to see how queens respond to priming agents early and in the middle of the bee season in Austria. Interestingly, we see a strong seasonal effect in the queen responses.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 148868

Behavioral impairments in paper wasp colonies due to neonicotinoid pesticide

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Neonicotinoids like imidacloprid are widely used for pest control but pose significant risks to beneficial social wasps, which provide vital ecosystem services as predators and pollinators. While individual mortality is documented, colony-level behavioral impacts remain largely unexplored. This study investigated how sublethal concentrations of imidacloprid affect the paper wasp Mischocyttarus cassununga. We conducted four bioassays: 1) a concentration-mortality test to determine LC50 and LC10; 2) a choice test to assess anti-feeding behavior; 3) walking behavior analysis using Ethoflow software; and 4) monitoring colony-level social interactions, including nest departures, trophallaxis, and aggression. Imidacloprid showed significant toxicity (LC50: 36.11 mg/L; LC10: 7.46 mg/L). Wasps failed to avoid contaminated food, indicating high field susceptibility. Sublethal exposure severely impaired locomotion, reducing distance walked while increasing stops and neurotoxic disorientation. At the colony level, imidacloprid significantly reduced nest departures, trophallaxis, aggression, and cell inspections, leading to increased lethargy and pause periods. Imidacloprid negatively affects M. cassununga at both individual and colony levels. The disruption of social interactions and locomotion suggests a functional collapse that threatens foraging efficiency and brood care. Ultimately, neonicotinoid use appears incompatible with the conservation of social wasps and their ecosystem services.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 149242

Towards an integrative taxonomy of ant genus Carebara in Asia using the colony composition and subcaste polymorphism

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The ant genus Carebara comprises 233 known species distributed across tropical and subtropical regions worldwide. Eighteen genera that had previously been established have been treated as synonyms under Carebara because their definitions are ambiguous and their diagnostic characters are considered convergent; this taxonomic treatment has also been supported by recent molecular phylogenetic analyses. Because many species have evolved similar morphologies as adaptation to cryptic environments, systematic studies based on synapomorphies are lacking. To reconstruct the higher classification of the genus, it is necessary to incorporate characters other than morphological traits. Here we focus on social structure such as colony composition in Asian species, and propose a classification system that integrates these data with morphological evidence. Among three species in which major workers account for less than 10% of the total worker individuals, shared character states are observed in head morphology; these three species also share intraspecific morphological variation within the major workers. Our results indicate that an integrative taxonomic approach combining morphological characters and social structure is effective for the genus. These results provide new insight, showing that morphological data in conjunction with social structure data can contribute to the construction of a more robust higher classification.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 149371

Drifting behaviour in bumblebees can be linked to both brood and kleptoparasitism.

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One of the defining traits of eusocial insects is reproductive division of labour, where workers refrain from reproducing and instead support their natal colony. However, this remarkable level of cooperation is not without vulnerabilities. ‘Drifters’, workers from other colonies, can accidentally enter another hive, but drifting may also be strategic, allowing workers to exploit this cooperation. Previous research has documented drifting as a reproductive strategy in eusocial insects such as the honeybee. Colonies lacking a queen are particularly susceptible to exploitation by non-natal workers, as these workers can reproduce in the queenless colony without being hindered by policing mechanisms. This study aimed to assess how the absence of a queen affects the drifting behaviour of Bombus terrestris workers. We quantified drifting and foraging from experimental colonies differing in queen status (queenright vs queenless). RFID monitoring provided time-stamped hive and feeder passages over a 2-week period, which were aggregated to individual drifting and foraging events across the experiment. Additionally, we examined worker size and ovary development to better understand how these factors influenced drifting behaviour. In general, drifters and foragers tended to be larger than intranidal workers as expected. Workers from queenright colonies were more likely to drift and were more actively foraging, but ovary development provided little support for brood parasitism: drifters and foragers had comparable ovary stages and, within drifters, queen status did not explain ovary stage. Overall, drifting appears shaped primarily by colony social context and size-related differences rather than by reproductive activation, consistent with a kleptoparasitic interpretation.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 149463

The Connection Between Grooming behavior and Flight Performance

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Grooming is a fundamental social behavior in honey bees, functioning both in individual hygiene and colony-level defense. In the context of host-parasite interactions, grooming, through autogrooming and allogrooming, represents a key behavioral defense against the ectoparasitic mite Varroa destructor. Here, we evaluate grooming as an extended behavioral phenotype in the Western honey bee (Apis mellifera), with particular emphasis on mite-biting behavior and its ecological and evolutionary consequences. We compared colonies with similar prevalence of mite infestation to assess variation in grooming effectiveness, quantified through the degree of mite damage. Feral colonies derived from wild populations exhibited significantly elevated mite-biting behavior, indicating enhanced defensive capacity likely shaped by natural selection under persistent parasite pressure. Despite growing interest in grooming as a resistance trait, its potential association with other performance-related traits has received little attention. We therefore examined the relationship between mite-biting behavior and individual flight performance, a trait central to foraging efficiency, dispersal, and overall colony health. Using a flight mill system, we measured flight distance, duration, and velocity of foragers from colonies exhibiting high versus low mite-biting behavior. We theorized that colonies associated with high-mite biting behavioral traits would also display higher flight performance values. By integrating behavioral defense with locomotor performance, this study explores potential trade-offs or synergies underlying parasite resistance and functional performance. Our findings provide insight into how social immunity traits may co-evolve with key ecological behaviors, contributing to the persistence and adaptive success of honey bee populations under parasite pressure.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 149736

Vegetation structure shapes horizontal and vertical stratification of ant assemblages in a Cerrado savanna

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Vegetation structure is a key but context-dependent driver of biodiversity, yet its influence on the vertical stratification of insect communities in tropical savannas remains poorly understood, particularly outside forest ecosystems. We evaluated how variation in woody vegetation structure along a Cerrado savanna gradient shapes both horizontal differentiation among physiognomies and vertical stratification between ground- and vegetation-dwelling ant assemblages. Ants were sampled simultaneously in ground and vegetation strata using standardized pitfall traps across four Cerrado physiognomies spanning a gradient from open savanna to forest-like formations, while woody aboveground biomass was quantified as an integrative proxy of vegetation structural complexity. Ant assemblages differed strongly between strata and among physiognomies, with vertical position accounting for most of the variation in species composition. Importantly, the compositional dissimilarity between ground and vegetation assemblages increased significantly with woody biomass, indicating that vertical segregation of ant communities intensifies as vegetation becomes denser, taller, and more vertically stratified. In open physiognomies, ground and vegetation assemblages were relatively similar, suggesting greater cross-stratum overlap, whereas in denser formations they became markedly distinct, consistent with increased microclimatic contrasts, resource compartmentalization, and physical separation between strata. Our findings demonstrate that woody encroachment in the Cerrado reorganizes ant assemblages primarily by strengthening vertical stratification rather than by uniformly increasing or decreasing diversity. These results highlight the need to incorporate multiple strata into ant sampling protocols and suggest that conserving mosaics of vegetation structure is essential to preserve both the taxonomic diversity and the vertical organization of ant assemblages in tropical savannas.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 149887

Population genetic reassessment of Vespa crabro subspecies: discordance between color variation and genetic lineages

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Traditional subspecies classification of Vespa crabro has relied largely on abdominal and thoracic color patterns, yet the evolutionary and population genetic validity of these traits remains poorly tested. In this study, we reassess subspecies boundaries in V. crabro with an emphasis on population-level genetic structure, focusing on Korean populations traditionally assigned to V. crabro crabroniformis and V. crabro flavofasciata. An examination of 163 Korean specimens revealed extensive color polymorphism, with 27 distinct color-pattern variants observed. Correlation analyses among thoracic and abdominal markings failed to identify any diagnostic combinations that reliably delimit subspecies. To evaluate genetic structure, we analyzed mitochondrial COI sequences from Korean populations and compared them with Japanese and European samples. Nine distinct haplotypes were identified within Korea, showing no correspondence with color-pattern–based subspecies assignments. Moreover, the Korean population possessed unique single nucleotide polymorphisms distinguishing it from Japanese and European populations. Notably, COI divergence was greatest between Korean and Japanese populations, despite their historical treatment as the same subspecies based on external coloration. Together, these results indicate that color-based subspecies designations in V. crabro obscure underlying population genetic structure and that the Korean subspecies are best treated as a single taxonomic unit. Building on these findings, we are conducting whole-genome sequencing analyses to further resolve population divergence, gene flow, and demographic history across East Asian and European populations. Our integrative, genome-informed framework highlights the importance of population genetic data in revising subspecies taxonomy in widely distributed social insects.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 149996

The density-dependent relationship between pheromones and the geometry of Argentine ant exploratory patterns

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Previous studies have shown that the geometry of individual ant's trajectories is density dependent. The reason underlying this density-dependent collective behavior is currently unknown. Here, we explore this question through experimental observations of Argentine ants exploring a novel area alone, or in groups of increasing sizes. While exploring, Argentine ants primarily communicate through physical contacts and chemical cues such as the trail pheromone, which is deposited on the ground constantly as individuals walk. We hypothesize that, as the group size increases, the probability of an ant crossing a pheromone trail will also increase. Since Argentine ants tend to change their movement direction to follow these trails, we expect that they will have more sinuous trajectories when exploring a new area as a larger group. Using a YOLO-based machine-learning tracking software, we measured the probability of an ant crossing the path of another ant at different time points during the experiment and related it to the sinuosity of its trajectory, controlling for the effect of direct collisions between ants and with the wall of the experimental arena. Our results will reveal whether the density-dependent sinuosity of Argentine ants is indeed a simple by-product of their constant trail laying behavior or whether a more complex explanation is required.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 152883

A novel tool to track ant movement in darkness to assess the role of vision in area-restricted search behaviour

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In recent work (doi: 10.1101/2025.06.25.661660) we found that the black garden ant Lasius niger is able to perform search behaviour, even in homogeneous white light or red light conditions. The present study aims to determine whether this search behavior is maintained in total darkness. To address this question, we present a novel experimental tool where trajectories are recorded using a LiDAR camera that maps the surface of the arena and reconstructs the ant's 3D position from 2D coordinates obtained during tracking. Individual trajectories are collected in a controlled arena (50 × 50 cm) under modulated infrared illumination (940 nm) emitted and perceived by the camera. This wave length corresponds to practical darkness for the ant. To detect search behaviour we model trajectories using a random-walk framework to extract several variables, including the distribution of free path lengths and reorientation angles as a function of ant orientation relative to the starting point. Since L. niger is preferentially active during darkness we will also test the diurnal ant Aphenogaster senilis and compare its movement to that of L. niger. This study will clarify the relative contribution of vision in the navigation process of these two species.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 152998

Improvment of Millettia laurentii (Fabaceae) production through floral visit by Apis mellifera (Hymenoptera: Apidae) at Dang (Ngaoundere, Cameroon)

Napoleon Nisso Djamo; Bernice Mireille Kingha Tekombo; Ezéchiel Nouama; Sanda Mazi; Sanda Mazi; Sanda Mazi; Fernand-Nestor Tchuenguem Fohouo

In Cameroon, demands for ornamental plants, honey and pollen as beehive products are high while their productions are low, due notably to the insufficiency of knowledge concerning relationships between bees and this plant species.

To assess the impact of flower visits by Apis mellifera on the production of Millettia laurentii, investigations were conducted on the behavior of this bee on Fabaceae flowers from February to December in 2020 and 2021 at Dang. During each investigation period, 540 flowers clusters in the bud stage were labeled and divided into four treatments: 120 unprotected flowers; 120 flowers protected from insects using gauze bags; 200 flowers protected from insects, which were uncovered once for a visit by A. mellifera and rebagged; and 100 insect-protected flowers, destined to be uncovered and protected again, without insects or any other organism visit. The results show that worker bees intensely harvested pollen and nectar on M. laurentii flowers. The mean duration of a visit per flower was 8.46 sec for nectar collection and 9.98 sec for pollen harvest. The mean foraging speed was 6.63 flowers/min. The average abundance of 56.50 individuals per 1000 flowers. Millettia laurentii is a highly polliniferous and nectariferous bees plant. Through its pollination efficiency, A. mellifera increased the percentage of mature fruit and normal seeds by 60.80% and the percentage of normal seeds by 29.06%. It is recommended to protect and establish A. mellifera colonies near M. laurentii plantation to enhance pepper production and improve pollen yield as a hive product.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 152999

Exploitation of the flowers of Capsicum annuum (Solanaceae) by Apis mellifera (Hymenoptera: Apidae) at Madem (Ngaoundere, Cameroon)

EZECHIEL NOUAMA; Denis Djonwangwé; Napoleon Nisso Djamo; Bernice Mireille Kingha Tekombo; Sanda Mazi; Fernand-Nestor Tchuenguem Fohouo

In Cameroon, demands for agricultural product, honey and pollen are high while their productions are low, due notably to the insufficiency of knowledge concerning relationships between bees and this plant species.

To assess the impact of flower visits by Apis mellifera on the production of Capsicum annuum, investigations were conducted on the behavior of this bee on Solanaceae flowers from August to December in 2021 and 2022 at Madem. During each investigation period, 540 flowers in the bud stage were labeled and divided into four treatments: 120 unprotected flowers; 120 flowers protected from insects using gauze bags; 200 flowers protected from insects, which were uncovered once for a visit by A. mellifera before being shielded once more; and 100 insect-protected flowers, left exposed and shielded once more, free from insect or other organism visits. The activity of A. mellifera was observed in treatments 1 and 3, where worker bees intensely harvested pollen and nectar. The mean foraging speed was 8.12 flowers per minute, with an average abundance of 136 individuals per 1000 flowers. Capsicum annuum is a highly polliniferous and faintly nectariferous plant for bees. Through its pollination efficiency, A. mellifera increased the fruiting rate by 12.94%, the mean number of seeds per fruit by 23.63% and the percentage of normal seeds by 11.31%. The contribution of A. mellifera to germination rates was 15.29%. It is recommended to protect and establish A. mellifera colonies near C. annuum fields to enhance pepper production and improve pollen yield as a hive product.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 153001

New insights into insect sociality: messages from social aphids

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Social behaviors have been recorded in a small proportion of aphids, a phytophagous hemipteran insect group usually with complex life cycles and various polyphenisms. Social aphids display significant diversity of traits and behaviors, making them good model for investigating social evolution and phenotypic plasticity. Using the social aphid system, we have been investigating behavioral and molecular mechanisms underlying caste differentiation, morphological plasticity and interspecific interaction. We found a novel type of maternal regulation of caste ratio involving reproductive differentiation of parthenogenetic mothers, which may be related to differences in sensilla types, cuticular chemical profiles and olfactory-related gene expression. We assembled a first chromosome-level social aphid genome with unique features in genome architecture and transcriptional regulation. Further integrated multi-omics and functional analyses revealed key regulators closely linked to developmental arrest (e.g. miRNA & 20E & nuclear receptor) and morphological specialization (e.g. paramyosin & leg enlargement, resilin & cuticle elasticity) in soldiers. The findings from social aphid system provide new insights into the diversity and evolution of insect sociality.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 154113

Morphological plasticity of Apis mellifera foragers across Urban–Rural land-use gradients and temporal scales in Southwest UK

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Honeybees live in some of the most human-altered landscapes on Earth, yet we still know surprisingly little about how their bodies respond to these environments. In this study, I compared the morphology of Apis mellifera foragers from urban and rural sites across Southwest UK during late summer. What I found was unexpected: city bees and country bees looked remarkably alike. Instead, the biggest changes happened over time, not space. Bees collected in September were noticeably smaller than those from August, and subtle shifts in body shape appeared between years. Even when I looked at the full 3-km landscapes around each colony, land-use differences explained only small, gentle trends, not major changes. Overall, these results suggest that for managed honeybees, seasonal conditions, like changing flowers and late-summer resource decline, shape their bodies far more than whether they live in an urban or rural setting.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 155381

Thermal Tolerance of Red Wood Ants and Their Hybrids in the Netherlands

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Ants of the Formica rufa-group are key ecosystem engineers in temperate forests, where they contribute to soil processes, trophic interactions, and pest control. Within this group, closely related species frequently co-occur and can hybridise, raising questions about how rapidly changing environmental conditions under climate change shape species boundaries and adaptive responses. In particular, it remains unclear if and how phenotypic plasticity of thermal tolerance differs between parental species and their hybrids, and how species and hybrids may respond to ongoing climate change.

Here, we examine the seasonal variation in heat tolerance before and after climate-change acclimation in the species F. rufa, F. polyctena, and F. pratensis and putative hybrids in the Netherlands. Using standardised CTmax assays, we test the organisms' responses to acute heat stress.

We hypothesise that species and hybrids differ in their thermal response over the season and due to acclimation, suggesting variations in heat tolerance and acclimation capacity. These differences may influence competitive dynamics and the stability of hybrid zones under rapidly changing temperature regimes predicted with climate change.

Our findings provide insight into how climate change may affect species interactions within the F. rufa-group, highlighting the importance of thermal physiology for predicting future distribution patterns and adaptive potential.

SYMPOSIUM 00 · Open Symposium
POSTER · Abstract ID 159226

When it gets hot, teamwork wins: ground warming boosts cooperative transport outcomes over solo carriers

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Ground temperature directly alters how ants move, grip, and navigate, with consequences that can scale up to colony-level performance. A key question is whether the effect of ground warming scale up equally for cooperative versus individual tasks. We used a portable warming setup to manipulate ground temperature and compare cooperative (CT) versus individual transport (IT) performance in the temperate ant Dorymyrmex tener, from the Patagonian steppe (Argentina). Under field conditions, we video-recorded standardized bait-removal trials across 32 colonies (259 videos; 173 CT and 86 IT) spanning 10.15–58.6 °C at the plate surface. From videos, we extracted transport metrics capturing efficiency and navigation accuracy, including removal success, transport velocity, path sinuosity, directional bias, and a composite food-transport rate (food weight*velocity/number of ants). We tested for thermal responses using mixed-effects models with plate temperature, transport mode (CT vs IT), and their interaction. Performance increased with temperature for both CT and IT models, but CT showed consistently stronger gains than IT. Ground warming increasingly favoured CT for key outcomes such as removal success, trajectory accuracy (directional bias/sinuosity), and food-transport rate. Further, when comparing food-transport rate responses in CT relative to IT, we found that CT performed ~2–5× better than IT under warmer conditions. These results suggest that warming can shift the functional payoffs of transport strategies, making cooperative food transport behaviour disproportionately advantageous over solo carriers. More broadly, our findings suggest that cooperation may be a more effective and potentially more resilient strategy for task performance under global warming scenarios.

The role of olfactory sensitivity on task specialization in the honey bee

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Division of labor and task specialization are key elements explaining the remarkable ecological success of human and animal societies. Social insect colonies are characterized by a highly effective division of labor, with workers specializing in brood care early in life and in foraging later in life. Various theoretical models have been proposed to explain division of labor, most prominently the response threshold model, which postulates that individuals differ in their response threshold to task-associated stimuli, and will engage in particular tasks depending on this threshold. While this model has received some experimental support, the current data

still do not explain how division of labor is implemented for all different tasks of a social insect colony.

The success of social insect colonies lies in the capacity of all its members to behave in a well-organized manner, which involves elaborate communication among colony members. Accordingly, social insects use a wide range of pheromones to regulate almost every aspect of their life. Astonishingly, the role of olfaction, the main sensory modality used by insects, on the division of labor has been greatly overlooked. Using the honey bee Apis mellifera as a model, we investigate the hypothesis that variation in olfactory perception and processing, especially regarding social pheromones, can give rise to division of labor. Using behavioral and neurophysiological approaches, we are comparing olfactory perception and processing in the hive’s different worker task groups (nurses, foragers etc.) to establish the role of olfactory perception on the division of labor.

A worker-specific role for neuroparsin A in regulating bee reproduction

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The reproductive division of labor is key to sociality, but the molecular mechanisms that regulate reproduction in social insects are not well understood. Specifically, the pathways that induce sterility in workers, and whether these same pathways are conserved in solitary species, remain unclear. Here, we examine the role of the neurohormone neuroparsin A (NPA) in bee reproduction.

To determine whether NPA is associated with reproductive status, we measured NPA gene expression in reproductive and non-reproductive females from six bee species with varying levels of sociality. In the two eusocial species tested, isolation from the queen and subsequent ovary activation were associated with reduced NPA expression in workers. Interestingly, we did not observe a negative association between NPA expression and reproduction in queens, nor in the solitary species tested. These findings suggest that NPA inhibits reproduction specifically in the worker caste and that the queen may manipulate NPA levels in workers to maintain her reproductive dominance.

To test whether NPA expression causally inhibits ovary activation in workers, we established an RNA interference protocol in the model Bombus impatiens. By injecting a cocktail of nanoparticle-packaged DsiRNAs through the antennal socket, we achieved a 35% reduction of NPA expression in workers' heads. We compared ovary development in NPA-DsiRNA-treated and untreated workers to determine whether NPA interference induces worker reproduction. Together, our work demonstrates a worker-specific role for NPA in bee reproduction that may underlie the reproductive division of labor in social bees.

SYMPOSIUM 01 · Adult phenotypic plasticity and the regulation of division of labor in social insects
ORAL · Thu 20 Aug · 11:00 · K10 · Session 54 · Abstract ID 149926

From Molecules to Societies: how queen pheromones enforce the reproductive division of labour

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The defining feature of eusociality is reproductive division of labour, where a single female, the queen, produces most of the offspring while workers perform all other tasks. In some insect societies this division is maintained through aggression or dominance interactions, but in highly eusocial insects reproduction is instead regulated by queen-produced semiochemicals.

The queen mandibular pheromone (QMP) of the honeybee, Apis mellifera, is one of the most chemically complex queen signals known. Produced in the mandibular glands, it coordinates worker behaviour and physiology, including reproductive suppression. Unlike queen pheromones of other eusocial hymenopterans, QMP comprises at least thirteen compounds, five major, raising fundamental questions about why honeybee queen signals evolved such exceptional chemical complexity.

Here I present our work examining how QMP represses reproduction in worker bees. By linking mechanism to function, we ask why this pheromone is so chemically complex and what this complexity reveals about the evolution of queen signalling. Our findings suggest that queen control emerges from interacting physiological processes rather than a single dedicated mechanism, and that these compounds exploit ancestral, conserved pathways that regulate reproduction in response to environmental cues. Ultimately, this work contributes to our understanding of how pheromonal control of reproduction may have shaped the evolution of eusociality.

SYMPOSIUM 01 · Adult phenotypic plasticity and the regulation of division of labor in social insects
ORAL · Thu 20 Aug · 11:15 · K10 · Session 54 · Abstract ID 146439

Neither caste nor sex: an ant species consisting entirely of queens

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Division of reproductive labor, which in ants is usually associated with pronounced phenotypic plasticity, is one of the key foundations of the evolutionary and ecological success of social insects. Nevertheless, caste differentiation has been lost in many ant species. This includes several workerless social parasites (inquilines), making them interesting subjects for studying the genomic changes underlying the loss of workers. The Japanese inquiline species Temnothorax kinomurai has gone a step further: not only has it lost the worker caste, but it has also evolved obligatory thelytokous parthenogenesis, resulting in the complete loss of males. It therefore is the only ant species known so far that consists exclusively of queens. We present data on the morphology and life history of this unusual and little-known species.

SYMPOSIUM 01 · Adult phenotypic plasticity and the regulation of division of labor in social insects
ORAL · Thu 20 Aug · 11:30 · K10 · Session 54 · Abstract ID 149720

Unmated queens show worker-like behavior and gene expression in polygynous colonies of the ant Stigmatomma pallipes

Maximilian F. Bolder[1]; Jannik S. Möllmann[1]; Thomas J. Colgan[1]; Romain Libbrecht[2]

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Insect societies function on a division of labor between queen and worker castes. While many studies have focused on the behavioral and physiological variation within the worker caste, such variation within the queen caste remains understudied, as it is generally considered that the sole function of queens is egg production. However, in polygynous colonies, queens may show variation in terms of physiology and behavior. To better understand the basis of such variation, we used the ant Stigmatomma pallipes to investigate: i) whether nestmate queens from polygynous colonies differed in behavior; and ii) whether this variation was associated with their mating status and underlying gene expression. Individual tracking and behavioral scoring identified two types of queens: low-mobility polygynous queens that behaved like monogynous queens and high-mobility polygynous queens with worker-like behavior. We found that only one queen per colony was mated, reproductively active, and consistently demonstrated lower mobility. Distinctions were also observed at the transcriptomic level, based on a genome generated specifically for this study, comparing gene expression in the brain and fat body. Mated low-mobility polygynous queens exhibited expression profiles similar to monogynous queens, whereas unmated high-mobility polygynous queens resembled workers. Such differences between low- and high-mobility queens were primarily associated with processes related to protein synthesis, transcription, and neural activity. Our finding that unmated queens in polygynous S. pallipes colonies exhibit worker-like behavior and gene expression challenges traditional views of queen specialization and provides new insights into reproductive division of labor in insect societies.

SYMPOSIUM 01 · Adult phenotypic plasticity and the regulation of division of labor in social insects
ORAL · Thu 20 Aug · 11:45 · K10 · Session 54 · Abstract ID 149303

Power and reproduction in an Australian paper wasp

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Multiple-queen societies have evolved repeatedly across the eusocial insects but pose a challenge for kin selection theory that underpins our understanding of social insect societies. The presence of multiple reproductives in groups should reduce intracolony relatedness and thereby increase potential for conflict between females in the group, raising questions of how the reproductive hierarchy is established and its stability in these systems. Here, I examine the stability of multiple-queen societies using Australia's little-studied primitively eusocial wasp, Ropalidia plebeiana. I used field experiments to address three questions. Firstly, to assess whether queens maintain their reproductive dominance via aggression, I filmed nests daily for one week to identify which individuals become queens, and to construct aggression networks. Secondly, to determine how perturbation of the social environment – namely loss of a queen – impacts behaviour of nestmates, I performed a queen removal manipulation, tracking changes to social networks and reproduction of nestmates over the following week. Finally, I tested stability of these changes to social networks and reproductive hierarchy by reintroducing removed queens to their nests, assessing whether reintroduced queens were reintegrated as egg-layers or aggressively challenged. The partitioning of reproduction in these groups and how this is maintained have important consequences for the genetic and social structures of cooperative groups, and hence for their evolution.

SYMPOSIUM 01 · Adult phenotypic plasticity and the regulation of division of labor in social insects
ORAL · Thu 20 Aug · 12:00 · K10 · Session 54 · Abstract ID 149733

Reproductive hierarchies of clonal ants with and without fertility signals

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Queenless ants use dominance hierarchies to sort reproductive conflicts and the division of labor, even in groups of clones such as the thelytokous parthenogenetic populations of Platythyrea punctata. Dominant females that achieve ovary development and egg production signal their fertility with cuticular hydrocarbon (CHC) profiles, but these profiles are distinguishable weeks after the division of labor can already be observed. While dominance hierarchies can be formed with self-organization processes that do not require chemical communication, the role of chemical communication in hierarchy reformation is less understood. We tested this by allowing young intranidal workers to form new hierarchies in isolated groups before merging these groups at “early” or “late” periods, to witness hierarchy reformation before or after CHC profiles signal fertility. We found that, despite fertility signals leading to more targeted dominance interactions and higher network centrality, hierarchies were equally linear and stable in both periods - arguably less stable in the late period with clear fertility signals. Given that fertility signals also shifted behaviors from more “ritualized” (antennal boxing) to “violent” (biting), we believe this chemical communication is not facilitating hierarchy reformation, but instead replacing dominance dynamics with policing dynamics, analogous to the policing observed in queen-right colonies that do not need dominance hierarchies to achieve their reproductive division of labor.

SYMPOSIUM 01 · Adult phenotypic plasticity and the regulation of division of labor in social insects
ORAL · Thu 20 Aug · 14:30 · K10 · Session 60 · Abstract ID 146097

Plasticity of non-nestmate discrimination in the clonal raider ant

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Social insects discriminate between foreigners and members of their own colony via complex olfactory cues. How plastic this discriminatory behavior is, and whether and under what circumstances ants can learn to accept genetically distinct individuals as nestmates, is poorly understood. Here, we study this question in the clonal raider ant, Ooceraea biroi, which provides unparalleled experimental control over the genotype of individuals and the genotypic composition of colonies. Using a cross-fostering design with mixed-genotype colonies of wild-type and transgenically labelled individuals, we show that ants become non-aggressive specifically toward their foster genotype. This tolerance is transient, and aggression resumes after two weeks of being isolated from the foster colony. However, even sporadic re-exposure to individuals from the foster colony is sufficient to maintain tolerance for over a month, while the same paradigm fails to establish tolerance in the first place. This shows that non-nestmate discrimination is remarkably plastic and that, once established, tolerance toward foreigners can be maintained by only intermittent contact. These dynamics echo general principles of social learning and contact-dependent tolerance described in other social species, including humans.

SYMPOSIUM 01 · Adult phenotypic plasticity and the regulation of division of labor in social insects
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Cooperation and competition in the clonal raider ant

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The evolution of social species is shaped by constant tension between cooperation and conflict. To study this evolutionary interplay in action, researchers have typically relied on microbial models - combining distinct conspecific strains into chimeric populations and tracking which outcompetes the other, why, and under which conditions. This paradigm has empirically grounded social evolution theory and revealed astonishing traits that are critical to microbial evolution yet invisible in monoclonal populations. However, practical constraints have prevented this paradigm from being applied to animals, and fundamental differences between microbial interactions and those of multicellular organisms limit how broadly microbial results generalize. The unusual biology of the clonal raider ant is well suited to this paradigm. This ant has no queens. Instead, workers reproduce clonally and distinct clonal lines have been collected from around the world. I am using fluorescently-labelled transgenic lines of the clonal raider ant to perform evolutionary mixing experiments - identifying which clonal lines outcompete which others over generations and, more importantly, why. My experiments have revealed that clonal lines can have strong effects on the survival and reproductive success of other clonal lines and have identified a suite of behavioral phenotypes that correlate with these fitness effects.

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Coordination of a rare task: Nightly door-closing behavior in harvester ants

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Florida harvester ant (Pogonomyrmex badius) workers change jobs as they age and develop. Door-closing is a behavior performed by a group of just 2-3 specialist workers, exactly once per day. How workers are allocated to this rare task is unknown. At one extreme, spatial task allocation models predict that workers are behaviorally ‘totipotent’, and proximity to cues dictates task participation, while task saturation limits excessive participation. In contrast, response threshold models predict that workers have intrinsic variation in cue sensitivity, that increased demand will not increase labor allocation, and that selection acts on adaptive labor ratios (demography). We used mark-recapture techniques to determine if the same workers act as door-closers on successive days, and to identify the larger demographic group from which door-closers were drawn. To investigate the relationship between demand for labor and labor allocation, we 1) added up to five additional entrances per nest, and 2) experimentally removed all door-closers from nests. Our findings suggest that ‘door-closers’ belong to a discrete, age-correlated group that included foragers. The addition of more entrances increased total nest closing time but did not increase the number of door-closers. Depleting the door-closer population prevented door-closing altogether, despite the availability of other workers on the nest mound. Closing times were idiosyncratic, and some colonies that closed before sunset excluded late-returning foragers. This talk will consider the value of studying rare behaviors in a phylogenetic context, discuss the costs and benefits of door closing, and review the many ‘door-closing’ methods employed by diverse ant species.

Tissue-Specific Transcriptional Activity Underlying Task Switching in the Ant Temnothorax longispinosus

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Insect societies exhibit a division of labor (DOL) in which task allocation remains flexible in adult workers. This flexibility is enabled by phenotypic plasticity, allowing individuals to modify behavioral traits in response to changing external conditions. In social insects, worker behavior and task performance are closely associated with gene expression. For example, elevated expression of vitellogenin-like A in the fat body is linked to brood care behavior in the ant Temnothorax longispinosus. Transcriptomic comparisons between nurses and foragers in this species further revealed approximately eightfold more differentially expressed genes in the antennae than in the brain. This pattern highlights the importance of the peripheral nervous system in task regulation and emphasizes the tissue specificity of transcriptional activity underlying DOL. Building on these findings, we investigated the transcriptional basis of behavioral transitions in worker ants. We experimentally induced task switching while disentangling the effects of age and task, and analyzed associated transcriptional changes across multiple tissues, including antennae, brain, and fat body. We are currently analyzing these expression data and predict rapid shifts in gene expression following task transitions, particularly in odorant receptor genes in the antennae and vitellogenin-like A in the fat body. Our study aims to identify which transcriptional changes occur most rapidly during behavioral transitions, in which tissues these changes arise, and which differences between nurses and foragers are attributable to age rather than task. Together, these results will advance our understanding of how tissue-specific gene expression underlies adult phenotypic plasticity and regulates DOL in social insect colonies.

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The structure of age-dependent nest defense plastically varies by threat type in paper wasps

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Division of labor is a defining feature of social insects, yet how specialized roles emerge in the absence of fixed castes remains poorly understood. Because most empirical work has focused on foraging, important axes of labor organization may be overlooked when task allocation is examined in only one ecological context. Here, we use colony defense as a lens for examining how labor is partitioned in the European paper wasp, Polistes dominula. Using nest-defense assays, we show that participation is highly skewed: most individuals rarely engage, while a subset consistently participates, revealing a clear division of defensive labor. Exposing nests to multiple threat types reveals context-dependent defensive engagement, behavioral tactics, and colony-level allocation that differ between conspecific wasp and heterospecific ant enemies. Critically, we found that the extent of age-based polyethism varied between wasp and ant threats, with older wasps preferentially engaging conspecifics while ant responses were distributed more evenly across ages. Transcriptomic analyses of wasp heads similarly highlighted both shared and threat-specific genomic mechanisms associated with defensive division of labor. Comparisons between more- and less-engaged individuals across threat types reveal differential gene expression related to cuticle function and metabolic processes consistent with age-associated physiological differences. Our results highlight that the age-dependence of labor can significantly vary, even within nest defense, depending on the ecological context of the enemy. Together, these results demonstrate that defensive division of labor can arise through behavioral plasticity, and that studying defense across multiple contexts reveals dynamic links between physiology, individual behavior and colony organization.

Behavioral and molecular variations in circadian clock set-up is related to colony reproduction in stingless bees

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In Apis mellifera, nurses show weak circadian rhythms, whereas foragers show strong circadian activity. We asked whether this also applies to other highly eusocial bees, such as the Meliponini, which display large variability in their life-history strategies. To address this, we investigated the circadian clock of Melipona quadrifasciata. We analyzed time-series data based on age (15- and 30-day-old workers) and task (nurses involved in the Provisioning Oviposition Process (POP) and foragers). Age-controlled workers showed synchronization, with significant oscillation in the clock genes per, cry-m, and clk in both age classes, although rhythms were stronger in the older bees. Conversely, task-based sampling revealed higher variability, with rhythmicity only for per and cry-m in foragers. Locomotor activity analyses showed robust rhythms for both nurses and foragers, indicating a functional clock across all bees. To test whether the nurses' rhythms depend on POP activity, we established a 10-days queenless condition, and then sampled 15-day-old workers. This led to significant changes in the clock setup, including strong oscillation of the cyc gene. Immunostaining for the clock neuropeptide Pigment-Dispersing Factor (PDF) revealed no difference in PDF-positive neuron number between tasks. Time-series analyses revealed daily rhythms in peptide release in both nurses and foragers. Preliminary studies with Scaptotrigona postica workers were contrasting, as compared to the foragers, POP nurses present attenuated locomotor rhythms, lower clock gene expression levels, and fewer PDF-positive neurons. Overall, circadian rhythms vary among stingless bee species and differ from honey bees, apparently associated with the work load placed on the nurse bees.

Dealing with the dead: an integrative approach to decode necrophoresis in ants

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In social species, individuals inevitably encounter dead group members, whose unattended corpses can rapidly become sources of disease outbreaks. Social insects have evolved stereotyped hygienic responses to dead nestmates that help prevent disease outbreaks and maintain colony health. This includes necrophoresis, sometimes referred to as “undertaking” or “corpse management,” is the active removal of dead colony members from the nest. It is a crucial innate hygienic behaviour of social insects, yet its chemosensory and neuronal underpinnings remain poorly understood. The clonal raider ant Ooceraea biroi, which possesses an expanded repertoire of olfactory receptors and relies heavily on olfaction as in most ants, also offers experimental control over group composition (e.g. number, age, and genotype of workers and brood) to investigate how different factors and mechanisms shape collective behaviours. Here, we integrated behavioural assays, chemical profiling, and neural imaging (in vivo calcium imaging) to elucidate the chemosensory and neuronal bases underlying necrophoresis. We observed O. biroi exhibits robust necrophoresis and its propensity differed by social context, such as the colony cycle phase. Chemical analyses of carcass extracts revealed quantitative increases in conserved necromones, which are fatty acids, in ant carcasses. Using in vivo calcium imaging, we quantified the temporal dynamics and spatial patterning of odour representations in the antennal lobe in response to various candidate necromones, and how it varies with colony cycle phase. By linking behavioural, chemical, and neural processes, this study provides insight into the mechanism of collective disease management.

Global peptidergic rewiring underlying reproductive role transition in ants

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Ant queens exhibit remarkable phenotypic plasticity based on reproductive status: inseminated queens are long-lived, nest-bound egg-layers, while un-inseminated gynes are short-lived and gradually display worker-like foraging behaviors. Yet, how their brains are molecularly and cellularly remodeled to orchestrate these profound physiological and behavioral shifts remains largely unknown. In this study, we constructed a dynamic single-cell transcriptomic atlas of pharaoh ant brains, profiling gynes and age-matched queens across multiple adult stages, from day 1, 5, 10, 15, 30, to day 60. We provide a comprehensive annotation of brain cell clusters, with an emphasis on characterizing the gene expression dynamics and intercellular communication of the whole-brain peptidergic system. We find that the peptidergic system is globally activated in aged gynes compared to queens, marked by widespread upregulation of peptidergic genes and increased abundance of peptidergic cells. A key exception is the Ilp2 cluster, which remains persistently active in queens but repressed in gynes. This gyne-biased peptidergic hyperactivity is linked to accelerated aging and the expression of worker-like exploratory and foraging behaviors, whereas queen-enriched Ilp2 signaling supports longevity and fecundity. These shifts involve extensive remodeling of neuro-neuronal and neuro-glial communication circuits and respond to juvenile hormone and ecdysteroid pathways. Notably, several core peptide genes—including Ilp2, CAPA, Prohormone2, TK, Dh31, and AstC—are evolutionarily co-opted for reproductive division of labor across diverse social insect lineages. Together, our results establish peptidergic rewiring as a fundamental mechanism underlying reproductive plasticity in social insects, shedding light on the neural substrates of social evolution.

Functional Insights into Osiris-Mediated Caste Differentiation in Harvester Ants

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The Osiris gene family is unique to insects and plays a critical role in development, including wing formation, ovary maturation, and the development of multiple sensory organs. The high degree of conservation in their genomic organization, combined with tightly regulated, stage-specific expression patterns, suggests that Osiris genes are key regulators of insect evolution. Notably, several Osiris genes have been implicated in organ systems that distinguish castes in eusocial insects such as ants. In ant colonies, queens develop wings for nuptial flight and fully matured ovaries for reproduction, whereas workers remain wingless with reduced ovarian development. Although specific Osiris genes have been associated with these traits, the relationship between their differential expression and caste-specific organ development remains poorly understood. Here, we investigate the functional role of Osiris genes in caste determination using an RNA interference (RNAi)–based approach in the harvester ant Pogonomyrmex barbatus. We systematically knocked down selected Osiris genes across multiple developmental stages, from larval to pupal transitions, and assessed resulting morphological and behavioral phenotypes. To determine how the functions of Osiris genes change between social and non-social insects, we also conducted parallel functional validation in the non-social beetle Tribolium castaneum. By integrating developmental, phenotypic, and comparative data, we aim to elucidate the regulatory roles of Osiris genes in caste-specific development and how their functions have diversified with the evolution of insect sociality. Ultimately, our findings will provide new insights into the genetic mechanisms underlying caste differentiation and the broader evolutionary significance of the Osiris gene family.

Honest bees dance more and gain confidence over time

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We investigated whether honey bee (Apis mellifera) recruits assess the reliability of waggle dance communication, and if dancers can gauge their own accuracy. Free-flying bees visited a feeder, and during the “learning phase” three personalities were imposed upon a focal dancer and evaluated during the “test phase”. Recruits following “honest” focal dancers received the advertised nectar at the feeder. “Liar” personality focal dancers advertised a nectar feeder that was available only to her. Recruits following “unverified” focal dancers were caught at the feeder for the remainder of the experiment to eliminate feedback. The focal dancer, for all personalities, danced for one feeder, and was later moved to a second feeder location to test the effects of the imposed personality on recruitment. Recruits in the test stage were more likely to follow, and attended more circuits performed by “honest” dancers, than by dancers that provided unverified or inaccurate information. “Honest” focal bees increased their recruitment effort by performing more circuits over time when advertising the second food source, as compared to those dancers who provided unverified or inaccurate reports. The confidence increase in honest dancers indicates an ability to assess the reliability of their own signal and provides a mechanism for evaluation for followers. “Liars” danced for the same duration and number of circuits per dance as “unverified” dancers. The effects were positive in honest experiments but not negative in liars. We provide evidence of the strength of the waggle dance as an autocatalytic reinforcement of useful information.

Effects of a Juvenile Hormone Analogue (JHA) on larval development and intercaste formation in Ooceraea biroi.

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In social insects, eusocial organization is characterized by the presence of distinct castes, typically a reproductive caste (queens) and non-reproductive castes (workers), which differ in morphology, physiology, and behavior. Caste fate is determined during embryonic or larval development, yet despite extensive research on adult caste differences, the developmental mechanisms and stimuli that drive caste differentiation remain incompletely understood.

In the clonal raider ant Ooceraea biroi, caste differentiation is reduced. Colonies are comprised of only workers exhibiting a cyclic reproductive strategy in which every individual reproduces and subsequently cares for the larvae until they reach adulthood, at which point the cycle is repeated. Nevertheless, colonies consistently contain a small proportion (~5%) of intercaste individuals, characterized by enhanced reproductive behavior and potential relative to their nestmates. Previous studies have shown that intercaste frequency increases under enhanced larval feeding, suggesting a developmental plasticity regulated by yet-unknown molecular and hormonal pathways. However, the juvenile hormone (JH) pathway may be involved, as increased levels of JH have been associated with reproductive or queen-like traits, suggesting a role in caste differentiation.

Here, we investigate the role of JH in this process by treating O. biroi larvae with methoprene, a juvenile hormone analog, during early and late larval instars to explore whether increased hormonal stimulation leads to an increase in intercaste individuals. This work explores the involvement of JH in caste differentiation as well as its effects during different larval instars.

Characterization of Dopaminergic and Octopaminergic Neurons in the Brain of the Red Harvester Ant

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Ants often display temporal polyethism or age-related task specialization. Young workers primarily nurse indoors, while matures forage outside the nest. Dopamine and octopamine are biogenic amines that modulate the function of specific neural circuits and may promote this behavioral transition. Yet, the anatomical description of aminergic neurons remains poorly studied.

In this work, we located dopaminergic and octopaminergic neurons in the brain using HCR RNA fluorescent in situ hybridization, by locating the mRNAs for the synthesis enzymes tyrosine hydroxylase and tyramine beta hydroxylase, respectively.

We found both types of aminergic neurons in the protocerebrum and subesophageal zone of the ant brain. In addition, we detected tyrosine hydroxylase mRNA in the optic lobes, whereas octopaminergic neurons were present in the antennal lobes.

Neurons producing dopamine and octopamine are thus located in neuropils involved in sensory processing, multimodal integration, and social behavior. This anatomical mapping of both aminergic systems provides a solid foundation for further studies on the modulation of social behavior.

Sex-specific caste development in termites is manipulated by endoparasitic flies

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Parasites manipulating with natural regulation of host's developmental processes provide a underused system for study of ontogenetic plasticity. Fly maggots from two unrelated families, Verticia fasciventris (Calliphoridae) and Misotermes mindeni (Phoridae), develop inside of Macrotermes termite heads and induce phenotypic and behavioral changes in the hosts. We discovered that both parasite species convergently redirect the ontogenetic development of either termite sex towards a large-headed phenotype that resembles female soldier caste. X-ray microtomography of parasitized and non-parasitized termites revealed that both parasitoid species deplete non-vital host head tissues and preserve vital nervous tissues. This tissue-selectivity is presumably achieved via adaptation of the maggot cephaloskeleton and the endopeptidase cocktail that is abundantly expressed throughout the maggot development. Our results reveal that host's ontogenetic plasticity is a convergently exploitable vulnerability, and we postulate it is a candidate factor promoting evolution of manipulative parasitic strategies. Disturbance of natural ontogenetic processes in social insect via parasitic interference provides a novel methodological approach to study the caste regulatory mechanisms.

Dynamic tissue- and caste-specific genomic imprinting in the ant Diacamma cf. indicum: implications for kinship and sexual antagonism theories

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Genomic imprinting—the differential expression of alleles based on their parental origin—provides a unique framework for evaluating the evolutionary drivers of social insect biology. Given their kinship-based social structures and sex-specific dispersal patterns, social insects allow for the simultaneous testing of the Kinship and Sexual Antagonism theories. This study examines parent-of-origin effects in allelic expression during adult caste differentiation in the Japanese queenless ant, Diacamma cf. indicum. By analyzing transcriptomes across various tissues including the brain, midleg, and the caste-determining gemma, we identified highly dynamic imprinting patterns. A pervasive maternal bias was observed across most adult tissues, a finding consistent with Sexual Antagonism theory under conditions of female-biased philopatry. In contrast, a localized paternal bias emerged in tissues associated with altruistic caste fate, supporting Kinship theory predictions for singly-mated Hymenoptera. These results suggest that genomic imprinting is not a static genomic feature but is instead a plastic, tissue-specific phenomenon shaped by multiple, non-exclusive selective pressures acting across different developmental stages and functional traits.

The molecular mechanisms of reverse brain plasticity in the ant Harpegnathos saltator

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Phenotypic plasticity enables organisms to adapt to dynamic environments by expressing alternative phenotypes from a shared genome, likely through the involvement of epigenetic mechanisms. Typically these alternative phenotypes are most noticeable when comparing states before and after key transitions during development and throughout the organisms life cycle, particularly in response to environmental or social cues. In the Jerdon's jumping ant, Harpegnathos saltator, adult workers can acquire a queen-like phenotype and become reproductive gamergates, a transition accompanied by substantial changes in both behaviour, reproductive physiology, and ageing. Previous work showed that this transition in caste identity and behaviour requires plastic changes in the cellular and molecular composition of their brains. Our current study investigates the limits of this plasticity by exploring whether, and to what extend these changes are reversible in adulthood. We removed all the workers from well-established colonies, leaving the gamergates without the work force. This setup induces a new dominance tournament to re-establish social hierarchies. Gamergates who lost these tournaments reverted to a worker-like phenotype, exhibiting changes in behaviour, ovarian status, and transcriptional profiles of key genes such as Kruppel-homolog-1 and Corazonin. Interestingly, we also observed reciprocal changes in this worker-less gamergates, indicating that the neuroepigenetic state of these dominant reproductive is in part maintained by external social stimuli originating from the presence of workers. These findings demonstrate that lack of the worker force can induce reversals in brain plasticity and behaviour in Harpegnathos, further expanding our understanding of the conditions under which phenotypic plasticity can be reversible

Dominance behaviour regulates division of labour in different ways in two congeneric sympatric species of social wasps

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Division of labour is a defining characteristic of eusocial insects. First, there is a division of reproductive labour between fertile queens (and kings) and sterile workers. Then there is the division of non-reproductive labour between intranidal and extranidal workers. Finally, there must be processes regulating the day-to-day and even hour-to-hour activities of both intranidal and extranidal workers. How does a forager know when to forage, what to bring, and how much? We have investigated such questions in the primitively eusocial wasps Ropalidia marginata and Ropalidia cyathiformis. In R. marginata, the division of both reproductive and non-reproductive labour emerges spontaneously in groups of two and three wasps, respectively, and both are mediated by dominance behaviour shown by the queen and the intranidal worker, respectively. In mature colonies, the queen's reproductive monopoly is mediated by pheromones, while intranidal activities such as foraging and feeding larvae are regulated by a process of decentralised self-organization mediated by worker dominance behaviour. In R. cyathiformis, on the other hand, reproductive monopoly appears to be mediated by the queen's and the potential queen' dominance behaviour, while non-reproductive activities, such as foraging and feeding larvae, are self-regulated by individual workers. The presence of pheromonal regulation of worker reproduction and decentralized self-organization of non-reproductive activities in R. marginata and their absence in R. cyathiformis suggest these two congeneric, sympatric species have achieved different levels of sophistication in their social organization. Their comparative study, therefore, promises rich dividends for our understanding of the evolution of social behaviour.

From Individuals to Groups: Metabolic rate as a driver of intra- and inter-specific variation in honeybees.

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The metabolic rate (MR) of an organism, by shaping energy acquisition and allocation, has been proposed as a fundamental driver of behavioral and life-history variation. In social insects, variation in MR has the potential to link individual physiology to behavior differences and colony-level performance, however, its role in a social insect context remains poorly understood. Using honeybees as a model system, we investigate how intra- and interspecific variation in MR influences individual behavior, performance, and colony function. In Apis mellifera, we use a marker-assisted selection breeding program, based on “slow” and “fast” malate dehydrogenase alleles, to generate genetic lines with low and high MR. Tracking lifetime behavioral and life-history traits in a common garden experiment, we demonstrate that MR drives consistent differences in individual activity and life-history. Flight mill and load-carrying assays further reveal MR dependent differences in flight performance and energetic capacity. To determine how these individual differences scale to the group level, we constructed colonies composed of distinct MR genotypes and quantified multiple metrics of colony performance, revealing that physiological variation among workers translates to differences in collective function. Finally, we extend this framework comparatively by assessing flight performance across Asian honeybee species (A. dorsata, A. florea, and A. cerana), providing insight into how evolutionary divergence has shaped MR and associated traits. Our results demonstrate that metabolic rate is a key physiological mechanism underlying individual and colony-level performance, highlighting its central role in the evolution and division of labor in social insects.

SYMPOSIUM 02 · New frontiers in the study of division of labour in social insects
ORAL · Wed 19 Aug · 15:15 · K6 · Session 38 · Abstract ID 149487

Spreading dynamics in clonal raider ant interaction networks

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The structure of interaction networks is theoretically predicted to affect spreading dynamics in social groups, including disease spread. However, few systems afford the degree of experimental control required to empirically test the link between network structure and pathogen spread.

The problem is alleviated in the clonal raider ant Ooceraea biroi, a queenless species in which workers reproduce synchronously and asexually. This unusual biology makes it possible to precisely control and replicate several colony traits that are expected to affect social network structure, including colony size, genetic and demographic structure. Here, we investigate the effect of colony genetic and demographic structure on network structure and disease spread.

Specifically, we use automated tracking to measure contact networks in clonal raider ant colonies with controlled variation in age and genetic composition. We show how these factors affect network structure, and in turn, predicted disease spread, and compare predictions with empirically measured spread of entomopathogenic fungus spores. This work provides the first step towards experimentally testing predictions from theoretical epidemiology and bridging the gap between simulated and real-world epidemics.

Do random variations drive inactivity in social groups?

Raphaël Jeanson
CNRS

A key feature of the ecological success of social insects is their division of labor, where each member fulfills a specific role, contributing to the colony's overall productivity. However, observations reveal that a significant portion of workers—sometimes more than half—remain idle. While multiple hypotheses have been proposed to explain this inactivity, none have achieved consensus. The expression of task specialization leverages variations among individuals, which are largely influenced by genetic factors outside the colony's control. As a result, individuals may also differ in the efficiency with which they perform tasks. This raises the hypothesis that colonies might produce a surplus of individuals to selectively recruit only the most efficient workers, despite the costs associated with producing and maintaining inactive members. To explore this idea, we have developed a model to explore the conditions under which variations in the scaling of worker production and maintenance costs, as well as activity costs, allow colonies to maintain a fraction of inactive workers. We simulated worker performance using different random distributions to reflect the natural variability in efficiency. Our findings suggest that the inactivity of a fraction of workers can actually benefit the colony across a broad range of conditions, provided it enables the selection of the most efficient individuals. In decentralized systems like insect societies, inactivity may reflect an inevitable outcome of the random processes involved in producing workers with unpredictable performance levels.

Molecular and cellular basis of worker-soldier polymorphic Carebara ants

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Division of labor is an important evolutionary innovation underlying the ecological success of social insects. In worker-polymorphic ants, non-reproductive individuals further differentiate into workers and soldiers that exhibit pronounced differences in morphology, physiology, and behavior, yet the regulatory basis of this behavioral specialization remains poorly understood. Carebara is a hyperdiverse ant genus encompassing species span the spectrum of worker polymorphism, from monomorphic to discrete, and continuous polymorphism. Here, we investigated worker–soldier division of labor in four Carebara species by integrating behavioral analyses with whole-body transcriptomics and brain single-cell transcriptomics. Whole-body RNA sequencing revealed consistent neuro–muscular differentiation between workers and soldiers in four species, with worker-biased expression of genes associated with synaptic signaling and soldier-biased expression of muscle-related genes. Single-cell analysis uncovered systematic caste-associated biases in brain cell-type composition, with soldiers exhibiting higher proportions of glia and workers enriched for neuron, which may contribute to behavioral differentiation. Additionally, single-cell gene co-expression network analysis identified a candidate gene that may regulate the behavior through modulation of hormonal level in the brain. Together, our result show that worker-soldier division of labor is associated with coordinated changes in gene expression, brain cellular composition and gene networks, offering insights into the regulation of social behavior.

SYMPOSIUM 02 · New frontiers in the study of division of labour in social insects
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Expanding the concept of division of labor: from social cooperation to levels of complexity

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Division of labor is a fundamental component of social organization across groups, and across levels of complexity. Studying division of labor in social insects can be frustrating, however, because of how narrowly the concept and terminology tend to be viewed by the broader research world. Thus, I suggest we provide a more expansive view of the phenomenon. If we consider division of labor in phenomenological terms as “outsourcing” of tasks between individuals, its relevance extends far beyond the social insect colony. Helping behavior in cooperatively social groups often manifests as division of labor. By considering it in that framework, we may find a more common language for comparing cooperative sociality in eusocial and non-eusocial societies, both vertebrate and invertebrate. These comparisons also highlight that division of labor varies considerably in its fitness costs and benefits across ecological contexts. Comparing the scaling of superorganism colonies to multicellular entities highlights how size and complexity impact social organization and metabolism and also highlights limitations on those capacities. And comparing division of labor within social groups to that of between-species mutualisms broadens our understanding of the expanse of functional relationships that can be achieved when individuals with very different capacities work together.

SYMPOSIUM 02 · New frontiers in the study of division of labour in social insects
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Role of Minor Workers in Weed Management in Odontotermes obesus

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Different castes in eusocial insects are selected to perform specific tasks. Although this division of labour is most pronounced in reproduction, it can also extend to other activities of the colony. The fungus-growing termite, Odontotermes obesus, has two different kinds of workers-major and minor. It is now known that the major workers can prevent weed invasion of their fungus combs by confining them with fungistatic soil boluses. This complex behaviour is also dependent upon the intensity of weed infection as more severe infestations elicit more complex behaviour than milder ones. However, what role, if any, minor workers play in this weed management remains unknown. In this study we describe the role of minor workers in weed management by challenging them with different intensities of weed-infected fungus combs. We compare the success and efficacy of minor workers with that of the major workers and identify critical roles that these two different castes perform in weed prevention.

SYMPOSIUM 02 · New frontiers in the study of division of labour in social insects
ORAL · Wed 19 Aug · 17:00 · K6 · Session 44 · Abstract ID 148037

Age-dependent energetics and flight performance in bumblebee workers

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Universität Regensburg | UR

Division of labour is key to the global success of social insects. While age-based polyethism is well-documented in the honeybee, the physiological transitions and underlying mechanisms mediating task allocation in its sister taxon, the bumblebee, remain puzzling. To gain a better understanding of energy homeostasis in worker development, we quantified flight performance, lipid reserves, and haemolymph sugar titres (fructose, glucose, and trehalose) across various age classes and body sizes in Bombus terrestris workers. Our findings suggest that age-dependent physiological shifts may be more pronounced than size-based differences in determining a worker’s energetic capacity. These results provide a mechanistic look at how age shapes the physiological traits associated with task performance in bumblebees, highlighting the importance of considering development age in the study of social organisation.

SYMPOSIUM 02 · New frontiers in the study of division of labour in social insects
ORAL · Wed 19 Aug · 17:15 · K6 · Session 44 · Abstract ID 145799

Division of what? Different axes of worker variation and their implications for colony organization

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The classic view of non-reproductive division of labor is that different groups or ‘castes’ of workers specialize on specific tasks, and that these workers then are cognitively, physiologically, or even morphologically optimized for those tasks. Indeed workers often differ along these axes; however, it is frequently not clear whether or how such differences contribute to performance in the tasks specialized on. Instead, in some species, older, bigger, or smarter workers may simply show higher performance in all tasks. If workers differ among a high-low performance continuum instead of belonging to groups optimized for different specific tasks, this has a variety of implications for colony organization. In particular, why would colonies even produce ‘low performance’ workers? We show from a theory perspective and using empirical data that there are several pathways through which this may become adaptive, and why a mix of high and low performance workers may be an optimal strategy.

Busy and Boxed in: How Space and Workload Divide Labor

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Division of labor is often considered a major reason for the success of social insects and other collective systems. In particular, worker specialization in social insect colonies is thought to increase productivity and reduce costs associated with task switching. The emergence of such specialization, however, may depend on the task structure and spatial configuration in the colony. When there are complex tasks, task partitioning may be a way to decrease travel times and error rates in workers. Alternatively, workers may decide to generalize in order to combat interruptions from bottlenecks of item delivery from adjacent task groups. Here, we study how another species of cooperative animal employs both specialization and generalization in tasks of varying complexity with group-level performance goals: humans. We use a complex task environment that nonetheless allows high controllability - the video game ‘Overcooked!’. We asked how task complexity affects a worker's decision on how much to specialize, as well as the presence of team communication. We also study the degree to which spatial constraints enable or prevent task performance and specialization, and how they affect communication. We compare our results on human team organization and performance to that of honey bee colonies and theoretical expectations. Our study allows us to broaden our understanding of the interplay of information and movement constraints in optimal and realized task allocation.

Olfactory sensitivity and division of labor in the honey bee Apis mellifera

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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 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.

Epigenetic regulation of division of labor in workers of the ant Temnothorax longispinosus

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Epigenetic regulation is a key mechanism underlying phenotypic plasticity in social insects, facilitating caste differentiation and reversible responses to environmental and social conditions. Division of labor is a complex phenotype regulated in part by post-translational histone modifications and non-coding RNA expression. miRNAs influence caste determination in termites, honeybees, and ants, and both miRNAs and piRNAs are associated with caste and task specialization in Temnothorax rugatulus. Post-translational histone modifications likewise regulate stress responses, circadian rhythms, and caste-related behaviors across taxa. Manipulation of histone (de)acetylation has demonstrated strong effects in ants, from modulating responses to queen loss in T. rugatulus to altering foraging behavior in Camponotus floridanus and T. longispinosus.

While several studies show epigenetic mechanisms influence caste determination and behavior in social insects, how these processes regulate flexible task allocation remains unexplored. Here, we take a multifaceted approach to examine two epigenetic processes associated with division of labor. Workers of the ant T. longispinosus may switch between nursing and foraging behavior in response to factors such as age and colony need. We show differential enrichment of H3K27ac and H3K27me3 in the brains of nurses and foragers using Cut&Tag and will link these patterns to task-associated gene expression with RNA-seq. We also explore task-specific differences in miRNA expression in the brain and fat body, aiming to predict mRNA targets. Initial results reveal mRNA and miRNA expression differ between nurses and foragers in the brain. Our analyses will provide insight into the epigenetic underpinnings of division of labor in a monomorphic worker caste.

A hybrid pipeline for fast and reliable automated tracking of tagged insects

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Studying division of labor in social insects requires individual tracking in large groups over extended time periods. Fiducial markers enable unambiguous identification of animals but detecting and decoding them in large video datasets is computationally demanding and time intensive.

We present a novel, lightweight, and fully automated pipeline for fast and reliable tracking of marked insects. Our method uses a two-stage approach combining a deep-learning detector (YOLO) with a classical fiducial decoding library (AprilTag). In the first stage, YOLO is trained to detect marker locations within very large video frames. Detected regions are then cropped and assembled into a compact composite image containing only tags. In the second stage, the AprilTag library is applied to decode tag identities.

This hybrid design leverages the strengths of both methods. YOLO is efficient at detecting small tags in high-resolution images. Training requires only a small dataset, which can be generated automatically. AprilTag, while computationally slow on large images, is reliable for decoding. By restricting its use to small, cropped regions, we drastically reduce computational cost and increase speed while preserving accuracy.

We demonstrate the performance of our method by continuously tracking 100 clonal raider ants for seven days at 10 fps using 4512x4512px video recordings. The entire dataset was processed in less than nine hours, compared to approximately a week using classic methods. Our approach provides an efficient and accessible solution for long-term tracking of social insects, opening new possibilities for large-scale behavioral studies and real time tracking for closed loop experiments.

Division of labor in sterile castes of the nasute termite Nasutitermes takasagoensis

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In eusocial insects, non-reproductive division of labor (DOL) is vital for colony maintenance. Termites, especially those in the family Termitidae, are ideal models for studying DOL. Although sterile castes include both sexes, multiple instars, and defense specialists (soldiers), the molecular basis of their DOL remains elusive. We focused on Nasutitermes takasagoensis, whose sterile castes consist of male nasute soldiers and male/female workers (3rd/4th instars). First, to investigate the state of DOL, we compared the caste compositions of termites present at nests and foraging sites. Foraging sites were dominated by soldiers and 4th-instar female workers, while nests had fewer soldiers and more male/female workers. Next, to determine whether individuals of different ages respond differently to soldier pheromone, we conducted behavioral assays using frontal gland secretions. Results revealed potential instar-dependent (3rd vs 4th) behavioral differences in female workers, as well as age-dependent differences within 4th-instar female workers, but not in soldiers. Finally, to identify the molecular basis of DOL, we focused on Vitellogenin (Vg) and foraging, based on previous studies in hymenopterans. All genes showed significantly higher expression in within-nest soldiers compared to outside-nest soldiers. Similarly, one Vg paralog showed higher expression in within-nest 4th-instar female workers. These results suggest that DOL in sterile castes exists among instars and ages, and may be regulated by molecular mechanisms similar to those in hymenopterans. Based on comparative RNA-seq analysis between individuals of different life history characteristics, we provide a comprehensive view of DOL in N. takasagoensis.

Before the snap: early developmental mandible asymmetry during soldier differentiation in Pericapritermes nitobei

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Left-right asymmetry is a fundamental feature of metazoan body organization and is best known from internal organ positioning and organogenesis. Although the molecular mechanisms underlying left–right asymmetry have been extensively studied in a limited number of model organisms, how asymmetric traits have been acquired through developmental modifications during evolution remains poorly understood.

Termites are eusocial insects whose societies consist of distinct castes with specialized morphologies and functions. Among these castes, soldiers exhibit remarkable diversity in head and mandible morphology across species. In several derived termite lineages, soldiers possess strongly curved, left–right asymmetric mandibles and defend their nests by snapping their mandibles. Despite the apparent ecological importance of this asymmetry for colony defense, when and how asymmetric mandibles are generated during soldier differentiation has remained unknown.

Here, we focus on the termite Pericapritermes nitobei, whose soldiers exhibit pronounced left–right asymmetric mandibles, to investigate the developmental origin of this asymmetry. By observing incipient colonies established from alates, we found that the fastest-growing juvenile individuals preferentially differentiated into soldiers. We examined mandible morphology in juveniles, presoldiers, and soldiers using morphological analyses combined with micro-computed tomography (μCT). Our analyses revealed that mandible asymmetry is already prominent at the presoldier stage. Although left–right asymmetry is not pronounced in juvenile mandibles externally, internal observations suggest the presence of differences in tissue organization between left and right mandible. These results suggest that asymmetric mandible formation in termite soldiers originates from early developmental asymmetries in internal mandibular patterning, prior to overt morphological differentiation.

SYMPOSIUM 03 · Stingless bees – emerging models for understanding life history diversity in highly eusocial bees
ORAL · Wed 19 Aug · 10:15 · K6 · Session 32 · Abstract ID 152884

Host-parasite interactions in stingless bees: robber bees and their victims

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Robber bees (e.g., Lestrimelitta) are specialised cleptoparasites that invade nests of other stingless bees and steal stored food resources and nesting material. These raids can have severe consequences for host colonies and have likely selected for a wide range of defensive strategies. This talk examines the behavioural and ecological dynamics of robber–host interactions in Neotropical stingless bees. Particular attention is given to colony defence mechanisms, including specialised entrance guards and coordinated responses to invading robber bees. Variation in guard numbers and defensive behaviour can influence the outcome of robber attacks and the survival of colonies. The costs of defence are also considered, such as potential reductions in foraging activity and other colony functions. These interactions highlight how parasitic pressure may shape the evolution of social organisation, including the emergence of soldier-like worker castes in some stingless bee species. Together, robber–host systems provide a fascinating model for understanding co-evolutionary processes and the ecological drivers of social complexity in insects.

SYMPOSIUM 03 · Stingless bees – emerging models for understanding life history diversity in highly eusocial bees
ORAL · Wed 19 Aug · 10:45 · K6 · Session 32 · Abstract ID 148726

Genomic insights from hybridisation at natural and artificial contact zones of an Australian stingless bee (Tetragonula hockingsi)

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The global proliferation of the honeybee Apis mellifera as a managed pollinator has led to a range of challenges, including the spread of diseases and parasites. Consequently, there is increased interest in the use of non-Apis pollinators. In Australia, eusocial stingless bees (Apidae: Meliponini) are increasingly being utilised for agricultural pollination and hobby beekeeping. However, the increased uptake in keeping and trading stingless bees (including Tetragonula hockingsi) has led to an increased movement of colonies between regions in Australia, with hive movement likely to increase even more in the future. One potential consequence of hive movement between populations is hybridisation, which could have problematic demographic and genetic impacts on both natural and managed populations. Here, we used whole genome sequencing to examine hybridisation between populations of T. hockingsi, a species with genetically distinct populations that are thought to be on the path towards speciation. We compared gene flow between populations at a natural hybrid zone with an artificial, recently established hybrid zone. Despite genetic divergence (particularly of mitochondrial genomes), ongoing hybridisation occurs at both locations. We examined a number of factors potentially limiting hybridisation, including differences in dispersal, climatic adaptations, and genetic incompatibilities. We compared introgression across the genome in the two hybrid zones to identify genes that may be incompatible in hybrids (including those involved in reproduction, environmental sensing, and in the mitochondria) and could be involved in the speciation process in T. hockingsi. These findings have implications for the movement of stingless bees, both in Australia and worldwide.

SYMPOSIUM 03 · Stingless bees – emerging models for understanding life history diversity in highly eusocial bees
ORAL · Wed 19 Aug · 11:00 · K6 · Session 32 · Abstract ID 149789

Queen-associated loci in Melipona bees

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Queen-worker differentiation in bees is mostly environmentally driven: queens and workers share the same genotype, and differential feeding steers development toward a reproductive or non-reproductive fate. The stingless bees of the genus Melipona are an exception to this rule. In these bees, females receive the same diet, and still up to 20-25% of them may become queens, even though most will never reproduce. This overproduction motivated a Mendelian “two-loci” hypothesis for queen determination, but the underlying loci were never found. Further, some authors have questioned this hypothesis and its supporting evidence, as the observed queen ratio is often smaller. We tested the two-loci hypothesis in two Melipona species (M. quadrifasciata and M. scutellaris) through comparative genomic analyses of queens and workers. In both species, we identified two loci consistently associated with caste, providing cross-species support for two major-effect genetic components in queen development. We also found species-specific genomic signatures. In M. scutellaris, the two-loci co-varied with additional single-nucleotide polymorphisms across the genome, consistent with polygenic modifiers affecting trait penetrance, explaining species-specific variation. We also found evidence that DNA methylation could affect the activation/deactivation of caste-associated genes. These results support an integrative gene-by-environment model, in which a queen-favorable genotype is necessary but not sufficient; females carrying this genotype develop as queens only when adequate provisioning triggers methylation shifts and activates the caste-differentiation gene cascade. This framework reconciles prior conflicting results, explains differences observed among Melipona species, and is consistent with caste-conflict evolutionary scenarios when environmental fluctuation is taken into consideration.

SYMPOSIUM 03 · Stingless bees – emerging models for understanding life history diversity in highly eusocial bees
ORAL · Wed 19 Aug · 11:15 · K6 · Session 32 · Abstract ID 150038

Insights into the evolution of eusocial stingless bees from large scale comparative genomics

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Stingless bees are one of the most diverse bees which evolved advanced eusociality and are major tropical pollinators. Yet, insights into their evolution are limited, nonetheless due to the lack of representatives with sequenced genomes. To fill this gap and ultimatively study patterns of evolution related to eusociality, cleptobiosis, stingloss, we generated high quality genome sequence assemblies and annotations for more than 15 species. With representatives sovering the entire tribus, we performed a large scale comparative analysis to uncover a high degree of synteny, expanded and contracted gene families, genes under positive and relaxed selection and unique genomic features such as satellite repeat islands. Our study helps characterize the evolution of stingless bees and eusociality in bees in general.

SYMPOSIUM 03 · Stingless bees – emerging models for understanding life history diversity in highly eusocial bees
ORAL · Wed 19 Aug · 11:30 · K6 · Session 32 · Abstract ID 150046

Evolution and gene family dynamics of cytochrome P450s in stingless bees (Apidae: Meliponini)

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Cytochrome P450 enzymes (CYPs) are a large multigene family involved in endogenous metabolism and xenobiotic detoxification, including plant-derived toxins. Bees are particularly suitable for studying CYP evolution due to their lifelong exposure to flavonoids in pollen and nectar, which are further concentrated in perennial eusocial species during the production of honey and bee bread. Here, we investigated the molecular evolution of CYPs in stingless bees (Meliponini), a diverse group of highly eusocial Neotropical pollinators. We analyzed 17 Meliponini species using a combination of publicly available genomes and newly generated data, identifying a total of 800 CYP sequences, with gene numbers ranging from 39 to 56 per species. These sequences were analyzed together with those from Apis mellifera and Bombus terrestris to infer phylogenetic relationships. We identified 43 minimum instability groups (MIGs) of CYP sequences, six of which showed significant gene family size changes across the phylogeny ($p < 0.05$). These MIGs correspond to the CYP305D subfamily (CYP2 clan) and five CYP3-clan groups, including two CYP6AS, two CYP9 (CYP9R/CYP9S and CYP9Q), and CYP336A. Lestrimelitta limao exhibited the greatest net contraction, affecting seven MIGs, mainly within the CYP6AS and CYP9 subfamilies. These families have been associated with quercetin metabolism, a plant flavonoid frequently found in honey. This contraction suggests a reduced relevance of quercetin metabolism in this cleptobiotic species, which acquires food resources already processed by other bee species. Together, these results advance our understanding of CYP evolution in stingless bees and provide insights into the evolutionary context of cleptobiosis.

SYMPOSIUM 03 · Stingless bees – emerging models for understanding life history diversity in highly eusocial bees
ORAL · Wed 19 Aug · 11:45 · K6 · Session 32 · Abstract ID 145752

Life-history plasticity in stingless bees (Meliponini): a comparative transcriptomics perspective

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Stingless bees are diverse and exhibit interspecific variation in key traits of social organization, including worker aggression and reproductive capacity. To reveal underlying molecular processes related to these traits we generated comparative transcriptomes of brains, ovaries, and fat body for workers of three stingless bee species, Scaptotrigona bipunctata, Melipona quadrifasciata, and Frieseomelitta varia, at four life stages: newly emerged workers, nurses, guards, and foragers. Across all species, brain transcriptomes displayed a conserved ontogenetic pattern. Multivariate analyses (PCA) showed that guards and foragers cluster together, whereas newly emerged bees and nurses form distinct groups. Functional enrichment analyses revealed that early life stages are dominated by cellular maintenance and neural maturation processes, while later stages showed enrichment of pathways related to neuronal signaling, synaptic plasticity, and increased metabolic demand. Notably, the more aggressive species, S. bipunctata, exhibited specific enrichment of genes associated with heat shock proteins and chromatin reorganization in guards, a pattern not observed in the more docile species. Reproductive differences among species were reflected in the ovarian transcriptomes. F. varia workers, which are sterile, show an ovarian expression profile with enrichment in cell death–related processes, indicating an early and pronounced reproductive repression. Species-specific differences were evident in the fat body, a central metabolic and immunity tissue. S. bipunctata workers showed strong enrichment in innate immunity and stimulus-response categories, whereas in F. varia basic metabolic and maintenance processes are dominant. Overall, this study unveils both conserved and species-specific molecular signatures underlying the behavioral and reproductive diversity in stingless bees.

SYMPOSIUM 03 · Stingless bees – emerging models for understanding life history diversity in highly eusocial bees
ORAL · Wed 19 Aug · 12:00 · K6 · Session 32 · Abstract ID 149193

Regulatory genes of worker ovary development in stingless bees with contrasting reproductive capacities

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Caste ovarian specialization and worker sterility are hallmarks of eusociality in bees, yet the developmental mechanisms that generate such divergent reproductive phenotypes across species remain poorly understood. Here, we compare ovary development in two stingless bee species with contrasting worker reproductive potentials: Scaptotrigona bipunctata, which maintains ovarian integrity, and Frieseomelitta varia, which undergoes programmed degeneration. Using an integrated framework that combines structural modeling with ovarian gene-expression profiling by RT-qPCR and tissue-level characterization by confocal microscopy, we show that species-specific ovary fate is primarily determined by differences in apoptotic permissiveness. Our results identify Ark as a central molecular candidate: its expression trajectory appear to shift the threshold for programmed cell death, thereby favoring ovarian maintenance in S. bipunctata and collapse in F. varia. In parallel, we demonstrate that the timing of decapentaplegic expression (of BMP signaling pathway) diverges sharply between species; early decapentaplegic activity in S. bipunctata correlates with germline maintenance, whereas delayed decapentaplegic expression in F. varia coincides with structural disintegration and tissue collapse. Notably, germline markers vasa and tudor persist even during advanced degeneration in F. varia, indicating that the retention of molecular germline identity does not necessarily translate into functional oogenesis. Together, these findings support the view that worker sterility in stingless bees is not a passive outcome of developmental constraint, but an actively regulated process shaped by heterochronic tuning of conserved apoptotic and signaling pathways, providing a mechanistic basis for the evolutionary diversification of reproductive castes.

SYMPOSIUM 03 · Stingless bees – emerging models for understanding life history diversity in highly eusocial bees
POSTER · Abstract ID 148168

Transposable Elements associated with cluster regions in bees with different levels of sociality

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Transposable elements (TE) are genomic repeats found in all eukaryotes that are characterized by their ability to transpose and replicate within host genomes. Here, we are identifying the structural and functional aspects of TE as regulatory factors related to the evolution of social behavior in bees. We examine genomic aspects in different ways, such as the whole genome and cluster regions. We used EDTA and Repeat Masker to: determine the proportion and location of TE associated with Major Royal Jelly Protein (MRJP) cluster and whole genome; describe their diversity and calculate Kimura Distance (K-D) to analyze evolutionary rates. TETrimmer was used to curate all data from EDTA annotations and improve the accuracy of TE bee libraries. We searched for chimeric transcripts using ChimeraTE from transcriptomic data. Our dataset comprises eusocial and solitary bees, totalizing 20 genomes. Among the analyzed species that represent each tribe, we highlight the abundance of TE in Frieseomelitta varia (5%), and Bombus terrestris (43%). We found some species (solitary and social) with TE associated with the MRJP cluster. The K-D analysis indicates that most of the TE (Class II) is recent in both species. Some TE are present in exonic and intronic regions of both species, and these results show that TE are related to gene regions, particularly the MRJP cluster. Our next step is to identify TE that are differentially expressed throughout transcriptomes and to compare their synteny in eusocial and solitary bee genomes.

Queen overproduction and intraspecific reproductive parasitism in Melipona stingless bees

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Queen overproduction is a striking and persistent feature of the neotropical stingless bees from the genus Melipona, in which most newly emerged queens are executed by workers shortly after emergence. Several hypotheses have been proposed to explain the maintenance of this system, including the idea that surviving queens adopt an alternative reproductive strategy by parasitizing unrelated conspecific colonies. This system could serve as a way for these bees to export copies of their genes to unrelated nests which would be completely decoupled from the resource expense of the original nest, serving as a high-risk-high-reward alternative reproductive strategy. Recent genetic work on M. scutellaris has shown that unrelated queens frequently invade and take over colonies following queen loss, suggesting that such events may be more common than previously assumed. Yet, evidence for queen parasitism remains mixed across the genus and is missing for other species such as M. beechei, raising questions about its evolutionary stability. In this research, we focus on what is currently known for two Melipona species native to north-east Brazil, M. subnitida and M. flavolineata, to assess whether queen parasitism also occurs in these systems through a microsatellite marker genetic study. By investigating whether similar processes operate in other Melipona species, we seek to determine whether queen parasitism is a marginal anomaly or a fundamental feature of the genus, with far-reaching consequences for its reproductive biology and ecological success.

SYMPOSIUM 03 · Stingless bees – emerging models for understanding life history diversity in highly eusocial bees
POSTER · Abstract ID 149454

Melipona Diversity and Meliponiculture in the Huallaga River Basin, Peruvian Amazon

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The genus Melipona Illiger 1806 comprises a diversity of stingless bees that have recently gained economic importance through meliponiculture in Latin America, particularly in the Peruvian Amazon. In the context of severe Amazonian forest destruction and associated biodiversity loss, controversy persists regarding the impacts of incipient meliponiculture on the conservation of these species. This study aimed to generate an inventory of Melipona species in the Huallaga River basin in the San Martín region, an ecologically transitional zone between the eastern Andean highlands and the Amazonian lowlands. Based on 771 specimens, we assessed the taxonomic identities of Melipona species using taxonomic keys, comparisons with reference collections, expert consultations, and COI-region molecular analyses. Additionally, we conducted interviews with 25 local meliponiculturists and developed a preliminary map of the geographic distribution of identified diversity. Six species were recognized, four assigned to the subgenus Michmelia, M. (Mouremelia) titania, and M. (Melikerria) grandis. Melipona illota showed the highest concentration of records in dry forest environments, while several morphotypes related to M. eburnea were found in upland rainforest up to 1,461 m a.s.l. Over one-third of the forest has been deforested, leaving natural Melipona colonies sporadic. According to local farmers, 75% of meliponaries housed colonies translocated from life zones beyond the species' natural local distribution. These findings highlight the potential role of meliponiculturists in the conservation of Melipona bees under increasing anthropogenic pressure and underscore the need for regulations to prevent the transfer of species between different ecosystems.

Gut microbiota of the stingless bee Melipona quadrifasciata in a Brazilian Savanna

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Social bees harbor a diverse and specific gut microbiota composed of a small number of conserved core bacteria species that are essential for nutrition, immunity, and host physiology. The composition of this microbiota can be influenced by diet, host genetics, and environmental factors, and some differences occur among the social corbiculate bees (Apini, Bombini, and Meliponini). Stingless bees (tribe Meliponini) represent the most diverse group of eusocial bees and display wide variation in life history traits, making them an important model for host-microbiota studies. Among Meliponini, Melipona represent a disctinct case, as they often lack core bacterial lineages typically associated with other social corbiculate bees, such as Snodgrassella and Gilliamella. In this study, we investigated the gut microbiota composition of Melipona quadrifasciata from colonies located in a campo rupestre area, a unique phytophysiognomy of the Brazilian savanna biome. Our result revealed the presence of the four main bacterial families commonly associated with Melipona microbiota: Acetobacteraceae, Lactobacillaceae, Streptococcaceae, and Bifidobacteriaceae. The dominant genera included Bombella, Commensalibacter, and Lactobacillus, as well as environmentally associated genera such as Floricoccus and Weissella. These bacterial taxa have also been reported in Melipona populations from other Brazilian biomes, indicating a conserved, species-specific core gut microbiota across distinct environmental contexts.

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SYMPOSIUM 03 · Stingless bees – emerging models for understanding life history diversity in highly eusocial bees
POSTER · Abstract ID 149726

Apibotanical resource competition inferred from the physicochemical properties of honeys produced by Apis mellifera and Tetragonisca angustula across two forest landscapes in the Huallaga Valley, Peruvian Amazon

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Honeybees and stingless bees (SB) represent groups of major relevance to humans, albeit with different roles and connotations. In the Peruvian Amazon, Apis mellifera L. 1758 dominates large-scale apicultural production, whereas the stingless bee Tetragonisca angustula (Latreille, 1811) plays a key role in conservation and people subsistence. This study aimed to assess the apibotanical resource use of A. mellifera and T. angustula through its effects on the physicochemical properties of their honeys in two ecosystems within the dry forest of the Huallaga Valley. During the dry season (July–September) 2025, the landscape of two 625-ha polygons was characterized, apibotanical richness was assessed, and honey samples were collected from colonies of A. mellifera and T. angustula for physicochemical analysis. The surveyed areas showed marked discrepancies in primary forest cover (43% versus 67%). Honeys from A. mellifera and T. angustula exhibited highly significant physicochemical differences. Tetragonisca angustula showed high sensitivity to landscape change, with increased variance in honey properties and significant color differences in the more anthropized landscape, in contrast to patterns observed in the predominantly forested area. Despite a moderate level of floristic similarity between zones, the distribution of non-shared species was markedly asymmetric, with the more forested zone harboring a higher number of exclusive species. Overall, these results suggest effects of competition and trophic niche displacement between A. mellifera and T. angustula in ecosystems with limited floral resources, as well as a more equitable partitioning of the trophic niche in areas with higher forest integrity.

SYMPOSIUM 04 · The evolution and regulation of reproductive division of labor across social insects
ORAL · Mon 17 Aug · 10:15 · K8 · Session 4 · Abstract ID 146427

Genome regulation and the evolution of social behavior in bees

Beryl Jones
University of Kentucky

Bees vary extensively in social traits and exhibit repeated gains and losses of sociality, facilitating studies to uncover the genetic mechanisms associated with social evolution. Here, I present recent progress integrating comparative genomics, population genetics, transcriptomics, quantitative assays of enhancer activity, and transcription factor binding site predictions to investigate the role of gene regulatory evolution in bee sociality. Within colonies, I provide evidence that transcriptomic plasticity between castes is regulated by factors also implicated in evolutionary changes across species. Next, by comparing enhancer activity and signatures of selection across populations of a socially flexible species, I identify regulatory loci and gene targets of these loci that are convergently modified during social transitions within this species. Strikingly, genes proximal to these regulatory elements are enriched among gene targets of fast-evolving regulatory loci across divergent social lineages spanning millions of years, suggesting convergence at the level of gene targets of regulatory evolution even when the specific regulatory elements being modified are distinct. Finally, I add to a growing body of evidence that gene regulatory expansions are a consistent signature of social evolution, but find that only a small subset of these expansions are quickly purged when sociality is secondarily lost. Together, these results highlight the critical role gene regulation has played in social evolution and identify promising candidates for uncovering the genetic changes driving sociality in bees.

Juvenile hormone signaling and social complexity in the Hymenoptera

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The seminal discovery that in adults of the highly social honey bee (Apis mellifera), juvenile hormone (JH) regulates age-related division of labor (DoL) but not adult fertility, unlike in most insects, has led to the hypothesis that the evolution of insect sociality involved modifications in JH signaling. Recent studies examining JH functions across the Hymenoptera provide two main insights: First, significant progress in studies of the bumble bee Bombus terrestris, which exhibits an intermediate level of social complexity relative to honey bees, shows that JH regulates multiple tissues involved in reproduction, but not task performance. JH also seems to function as a primary gonadotropin in bees showing solitary lifestyles or low levels of social complexity, highlighting a marked contrast with its roles in honey bees. Second, this association between JH function and social complexity in bees does not generalize to other lineages. The few studies on JH function in highly social stingless bees are not consistent with the honey bee model. In wasps and hornets, JH typically influences both fertility and age-related DoL. There is substantial variability across ant species, offering no consistent model linking JH function to social complexity. We propose that although JH signaling is commonly modified in social insects, the specific changes differ between — and sometimes within — lineages. There is no one model linking JH function to social complexity across major lineages, likely due to changes in related pathways. These modifications enable social insects to circumvent the trade-off between reproduction and maintenance.

The regulation of a simple behavior toolkit is sufficient to produce the social diversity of bees

Daniel Jorge; Sarah Kocher; Corina Tarnita
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Social groups are widespread, yet their organization can vary drastically even among closely related species. To better understand the evolutionary paths that can lead to such diversity, we leverage the extensive variation found in bees. Bees exhibit a broad range of social organizations, from solitary individuals to communal groups and eusocial colonies. The repeated evolution of these forms suggests that the building blocks of sociality may have already been present in solitary ancestors. Because many of the behaviors of queens and workers are subsets of the behavioral repertoire of solitary females, decoupling reproductive and provisioning behaviors has long been proposed as a key step in social evolution. However, if and how a set of ancestral behaviors could give rise to the full range of bee social organizations remains unclear. To address this, we modeled colony development as an emergent property of individual behaviors regulated by social interactions across two behavioral dimensions: social tolerance and reproductive inhibition. By varying the regulation rules of these two behavioral traits, our model reproduces naturally occurring variation in social organization observed across bee species. Variation in social tolerance regulates group size: low social tolerance leads to dispersal, while high social tolerance facilitates group formation. In contrast, reproductive inhibition establishes hierarchy: low inhibition leads to communal nests while high inhibition leads to eusocial or semisocial colonies with a single reproductive. Ultimately, this work provides a simple yet powerful framework for understanding social diversity.

Social insect castes evolved by re-timing ancient, seasonally expressed pathways

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How novel, complex phenotypes like queen and worker castes arise from ancestral developmental toolkits is a fundamental question in evolutionary biology. A leading hypothesis is that such innovations evolve by repurposing pre-existing gene regulatory networks. Here, we provide the first developmental genomic test of this in wasps by comparing a species with fixed morphological castes (Vespula vulgaris) to one without (Polistes dominula). We discovered that the transcriptomic signatures that define queen versus worker development in Vespula are a direct, time-shifted echo of seasonal, nutritionally-plastic gene expression in its primitively social relative. Specifically, gene networks associated with diapause and metabolism in late-stage Polistes larvae are redeployed earlier in the development of queen-destined Vespula larvae. This molecular co-option includes the insulin signalling pathway, a key regulator of caste development that has been convergently recruited across several independent origins of sociality, including in ants and bees. Our findings demonstrate that the evolution of one of the most complex social phenotypes was not due to genetic novelty, but more simple developmental re-timing, where an ancestral program for seasonal plasticity was canalized to create a new and stable division of labour. This reveals a generic route by which ancestral plasticity was refactored to fuel macroevolutionary innovation.

Transcriptomes of solitary and social halictid bees support the ovarian ground plan hypothesis as mechanistic explanation for the evolution of eusociality

Mozhgan Khodadadi[1]; Robert Paxton; Antonella Soro

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Reproductive division of labour, whereby queens specialise in reproduction and workers in brood care, is a defining feature of eusociality. The ovarian ground plan hypothesis (OGPH) proposes that eusociality evolved through the decoupling of reproduction and brood care, thought to be coupled in solitary ancestors, and decoupled between reproductive queens and brood caring workers in eusocial descendants. We tested the OGPH in halictid bees, a socially variable lineage in which eusociality has independently evolved twice, and been lost repeatedly. We compared female brain and fat body transcriptomes of solitary and eusocial species. If the OGPH holds, we expected foundress transcriptomes in eusocial species (in which females establish nests haplometrotically) to be most similar to transcriptomes in solitary species, and intermediate between queens and workers.

In the annual eusocial Lasioglossum malachurum, foundress transcriptomes were indeed intermediate between those of workers and queens, as expected under the premises of the OGPH. In the perennial eusocial Lasioglossum marginatum, foundress and worker transcriptomes clustered together, reflecting the behavioural equivalence of these two phenotypes in this species. In interspecific comparisons, transcriptomes of L. malachurum and L. marginatum foundresses overlapped with the transcriptomes of the ancestrally solitary Nomia melanderi and derived solitary Halictus quadricinctus, again in support of the OPGH, whereby pre-existing maternal traits in solitary ancestors are re-organised through decoupling in eusocial descendants. These results suggest that the social phenotypes of eusocial halictid bees might have emerged through changes in the regulation of ancient genes, highlighting the role of phenotypic plasticity in driving evolutionary innovation.

The genomic basis of termite sociality

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Reproductive division of labour is a hallmark of social insects. Individuals within colonies of social insects have different reproductive potential, where in extreme cases sterile castes (workers, soldiers) have lost the ability to become reproductives. In termites, the reproductive potential is tightly linked to their developmental trajectories: in species with linear development, the “false” workers retain full potential to become other castes, including reproductives. However, in termites with bifurcated development, the “true” workers have limited to no reproductive potential. In this study, we assembled near-chromosome-quality genomes from 29 cockroach and termite species and compared genomes of multiple independent lineages of termites with true workers to look into the genomic changes associated with the reproductive division of labour in termites. We found that the reproductive division of labour, which was proposed to reduce effective population size and therefore reduce selection pressure acting on genes, does not significantly affect selection pressure. Instead, we find relaxed selection predating the emergence of the reproductive division of labour and unaffected by its elaboration in termites. We also find that the evolution of reproductive division of labour in termites was accompanied by gene-family and regulatory changes in distinct sensory and communication functions of termite castes.

Large-scale genomic rearrangements may be the basis for reproductive isolation in the Pogonomyrmex dependent-lineage system

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Chromosomal rearrangements are a potent source of genetic variation. In the dependent-lineage system of the ant Pogonomyrmex barbatus, two apparently reproductively isolated lineages (J1/J2) need to mate with each other to establish functional colonies. Queens from each lineage must mate with males from the other lineage to produce workers, but these hybrid daughters do not reproduce, so the genomes of the two lineages do not recombine. We discovered a large-scale genomic rearrangement that may contribute to the reproductive isolation of the two lineages.

We assembled two almost chromosome-level genome assemblies from one male from each lineage. A comparison of the two genomes revealed multiple translocation mutations that rearranged several large chromosomal segments. Most notably, one large chromosome in J1 (at least 30Mbp) is composed of three large chromosome segments, with one very large gap between them (3Mbp) that shows an extreme level of rearrangement and is enriched with transposon-related genes.

This work provides a first detailed comparison of structural genomic variants between a pair of dependent lineages. Future studies in other dependent-lineage systems will show if this is a general mechanism in the evolution of such unusual reproductive systems. Our findings contribute to a growing understanding of how structural variation drives the evolution of new species and gives rise to reproductive isolation.

Intraspecific variation in recombination landscapes in the California harvester ant, Pogonomyrmex californicus

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Meiotic recombination is fundamental to sexual reproduction, ensuring proper segregation of homologous chromosomes and generating genetic variation that fuels phenotypic diversity. Recombination rates vary widely across taxa, with social Hymenoptera exhibiting the highest rates reported among multicellular animals, yet the causes and evolutionary consequences of this extreme recombination remain unclear.

We analyzed three linkage maps of the California harvester ant, Pogonomyrmex californicus, derived from populations that vary in social organization. Using a newly generated chromosome-level genome assembly, we examined how local recombination rates relate to genome architecture and found strong similarities, indicating species-level regulation of recombination landscapes. These landscapes are shaped by gene and transposable element density, chromatin structure, and selection against ectopic recombination in functionally constrained regions. GO enrichment analyses further revealed biological functions associated with consistently high- and low-recombination regions across maps. Additionally, we found no association between recombination and evolutionary rates, suggesting that recombination does not modulate selection efficacy and calling into question the view that increased recombination facilitated the evolution of sociality via enhanced selection efficiency. Instead, our results suggest that extreme recombination primarily benefits colonies by increasing offspring genetic diversity, providing raw material for socially relevant phenotypic variation.

By integrating linkage maps from multiple populations, our study provides new insights into intraspecific variation in recombination and contributes to a broader understanding of how extreme recombination rates shape genomic and phenotypic evolution in ants and other social insects.

Transgenerational epigenetic inheritance in caste determination of termites

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Reproductive division of labor is a defining feature of social insect societies and is realized through caste-specific developmental pathways. In termites, caste determination has long been regarded as a highly plastic process controlled primarily by social and environmental factors. However, accumulating evidence indicates that parental influences systematically bias offspring caste fate, suggesting the involvement of additional inherited factors beyond environmental regulation. In this presentation, we examine the role of transgenerational epigenetic inheritance in caste determination of termites, focusing on recent theoretical and empirical advances. Studies in the Japanese subterranean termite Reticulitermes speratus demonstrate that parental conditions, such as reproductive phenotype and age, affect offspring caste differentiation independently of DNA sequence variation. In particular, age-dependent changes in sperm DNA methylation provide direct evidence that epigenetic states in gametes can be transmitted across generations and influence developmental trajectories of offspring. These findings indicate that caste fate is shaped not only by the social environment experienced by developing larvae but also by epigenetic information inherited from parents. We argue that transgenerational epigenetic inheritance offers a unifying framework for understanding persistent parental effects on caste differentiation in termites and may help explain how complex reproductive systems, such as asexual queen succession, have evolved. More broadly, this perspective highlights the importance of epigenetic mechanisms in linking phenotypic plasticity with evolutionary processes in social insects, thereby contributing to an expanded view of heredity beyond classical Mendelian genetics.

Gene duplication and caste-specific gene regulation in termite social evolution

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Genomic and transcriptomic analyses of two lower termites (Zootermopsis nevadensis and Reticulitermes speratus) have suggested that gene duplication plays an important role in the evolution of termite sociality (Shigenobu et al. 2022; Fujiwara et al. 2025). To examine whether this pattern also holds in the family Termitidae, which comprises approximately 80% of all described termite species, we analyzed the genome and transcriptome (across castes, sexes, and body parts) of the nasute termite Nasutitermes takasagoensis. Our results revealed that, in this species as well, duplicated genes exhibit more caste-specific expression than single-copy genes. Next, we investigated how the caste-specific expression of duplicated genes is regulated. We examined the expression patterns of two paralogs arranged in tandem on the genome of the beta-glucosidase (BG) gene in three species. In termites, BG has been shown to function not only as a cellulase but also to play a social role in regulating interactions among individuals. RNA-seq based expression analyses revealed that these two paralogs were highly expressed in queens and soldiers, respectively. Furthermore, ATAC-seq analysis of tissues in which these genes were expressed in Z. nevadensis (the queen ovarian accessory glands and soldier mandibular glands) revealed distinct differences in the open chromatin regions upstream of each paralog. Finally, we examined transcription factors that show caste-specific expression conserved across species and discuss the importance of gene duplication in termite evolution.

lncRNAs contribute to caste differentiation as a regulatory layer in ants

Guo Ding; Fuqiang Lin; Jixuan Zheng; Weiwei Liu; Guojie Zhang

Caste differentiation in ants represents a major evolutionary transition and provides a unique model for studying developmental mechanisms underlying division of labor. Genetically identical individuals follow divergent epigenetically-regulated developmental trajectories that generate distinct morphologies and behaviors. While long non-coding RNAs (lncRNAs) are emerging as key epigenetic regulators across diverse biological systems, their specific contributions to caste development in social insects remain largely unexplored. Here, we conducted comprehensive transcriptomic analyses across major developmental stages of two evolutionarily and ecologically distinct ants Monomorium pharaonis and Acromyrmex echinatior, identifying over 10,000 lncRNAs. We demonstrate that lncRNAs exhibit dynamic, caste-specific expression patterns throughout development. We also identified a subset of lncRNAs displaying canalized expression patterns, characterized by progressively increasing caste bias and decreasing within-caste variation as development proceeds. Co-expression analyses revealed that canalized lncRNAs are functionally linked to canalized protein-coding genes, which are crucial regulators for caste differentiation. These canalized lncRNAs show striking tissue-specific enrichment consistent with canalized protein-coding genes. Functional validation through RNA interference revealed that canalized lncRNAs directly regulate caste-specific traits. Furthermore, juvenile hormone treatment capable of redirecting worker lncRNA expression profiles toward gyne-like patterns. These changes mirrored the expression shifts and tissue specificity previously observed in JH-responsive protein-coding genes . This appears to functionally connect lncRNA regulation to the well-established hormonal pathways controlling caste fate. Our findings thus establish lncRNAs as active architects of caste differentiation in social insects, demonstrating that these rapidly-evolving regulatory molecules contribute to the evolution and maintenance of social phenotypes through tissue-specific regulation of caste-associated developmental programs.

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The evolution of queen-worker dimorphism in ants

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Queen-worker dimorphism varies dramatically across ants, ranging from nonexistent or weak dimorphism to very strong dimorphism. Many questions remain unanswered about how such queen-worker dimorphism has evolved: to what degree are queen and worker traits evolutionarily integrated, and hence constrained to evolve independently? Did phenotypic evolution of queen or worker phenotypes drive most of ant morphological evolution? How has the allometric relationship between body size and caste-related traits evolved? I will discuss recent work from my lab investigating these questions across ants.

Evolution of social parasitism in the leaf-cutting ants

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Social parasitism is a form of brood parasitism in which a parasitic species depends on its host's social organization for survival and reproduction. In ants, social parasitism is particularly intriguing because social parasites evolved repeatedly throughout the ant tree of life, and both parasite and host coexist in a permanent, obligate relationship, which raises questions about the repeated convergent evolution of these highly specialized species interactions. To test competing evolutionary hypotheses about social parasite evolution, we studied Neotropical leaf-cutting ants, because at least five inquiline social parasite species are known in the group, each exhibiting a mosaic of morphological, behavioral, and life-history traits. To unravel the speciation mechanisms of the social parasite species, we reconstructed a comprehensive phylogeny of the leaf-cutting ants, including a thorough sampling of host and parasite populations, using Ultraconserved Elements (UCE) as molecular markers. This phylogenomic framework allowed us to test competing hypotheses regarding the origin and evolution of social parasitism. We tested whether social parasite species speciated in direct sympatry from their hosts via the intra-specific route of social parasite evolution, or whether they speciated in allopatry via the inter-specific route. Our results suggest that social parasitism evolved at least three times in leaf-cutting ants, with both sympatric and allopatric speciation contributing to the diversity of social parasitism. Our findings that allopatric speciation also contributes to parasite divergence emphasize the diversity of convergent evolutionary pathways resulting in highly similar parasitic life histories.

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Evolution of sex chromosomes and chromosomal chains in termites

Ann Kathrin Huylmans
Johannes Gutenberg-University Mainz

In contrast to eusocial hymenopterans, sex in termites is determined via XX/XY sex chromosomes and both sexes are usually present in the different castes. In addition to this, in many species of termites chains of multiple chromosomes exist during male meiosis. These meiotic chains contain the sex chromosomes and are thought to effectively transform linked autosomes into neo-sex chromosomes. The presence and number of chromosomes in these meiotic chains can vary quite drastically between and even within species. We here show that termite sex chromosomes likely evolved via sex chromosome turnover from a X0 karyotype in the ancestral roaches and that different termite species differ quite strongly in the degree of sex chromosome differentiation. Especially interesting are European species where we can study early patterns of differentiation and within-species diversity of male meiotic chains.

Decoding the building blocks of social dominance in queenless bumble bee colonies (Bombus impatiens)

Ian Traniello; Scott Wolf; Sarthok Rahman; Andrew Webb; Eli Wyman; Sarah Kocher
Princeton University

Queenless bumble bee workers (Bombus impatiens) form dominance hierarchies in which individuals compete to activate their ovaries and monopolize egg-laying behaviors. Latent behavioral dynamics within these “orphan” colonies facilitate the rapid emergence of reproductive division of labor, a hallmark of all insect societies. However, the behavioral and molecular mechanisms that drive the formation of this organizational strategy remain largely unknown. We performed automated, high-throughput tracking of dozens of queenless bumble bee colonies and leveraged machine vision to decode behavioral features associated with hierarchy structure and formation. We show that low-dimensional social and kinematic behaviors are highly predictive of higher-order social network properties, some of which predict dominance rank days before ovary development begins. To identify the neurogenomic correlates of dominance, we combined RNA- and ATAC-Sequencing to identify signatures of gene expression and regulation in the brain. We then aligned these molecular signatures with queen and worker spatial transcriptomic atlases to determine if the brain of a dominant worker recapitulates the neurogenomic landscape of an anatomically distinct queen or represents a distinct state. Taken together, our findings provide a mechanistic framework for understanding the behavioral and molecular building blocks that support the organization of social life.

Pairwise social interactions and social flexibility in the sweat bee, Lasioglossum baleicum

Michelle L. White[1]; Scott W. Wolf[2]; Kennedy S. Omufwoko[3]; Joanna D. Shoubaki[4]; Eli S. Wyman[1]; Andrew E. Webb[5]; Sarah D. Kocher[5]

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Pairwise interactions among conspecifics represent the “building blocks” of social groups. Interactions between non-social individuals can often be antagonistic or aggressive, but individuals living in social groups often display a mix of both aggressive and affiliative interactions. For example, individuals living in social groups frequently coordinate tasks among group members and can often rely on dominance hierarchies to establish and maintain a reproductive division of labor. To identify if and how behavioral interactions vary among social and solitary individuals, we examined differences in fine-scale, pairwise interactions in the socially flexible sweat bee, Lasioglossum baleicum (Hymenoptera: Halictidae). Individuals from a single population can exhibit both eusocial and solitary reproductive strategies, providing a unique opportunity to examine how the behavioral repertoires of social and solitary individuals vary within a single species. We examined L. baleicum across a range of social forms and contexts, including social pairs of social nestmates and social non-nestmates, pairs of solitary individuals, and social-solitary pairs. Our behavioral assays were conducted and filmed in a circular arena that facilitated tracking of fine-scale social interactions as well as individual identity. We used a deep learning platform, NAPS, and an ethogram event-logging software, BORIS, to quantify the behavioral repertoires of individual bees in these pairwise assays. Our results show that body size disparity is a better predictor of pairwise interactions in L. baleicum than caste, with greater disparities resulting in less affiliation, particularly those affiliations that are aggressive, neutral, or avoidant, but not cooperative.

Nutritional specialization and social evolution in woodroaches and termites

Sheng LI

Woodroach biparental-care and termite sibling-altruism evolved from solitary cockroach ancestors following nutritional specialization on nutrient-deficient dead-wood, but the accompanying genomic changes remained unclear. We sequenced eight new Blattodea species showing stepwise contracted genomes. Woodroach brood-rearing remained constrained by deactivated oxidative phosphorylation and peroxisome genes, consistent with slow immature growth. Termites lost key genes mediating sperm motility, corroborating that reproductive division of labor required monogamous colony-founding. They also co-opted many genes from fundamental nutrition-sensitive juvenile hormone, insulin, EGFR and Dpp signaling pathways. Thus, most larvae develop as workers via high energy metabolism early on, while reproductive nymphs highly express energy metabolism genes late in development. These pathways are consistent with obligate dependence on provisioning by specialized workers and feedback loops allowing large homeostatic colonies to evolve.

Caste specialisation of cellular identities in the termite Zootermopsis nevadensis

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Multicellularity is achieved through division of labour among multiple cell types, each adjusting its distinct transcriptional program towards overall body homeostasis. This pattern is reproduced at the societal level in social insects, as each individual belongs to a caste fulfilling distinct tasks towards overall colony homeostasis. How adjustments in cell-type proportions and gene expression allow distinct castes to arise from a single genome is poorly understood. Here, we investigated differential gene expression and composition across cell types and termite castes using whole-body cell atlases constructed via single-nuclei RNA-seq for each caste of Zootermopsis nevadensis. We found that the relative abundance of cell types differs among castes. Caste-restricted cell types included reproductive cells, several royalty-enriched cells, including stem and progenitor cells, and royalty-depleted cells, including neurons and muscle cells. Caste-associated transcriptional plasticity was detected within most cell types. While some genes were specific to one cell type or one caste, others showed dual specialisation and were upregulated in specific sets of cell types of several, often different, specific castes. This study illuminates with unprecedented resolution the complex relationships between division of labour at cellular and organismal levels and reveals the complex expression patterns of some caste-specific genes.

How does early experience determine reproductive hierarchies in clonal Platythyrea punctata ants?

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The reproductive division of labor (DOL) is one of the major evolutionary transitions in the evolution of animal societies. The reproductive DOL is characterized by a strong reproductive skew, whereby one or a few females monopolize reproduction, while the others take care of non-reproductive tasks. In eusocial insects, DOL is shaped by a complex interplay of factors, including age, size, genotype, and social environment. Species where individuals are totipotent often exhibit dominance hierarchies that regulate reproduction. However, the mechanisms underlying these dominance hierarchies remain unclear. The clonal ant Platythyrea punctata provides a unique model to investigate this question. Within a colony of genetically identical workers, a clear reproductive hierarchy forms through aggressive interactions, resulting in a dominant egg-layer and subordinate workers. To identify the intrinsic traits that determine an individual’s rank, we examined young workers from the time of their emergence until hierarchy establishment with a clonemate. We monitored 68 young ants from emergence until hierarchy formation and ovary development. We assessed a range of potential predictors, including physiological and morphological traits, early social behaviors, and behavioral personality. Our analysis revealed that early social behavior (specifically, an individual's nest position during the initial days), was the only significant predictor of future social rank. There was no correlation between social rank and physiological, morphological, or personality measures among these young adults. These findings suggest that clonal colonies

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What Drives the Reproductive Division of Labor in Small Carpenter Bees? A Case Study of Ceratina albosticta

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To understand the origin of eusociality, it is crucial to evaluate reproductive division of labor in simple insect societies and to identify the factors that shape it. At present, the drivers of task specialization in such societies are less well understood than those in complex eusocial systems. For this reason, our study examines how season, colony size, body size, and relatedness influence the division of labor in a simple social species. Small carpenter bees (Ceratina) represent an excellent model for studying these phenomena. Ceratina bees nest in broken sticks, and facultative eusociality occurs in most behaviorally studied species, although social nests are relatively rare. We investigate reproductive division of labor in the North African small carpenter bee Ceratina albosticta, which exhibits a relatively high proportion of social nesting (approximately 20%) and is common in rose plantations. We dissected nests and analyzed the relatedness of colony members in social nests of this species. We tested the influence of multiple factors on reproductive division of labor, including ecological pressures (season), social dynamics (colony size and relatedness), and individual differences (body size and wing wear). Our results suggest that, in all cases, only a single female reproduces within a nest, although the factors leading to reproductive dominance appear to be complex.

Demographic control via brood cannibalism in ants

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Universitat Autònoma de Barcelona (UAB)

Ant societies exhibit a remarkable division of labour between reproductive queens and the mostly sterile worker caste. However, because queens and workers are not clones, this specialization can create divergent evolutionary interests: the optimal allocation of reproductive and non-reproductive castes may differ at the individual and group levels. This caste-fate conflict has played a pivotal role in shaping the evolutionary history of ant societies. In several species, workers are at an advantage when castes are determined by differential feeding. In other species, queens exert control over caste fate by regulating the levels of juvenile hormone deposited in the eggs. Here, we describe a novel mechanism by which workers reclaim control of caste fate by cannibalizing excess sexual brood. This mechanism is especially relevant in polygynous species, where co-nesting queens might attempt to exploit an unrelated worker force to rear a greater share of their sexual offspring. Through hormone treatments and behavioural assays in two supercolonial ant species, Tapinoma darioi and Linepithema humile, we demonstrate that workers can detect and eliminate surplus reproductive larvae before adult emergence. Furthermore, we show that the production of sexuals and the extent of subsequent cannibalism depend on hormone treatment levels. Finally, a cross-fostering experiment reveals that workers selectively cull unrelated sexual larvae at higher rates than their own sisters. Overall, our findings illustrate how control over caste determination has shifted from queens to workers, culminating in a demographic regulation mechanism mediated by worker-driven brood cannibalism that ensures colony-level optimization of caste ratios.

Wings to Ovaries to Behavior: The Role of Wings in the Reproductive Ground Plan

Ian Brush; Srijan Seal; Chris Smith
Utah State University

Reproductive division of labor is the hallmark of eusociality, but reproductive differences in ants

may occur downstream of wing polymorphisms. In this study we test whether differences in the

loss of wing muscle volume in queens regulates behavioral and reproductive differences

between them. In pleometrotic associations, multiple ant queens jointly found a colony, often

leading to reproductive skew and behavioral differentiation. In this study, we investigate the

physiological mechanisms underlying queen division of labor, by examining wing-muscle

resource reallocation to ovary development. The reproductive ground plan hypothesis links

reproductive physiology and behavior in specialization among individuals. We hypothesize that

queens exhibiting accelerated rates of flight muscle histolysis will show enhanced ovarian

activation and assume reproductive dominance, while their partners adopt “worker-like” roles

with reduced fecundity. To test this, paired queens of Tetramorium immigrans were monitored

for behavioral differences, and physiological traits were quantified via MicroCT imaging.

Volumetric wing-muscle decay and oocyte counts provide direct measures of physiological

reinvestment. Microsatellite analysis of the workers produced will be used to assign parentage

and quantify reproductive contribution, enabling genetic validation of observed behavioral

roles. We anticipate that dominant queens will display greater ovary development and produce

more offspring, while subordinate queens will metabolize their flight muscles more slowly and

engage in non-reproductive, “worker-like” tasks. Our results will link the dynamics of wing

muscle loss to reproductive and behavioral division of labor. More broadly, this work will

highlight the importance of wings, and wing polymorphism, in the evolution of cooperation and

sociality

Age, caste, and social context shape ovarian morphology and transcriptomic profiles in red harvester ants

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In most animals, reproduction comes at the cost of longevity, as energy allocated to reproduction reduces resources for somatic maintenance, shortening lifespan and accelerating aging. However, this trade-off seems to be absent in eusocial insects such as ants, where queens can remain highly fertile for decades while non-reproductive workers have dramatically shorter lifespans. Yet, some workers retain rudimentary ovaries, raising questions about latent reproductive potential and how ovarian structure and regulation contribute to reproductive suppression and aging in eusocial systems. Here, we investigated ovarian anatomy, ultrastructure, and gene expression in the red harvester ant Pogonomyrmex barbatus, comparing queens and workers across age and social contexts. Although workers are functionally sterile, both castes possess ovaries. Histological analyses revealed large, yolk-rich oocytes in queens, consistent with active vitellogenesis, whereas worker ovaries showed regression. Ultrastructural analyses showed that queen ovaries exhibit abundant oocyte microvilli, high mitochondrial density in follicular cells, and distinct lipid and vacuolar protein accumulation. In contrast, old workers displayed signs of cellular deterioration, including degraded mitochondria and disrupted nuclear membranes, indicative of ovarian aging. Ovarian development in workers declined with age and was further reduced in queenless conditions. Transcriptomic analyses identified approximately 2,000 caste-specific differentially expressed genes, including pathways related to metabolism, hormonal signaling, and epigenetic regulation. Queenless workers upregulated a fertility-associated gene while downregulating lipid metabolism genes. Together, our results show that age and social context influence ovarian state, highlighting complex regulation of reproductive suppression and offering insight into reproductive senescence in eusocial systems.

Photoperiod and social regulation determine caste fate in the temperate paper wasp

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The reproductive division of labor in temperate paper wasps with annual colony cycles is strongly constrained by seasonality. Reproductive castes (gynes: queen candidates) must overwinter before establishing their own colonies and are therefore thought to perceive seasonal changes through environmental cues such as photoperiod. To clarify the role of photoperiod in adult caste determination, we examined its effects under both isolated conditions and conditions with social interaction among colony members. Our results demonstrated that photoperiod strongly influenced caste fate. Under long-day conditions (light 16 hrs.: dark 8 hrs.), emerged females tended to develop into non-reproductive castes (workers), whereas under short-day conditions (12:12), they became gynes. These findings support the hypothesis that photoperiod serves as a reliable cue for seasonal prediction and plays a critical role in determining caste-specific physiological states. Importantly, this tendency was observed not only in isolated individuals but also under social conditions, indicating that photoperiodic regulation is robust across different contexts. Furthermore, under conditions with social interaction, only a few workers developed ovaries (i.e., reproductive workers). This suggests that worker reproduction is strongly suppressed by colony members, highlighting the importance of social regulation in maintaining reproductive division of labor. Taken together, our study indicates that reproductive division of labor in temperate paper wasps is established through environmental cues, particularly photoperiod, and reinforced by social interactions within colonies. This dual regulation ensures the adaptive timing of caste differentiation in species with annual colony cycles.

Worker reproductive constraints across Temnothorax

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Reproductive division of labor is a hallmark of eusociality which is tightly linked to phenotypic differences between castes. In ants, these differences often manifest as physiologically-mediated limits on the reproductive capabilities of workers, such as the suppression of ovary development. In many ants, these constraints are relaxed in the absence of a queen, but the degree and timing of worker ovarian activation are species-dependent and poorly understood. In my thesis project, I am characterizing reproductive constraints in worker ants by measuring ovary expression and egg viability across a model clade of Temnothorax. Temnothorax is a speciose, highly diverse genus with facultatively sterile workers which readily activate their ovaries when isolated from their queens. By comparing between species of Temnothorax, I also aim to identify how variance in degrees of worker reproductive constraint correlates with differences in life history traits.

Cellular and evolutionary mechanisms of social caste differentiation in the ant brain

Xiaoxu Xu; Guojie Zhang

Brain specialization among individuals within the colony is an important mechanism that contributes to the complex social organization of ants, alongside reproductive specialization. However, the molecular, cellular, and evolutionary mechanisms underlying queen/worker social caste differentiation across species remain poorly understood. To address this, we constructed a comprehensive cross-species single-cell brain atlas by profiling 858 brain samples from 10 ant species, comprising 1,174,303 nuclei, and resolving major neuronal and glial types. This atlas revealed caste-associated shifts in specific cell populations, with large Kenyon cell I (KCI) neurons consistently having higher proportions in workers while optic-lobe (OL) neurons more expand in gynes. These patterns reflect caste-specific behavioral specialization and visual demands, and remarkably conserved across all species studied. Integrating phylogeny, cellular composition and single-cell gene expression profiles, we found that the gyne brains exhibit greater evolutionary conservation than those of workers, enabling quantitative assessment of worker-specific divergence across clades. We further identified a set of genes with conserved caste-biased expression, including candidates related to the extreme longevity of gynes. Together, these findings uncover conserved and divergent cellular architectures underlying caste differentiation and reveal molecular innovations associated with evolution of social complexity in ants. Our work provides a mechanistic framework for understanding how complex social brain organization emerges in superorganisms.

Reproductive differentiation through mutilation is a time bound process in a ponerine ant Diacamma indicum

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Unlike complex insect societies characterised by rigid pre-imaginal caste determination, simple eusocial groups often retain worker totipotency. This strategy often leads to behavioural plasticity in nest members, enabling them to switch castes, but renders colonies inherently susceptible to internal reproductive conflict. In the monomorphic ponerine ant Diacamma indicum, the gamergate (sole reproductive individual) resolves this tension by physically mutilating the thoracic appendage called gemmae of newly eclosed workers, permanently arresting their reproductive potential. However, a critical knowledge gap remains regarding the temporal flexibility of this policing mechanism.

We address this by monitoring interaction dynamics with callows of varying ages (n=44). We found the success of mutilation is strictly time-bound: mutilation was 100% successful within 24 hours of eclosion (1-Day Callow) but failed in 85% of cases involving callows aged 24–48 hours (2- Day Callows). Network analysis revealed that this failure stems from a rapid behavioural shift: while 1-day callows were behaviorally submissive, older callows actively resisted, displaying aggression levels comparable to the gamergate. Our results further demonstrated that this resistance fundamentally altered the colony’s social structure, transforming a simple dyadic interaction into a coalitional conflict that necessitated the recruitment of "helper" workers to assist in suppression. These findings define a narrow, non-negotiable 24-hour window for conflict resolution. We propose that this temporal rigidity represents an evolutionary trade-off, where colony stability relies on the immediate response of the gamergate before developmental shifts render enforcement energetically costly and ineffective.

Modifications in Doublesex characteristics drive termite eusocial evolution

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Unlike their sister group Cryptocercus, termites exhibit a specialized reproductive division of labor. In Cryptocercus, reproductive organs mature in all individuals during development, whereas in termites, gonad development is primarily restricted to reproductives (king and queen). Therefore, an analysis of Doublesex (Dsx), a master regulator of gonad development, is essential for elucidating the molecular basis underpinning the reproductive division of labor. Here, we characterized Dsx in Cryptocercus and various termite species to examine the relationship between Dsx and termite evolution. We found that Dsx characteristics notably differed between Cryptocercus and termites. While Cryptocercus Dsx possessed both a DNA-binding domain (DM) and an oligomerization domain (OD) with sex-specific splicing, an OD was not present in termite Dsx (except in Mastotermes). Moreover, Dsx was expressed only in males, indicating a loss of sex-specific splicing. Dsx characteristics varied within termite lineages, particularly between species with linear and bifurcated developmental pathways. In Zootermopsis nevadensis (linear pathway), Dsx was equally expressed across all male castes, whereas in Reticulitermes speratus (bifurcated pathway), Dsx was highly expressed only in kings. Notably, transcriptome analysis revealed that Z. nevadensis exhibited sex-biased gene expression pattern across all castes, while R. speratus exhibited this pattern only in reproductives. This difference in genome-wide expression patterns is potentially regulated by Dsx, which may play a crucial role in the diversification of caste developmental pathways. Our results suggest that modifications in Dsx characteristics were key factors driving the acquisition of eusociality and the diversification of caste developmental pathways in termites.

From nutrition to reproductive fate: transcriptional programs of ovary differentiation in the honey bee Apis mellifera

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Reproductive division of labor in eusocial insects arises when differential larval nutrition biases female development toward queen or worker ovaries, a process mediated by coordinated changes in gene regulation across development. We analyzed ovary transcriptomes from queens and workers of the honey bee Apis mellifera across four developmental stages (L5F1, L5F3, L5S, prepupae, PP) to resolve the temporal structure of caste-biased gene expression and its organization into coexpression networks. Transcriptomic variation was primarily structured by developmental stage, while caste differences emerged in a strongly stage-dependent manner. Thousands of genes differed between queens and workers at each stage, with the greatest divergence at late development (PP; 2,580 differentially expressed genes). Most caste-biased genes were stage-restricted, indicating that queen and worker ovaries deploy distinct regulatory programs at successive developmental windows rather than relying on a single caste-specific gene set. A smaller core of genes showed consistent caste bias across development, including worker-biased genes associated with metabolism, detoxification, nutrient uptake, and hormone signaling, and queen-biased genes linked to oogenesis, mitochondrial activity, and ribosomal function. Beyond expression magnitude, caste differences extended to developmental dynamics: genes with caste-dependent trajectories partitioned into four major temporal programs, including early and late queen activation, late worker activation, and progressive repression in workers. Coexpression network analysis revealed discrete caste-biased modules enriched for caste-biased genes and highly connected hub genes, nominating candidate regulators of ovary differentiation. Together, these results show that queen and worker ovary divergence in A.mellifera is achieved through coordinated, stage-specific transcriptional programs organized into modular regulatory networks.

Social Evolution in Beetles

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The order Coleoptera is the most species-rich of all animal orders: beetles account for around 40% of all insect species and 25% of all animal species, with hundreds of new species being described every year. Beetles have successfully colonised all terrestrial habitats and display the widest diversity of social systems of any insect. These include simple mother-offspring associations, complex parental care, adult aggregations, larval societies, cooperative brood care, and eusociality.

However, their social interactions are often hidden away: inside burrows, carrion, dung, plant tissues, or under the bark of trees. This cryptic lifestyle means beetles are underrepresented in social evolution literature, especially compared to the charismatic Hymenoptera and Isoptera, whose large colonies are relatively conspicuous. The most recent non-exhaustive review of beetle sociality was published over a decade ago by James Costa in his excellent book, 'The Other Insect Societies'. Since then, entomologists have made new discoveries, expanding our knowledge of the social systems of beetles, including a confirmed case of obligate eusociality in the Platypodinae. Despite this progress, an updated, comprehensive overview of coleopteran sociality is still lacking. In this study, we aim to broaden our perspective on the evolution of social insects and present the ecological drivers of social behaviours in Coleoptera, the most prolific animal order on Earth.

Exogenous farnesol induces nursing behaviour in older workers of the stingless bee Melipona quadrifasciata

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While foraging, stingless bees of the tribe Meliponini may be exposed to farnesol, a plant-derived precursor of juvenile hormone (JH). JH plays a central role in insect development and reproduction, regulating division of labour and caste differentiation in eusocial insects. In Apis mellifera, low doses of farnesol accelerate worker development, increase activity, and upregulate genes involved in JH signalling, whereas higher doses are toxic. Because JH profiles in adult Melipona workers differ from A. mellifera, we hypothesized that Melipona workers would respond differently or show reduced sensitivity to exogenous farnesol. To test this hypothesis, we evaluated the effects of farnesol doses equivalent to those used in A. mellifera on M. quadrifasciata foragers by measuring the following parameters: (i) food consumption over a 72-h period, (ii) survival, and (iii) behavioural metrics associated with extra-nest activity under artificial conditions. Assays included daily food intake, survival, and behavioural analyses at 24, 48, and 72 h using Ethoflow software. Exogenous farnesol did not affect food consumption ($p=0.5$) but significantly reduced worker lifespan ($p=0.0002$). It decreased distance travelled ($p=0.004$), maximum speed ($p=0.0005$), number of fast movements ($p=0.0005$), and mean duration of fast movements ($p=0.0005$), while increasing group interactions ($p=0.01$) and mean turning angle ($p=0.0008$). Together, these results suggest that the collection of farnesol-containing resins by M. quadrifasciata may alter normal colony development. However, in contrast to the exotic species, farnesol appears to promote nursing behaviour in older M. quadrifasciata workers, pointing to a reversed physiological response to this compound.

Identification of the terpene synthase responsible for biosynthesis of the queen pheromone in the Pharaoh ant, Monomorium pharaonis

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Queen pheromones are crucial for reproductive caste regulation in advanced eusocial insects. Secreted by fertile queens, they inform the nestmates of queen's presence, which ultimately allows regulation of the number of reproductives in the nest. Queen pheromones have a wide array of effects on the receivers, ranging from physiological effects on their development and fertility to behavioural effects which result in differential breeding of reproductive phenotypes.

The queens of the pharaoh ant, Monomorium pharaonis, produce a monocyclic diterpene neocembrene in their Dufour's gland. After decades of suspicion that it could function as a queen pheromone, it was only recently confirmed to affect rearing of new queens and males by M. pharaonis workers.

Here, we expound the biosynthesis of neocembrene in M. pharaonis. Drawing on current knowledge on terpene biosynthesis in several insect lineages, where terpene synthases have evolved via duplication and neofunctionalization of isoprenyl diphosphate synthase genes, we searched publicly available sequence data for duplications in isoprenyl diphosphate synthase genes. We identified such multiplication in farnesyl diphosphate synthase genes, some of which were upregulated in abdomens of mated queens. Using recombinant proteins, we showed that one of these, MpFPPS1, converted the terpenoid precursor geranylgeranyl diphosphate to neocembrene in vitro. Thus, MpFPPS1 adds to the list of terpene synthases which have independently evolved from isoprenyl diphosphate genes in multiple insect lineages. We propose that MpFPPS1 represents the enzyme responsible for queen pheromone production in M. pharaonis and we plan to complement our results with upcoming in vivo experiments.

SYMPOSIUM 05 · Life-history evolution in social insects – fertility and ageing
ORAL · Tue 18 Aug · 18:30 · K10 · Session 30 · presented in Symposium 00 · Abstract ID 148919

Effects of colony fusions and relatedness on colony size in the drywood termite Cryptotermes secundus: Theory meets data

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The transition from independent organisms to a cooperating “super-organism” is thought to link individual and colony reproductive success, reducing intracolonial conflict and permitting larger colonies. In the drywood termite Cryptotermes secundus, a species with totipotent workers and low superorganismality, we found the opposite pattern: lower genetic relatedness was linked to greater intracolonial divergence in fitness and it is associated with larger colonies and higher production of dispersing reproductive individuals. We genotyped 268 workers from 27 natural colonies to calculate within-colony relatedness. Both total colony size and the number of nymphs/alates/dealates declined with increasing mean relatedness, the latter significantly. To probe the underlying dynamics, we built an individual-based model of the C. secundus life-cycle. Workers inherit a continuous trait deciding the colony size at which they leave with a 50 % annual probability. Each run is set with a fixed yearly fusion probability at which colonies may fuse and a peaceful-fusion probability, determining whether both royal pairs survive. Fusion probability serves as a proxy for relatedness as colony fusion is a common, natural cause of relatedness to vary within C. secundus colonies. Simulations revealed a step-like increase in both trait and dispersing reproductive individuals once fusion probability exceeded a threshold. Together, the empirical data and simulations show that colony fusion, by lowering relatedness, drives the evolution of optimal colony size and dispersal strategies in C. secundus. Totipotency may be the primary factor behind the unexpected association, thereby challenging the view that reduced kin conflict alone always promotes larger colonies.

SYMPOSIUM 05 · Life-history evolution in social insects – fertility and ageing
ORAL · Wed 19 Aug · 14:30 · K8 · Session 40 · Abstract ID 149470

Social drivers of lifespan extension in a facultatively eusocial bee

Karen Kapheim[1]; Ana Gutiérrez-Zuluaga[1]; Priscila K. F. Santos[1]; Frances K. Hunter[1]; Ren Weinstock[1]; Arthur Matte[2]; William Wcislo[3]; Adria C. LeBoeuf[4]; Nicolas Pichaud[5]

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Social insects seemingly violate the rules of life history theory governing trade-offs between longevity and fecundity: queens are long-lived and highly fecund, while their sisters and daughters that work and neither mate nor reproduce have drastically shorter lifespans. One potential explanation for this phenomenon is the “molecular rewiring” hypothesis that proposes elements of nutrient-sensing and endocrine pathways were decoupled to allow simultaneous investment in lifespan and fecundity. According to the “energetic resources” hypothesis, queens may simultaneously increase investments in both lifespan and fecundity due to the abundance of resources provided by the workers in the colony, increasing their total energy reserves. We tested these two hypotheses in a facultatively eusocial sweat bee, Megalopta genalis, that allows for ecologically relevant manipulation of the social environment. We compared immunity, oxidative stress, mitochondrial function, and gene expression among solitary nesting females and queens of social nests both prior to and after the emergence of offspring, as well as after the experimental removal of workers in social nests. Results provided partial support for both hypotheses and suggested that queen physiology is highly influenced by the presence of workers. We further investigated the mechanisms by which workers influence queen performance by characterizing the proteins present in the trophallactic fluid exchanged between adult queens and workers and experimentally assayed the functional benefits for queens. Together, these experiments provide insights into the early evolutionary history of the processes that led to capabilities of social insect queens that lay thousands of eggs over exaggerated lifespans.

SYMPOSIUM 05 · Life-history evolution in social insects – fertility and ageing
ORAL · Wed 19 Aug · 14:45 · K8 · Session 40 · Abstract ID 149967

Social status, flight activity and DNA damage in large carpenter bees

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In eastern carpenter bees, Xylocopa virginica, females live in small colonies structured around reproductive queues. Primary females monopolize egg-laying, secondaries queue for reproductive opportunities, and tertiaries remain inside their natal nests, postponing reproduction. Primaries and secondaries live about 1 year, whereas tertiaries live about two years. In spring, males defend territories by hovering and chasing rivals, usually dying within a few weeks. These patterns suggest a link between flight activity and lifespan. Flight activity is associated with wing damage, oxidative and thermal stress, and UV exposure; we propose that this causes tissue, cell, and genomic damage that leads to earlier senescence. We will test several hypotheses. H1: In females, flight activity correlates with social roles, so primaries that provision brood should accumulate the most damage and tertiaries that remain inside nests, should accumulate the least. H2: In males, flight activity correlates with territorial success, so more successful males should accumulate more damage. An added wrinkle is that the haploid genomes of males lack “backup” alleles and DNA repair systems that operate effectively in diploid females, so we also predict H3: Males should accumulate genomic damage and senesce faster than females. We employ RNAseq analyses and other techniques to measure a variety of proxy parameters for measuring cellular and genomic damage, such as sequence quality scores, average length of reads, and assembly statistics, and expression levels of stress response genes. We expect that this new model system will provide unique insights linking social behaviour, physiological performance, and genomic quality.

SYMPOSIUM 05 · Life-history evolution in social insects – fertility and ageing
ORAL · Wed 19 Aug · 15:00 · K8 · Session 40 · Abstract ID 149220

Having their cake and eating it too: stressperiments in ants

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Reproductive eusocial insect castes are among the most long-lived insects with lifespans often exceeding decades, while lifespans of non-reproductive workers of the same species rarely exceed 6-12 months. Because caste is typically environmentally and not genetically determined, eusocial insects represent outstanding systems within which to study the still poorly understood process of cellular and organismal aging. Using the ponerine ant H. saltator, we previously showed that adult-inducible reproductive workers are refractory to heat stress relative to their non-reproductive counterparts. Along with dramatically enhanced survival under heat stress, long lived reproductive workers exhibit elevated expression of a suite of chaperone proteins under normal (as well as stress) conditions, suggesting basal up-regulation of the heat shock response pathway to mitigate age-associated proteostatic decline. Here, we take the extremely creative approach of repeating these experiments using multiple other stressors linked to lifespan: oxidative stress, DNA damage, hypoxia, and nutritional stress. For each of these we find considerable differences in transcriptomic stress response as well as survival between reproductive and non-reproductive workers. Further, despite differences in stressors and the molecular regulation of the associated stress response, our data indicate shared upstream regulation via caste-specific engagement of several conserved transcription factors as well as attenuated activation in reproductive workers without stress. Together, our data suggest that caste-specific basal activation of multiple stress response pathways via shared upstream regulation is one component underlying the circumvention of the reproduction:lifespan tradeoff seen in eusocial insects, and will also probably fix all the world’s problems.

Ageing affecting evolution of genes and their expression across tissues in social insects

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When organisms age, the strength of selection against senescence declines, a pattern known as the “selection shadow”. Consequently, genes with old-biased expression show weaker sequence conservation than genes expressed earlier in life in model organisms. Contrary to this expectation, studies in the ant Cardiocondyla obscurior have shown that old-biased genes in queens are under stronger purifying selection than young-biased genes, suggesting a delayed selection shadow and extended health-span in social insect reproductives. Our project will test how sociality affects the selection shadow across tissues in a superorganism. Specifically, we ask: Do social insect queens maintain purifying selection on old-biased genes longer than solitary insects? Does selection weaken earlier in somatic tissues than in the germline? How does selection strength vary among cell-types? For this, we will generate a single-cell RNA-seq data from C. obscurior queens sampled at different ages, and from both somatic and germline tissues. We will derive a selection index linking expression, evolutionary rates and conservation of age-biased genes. Comparative analyses with flies and Caenorhabditis elegans will place queen ageing trajectories in the context of solitary model organisms. We expect that germline tissues will retain the strongest conservation into late life. Our project will elucidate how reproductives sustain strong selection for most of their lifespan, followed by a brief period of senescence. By linking cellular ageing, gene expression, and molecular evolution, we will test how sociality reshapes the selection shadow. A comparative framework will be established linking the reproductive specialization to the evolution of senescence in superorganisms.

H3K9me3-mediated repression of transposable elements linked to long lifespan in the drywood termite, Cryptotermes secundus

Louis Allan Okwaro[1]; Bitao Qiu[2]; Annalisa Izzo[2]; Tanja Vogel[2]; Judith Korb[2]

[1] University of Zurich; [2] University of Freiburg

Transposable elements (TEs) have been associated with ageing in several animal species. In solitary organisms, histone H3 lysine 9 trimethylation (H3K9me3) is associated with the repression of TEs. Social insects show remarkable phenotypic plasticity, with queens and workers differing enormously in lifespan despite having a similar genetic background. In this study, we investigated whether H3K9me3 enrichment varies with age in queens and workers of the drywood termite Cryptotermes secundus, a species in which workers commonly develop into reproductives. To address this question, we analysed chromatin immunoprecipitation sequencing data from head/prothorax tissues of workers and queens of various ages. We found high levels of H3K9me3 enrichment in young queens compared to old queens and workers. Interestingly, old workers also had high levels of the H3K9me3 marks compared to old queens, suggesting a potential robust genomic maintenance mechanism in preparation for becoming reproductives. There was a strong overlap between H3K9me3-enriched sites and TE loci with LINE/RTE-BovB, tRNA-derived TEs, and DNA/TcMAr-Mariner overlapping with H3K9me3 enriched sites in young queens compared with old queens. Importantly, several of the overlapping TEs belonged to young TEs, that recently invaded the genome and that are not constitutively silenced and can be active. Taken together, our results demonstrate that H3K9me3 could play a significant role in regulating TE-activity in C. secundus, thereby contributing to explain termite longevity.

SYMPOSIUM 05 · Life-history evolution in social insects – fertility and ageing
ORAL · Wed 19 Aug · 15:45 · K8 · Session 40 · Abstract ID 145625

Sperm metabolism dynamics during storage in long-lived ant queens

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How queens of social Hymenoptera keep sperm alive for exceptionally long periods (up to 30 years in some species) remains a longstanding puzzle. Known mechanisms supporting sperm viability in the spermatheca include nutritional provisioning and protection against pathogens and oxidative stress. A key hypothesis is that queens achieve long-term sperm preservation by suppressing sperm metabolism, pushing stored sperm into a quiescent state. Yet, despite the major fitness consequences, the dynamics of sperm metabolism in the spermatheca has been investigated only sparingly, and studies have provided only indirect evidence for metabolic suppression.

By combining measurements of ATP content, mitochondrial activity, and ROS levels, we demonstrate a clear and substantial reduction in sperm metabolic activity in the queen spermatheca after mating. Proteomic analyses further highlight molecular pathways underlying this metabolic shift, offering new insight into how queens sustain long-term sperm storage.

SYMPOSIUM 05 · Life-history evolution in social insects – fertility and ageing
ORAL · Wed 19 Aug · 16:00 · K8 · Session 40 · Abstract ID 145750

Slow sperm aging in males of the buff-tailed bumblebee (Bombus terrestris)

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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.

SYMPOSIUM 05 · Life-history evolution in social insects – fertility and ageing
ORAL · Wed 19 Aug · 16:15 · K8 · Session 40 · Abstract ID 146372

The fecundity–longevity trade-off in a clonal eusocial insect: subordinate workers match dominants in reproductive capacity

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Reproductive division of labor (DOL) is key to the ecological success of eusocial insects such as ants, bees and wasps, in which queens reproduce while workers perform non-reproductive tasks. DOL is often associated with a shift in the fecundity-longevity trade-off, with queens outliving non-reproductive workers. In most species, reproductive and non-reproductive individuals differ significantly (e.g., in ontogeny or morphology), which may contribute to this phenomenon. In contrast, in the ant Platythyrea punctata, females are clonally identical and socially dominant workers produce female offspring from unfertilized eggs by thelytokous parthenogenesis. In this study, we investigated whether all workers, i.e. dominants and subordinates, reproduce when given the opportunity. We found that nearly 88% of workers, regardless of social rank, activated their ovaries in isolation. However, fewer subordinates developed functional ovaries, i.e., reproductive ability differs among workers. Reproductively active subordinates matched dominants in egg-laying rate, with no apparent trade-off between fecundity and longevity. Reproductive costs were evident for both workers in isolation, as egg-laying rates declined over time in the absence of supportive workers. These results highlight the complex interplay between reproduction, longevity, and social status in eusocial insects and provide insights into how eusociality has shaped aging and life history evolution.

Caste-specific ageing and age polyethism emerge from the evolution of resource allocation in eusocial insects

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Queens and workers of eusocial insects often have extremely divergent lifespans. How has this intraspecific lifespan variation evolved? Several studies have invoked the disposable soma theory to explain the evolution of caste-specific ageing, which proposes that senescence results from a resource allocation trade-off between maintenance vs. reproduction. A reasonable extension of this theory to social insects is that caste-specific ageing could emerge from a resource allocation trade-off between castes. However, to date no theoretical model has tested this idea. Here, we present an individual-based model for the evolution of ageing in social insects. In our model, queens and workers die when their nutrition level becomes too low. Workers transition from nursing the brood to foraging when their nutrition level declines. The resource allocation of queens and workers evolves: foragers allocate between themselves vs. nurses, nurses between themselves vs. larvae vs. the queen, the queen between herself vs. reproduction. We find that lifespan differences between queens and workers emerge as a consequence of the evolved resource allocation within colonies. Queens obtain large amounts of resources, which liberates them from the trade-off between maintenance vs. reproduction, whereas workers evolve to give resources away to enhance the queen’s reproduction and thereby their indirect fitness. We also observe that age polyethism emerges, where young workers nurse the brood and older workers forage. Overall, our model demonstrates that caste-specific ageing and age-related worker division of labour emerge as a consequence of a common mechanisms, which is how resources evolve to be allocated within colonies.

When evolution makes things worse: coevolution between selfish traits and colony lifespan in social insects

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Social insects construct integrated societies through altruistic behaviors, with the colony serving as the functional unit. However, individual interests do not necessarily align with colony-level productivity, and selfish traits arising from conflicts among individuals can reduce overall colony performance. The evolutionary dynamics of such conflicts are often analyzed using game theory. Yet, when colony-level traits such as colony lifespan are themselves subject to evolution, the payoff structure of the game can change over evolutionary time, making standard game-theoretical approaches inadequate. Here, we present a theoretical analysis of the coevolution between colony lifespan and selfish traits, using queen succession conflicts in termites as a focal biological context. We first examined the evolution of selfish traits under conditions with colony lifespan fixed at different values. In this scenario, longer lifespans promoted the evolution of stronger selfish traits, thereby reducing colony productivity. Consequently, the colony lifespan that maximizes lifetime fitness of colonies became shorter than in cases where selfish traits were absent. In contrast, when colony lifespan and selfish traits were allowed to evolve simultaneously, colony lifespan did not converge to this fitness-maximizing optimum. Instead, it evolved to the same length as in the absence of selfish traits. Subsequently, selfish traits became expressed, producing an evolutionary trajectory that appeared as though the evolution of longer lifespan itself caused a decline in fitness. These results demonstrate that interactions between traits operating at different hierarchical levels—individuals and colonies—can generate complex and counterintuitive evolutionary outcomes.

SYMPOSIUM 05 · Life-history evolution in social insects – fertility and ageing
ORAL · Wed 19 Aug · 17:30 · K8 · Session 46 · Abstract ID 145559

Reproductive and developmental dynamics in Lasioglossum marginatum (Halictidae), a bee with an exceptionally long nesting cycle

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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 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.

Are wound care behaviours key to the ecological success of ants? How saving the injured boosts colony growth.

Erik Frank
Würzburg University

Open wounds represent a significant risk of infection and mortality, driving diverse ant species to evolve sophisticated social wound care strategies. Termite hunting ants employ therapeutic treatments on infected wounds with antimicrobial secretions from the metapleural gland, dramatically reducing mortality. Carpenter ants perform prophylactic limb amputations to halt infection spread. Ants with a simpler social hierarchy and colonies of only a few dozen ants, like Dinoponera, conduct self-wound care using their front legs, while Eciton army ants, with colonies reaching over one million individuals, exhibit “first aid” wound care behaviours near the raiding sites, followed by antimicrobial care inside the bivouac. Over the past 10 years, we have detected diverse social wound care behaviours in 31 species of ants across all major ant lineages. A central-European analysis of ant injury rates across species and populations of thousands of foragers found that injuries (and wound care) are ubiquitous across all tested species, with injury rates for foragers ranging between 5 and 40% in most species. More importantly, theoretical models on the value of wound care behaviours for the colony suggest that its presence can accelerate colony growth rates between 30 and 80%, depending on the species, suggesting that saving the injured has immense fitness benefits. Wound care therefore emerges as a widespread and essential behavioural trait in ants, and its considerable fitness benefits suggest that it may be as crucial to their ecological and evolutionary success as their better-studied altruistic sacrifices.

Molecular causes and consequences of reproductive plasticity in honey bees

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Social insects exhibit pronounced reproductive plasticity between and within castes but the molecular causes and consequences of this plasticity is not yet fully understood. Drawing from several studies in the model Apis mellifera, we will compare molecular patterns that are associated with reproductive activation of queenless worker and reproductive deactivation of swarming queens. The results from these complementary studies will also be connected to differences between castes and social evolution in general.

The effects of urbanization on ant life history

Lia Romanotto; Anna Dornhaus
University of Arizona

Both individuals and species differ in their life history strategies, which are thought to be a syndrome, a set of highly correlated traits which includes but is not limited to lifespan, timing of reproduction, and metabolic rate. Environmental factors are known to impact the evolution and plastic development of life history traits, and urbanization is a known and increasingly common cause of environmental change. Urbanization is in particular thought to correlate with disturbance and microclimatic variables, but it also substantially affects ground substrate and many other environmental factors. Here we investigated which environmental properties of urbanization may most strongly impact ant life history. In particular, we analyze whether the unique combination of environmental factors found in cities may drive a disruption of the life history syndrome, i.e. a disassociation of typically correlated life history traits, within or across species. We use ant forager movement speed as a proxy for individual-level “pace of life,” as it has previously shown to relate to a number of other behavioral and metabolic traits such as “tempo.” We examine the relationship of ant forager movement speed with human population density and the mechanisms that may drive this relationship. We argue that it may be time for a trait-based ecology of ants.

Testing prezygotic reproductive isolation between two sympatric lineages of the leaf-cutting ant Atta laevigata (Smith, 1858)

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Atta laevigata (Smith, 1858), a widespread Neotropical leaf-cutting ant, provides a model for sympatric speciation, as two recognized mitochondrial lineages co-occur in southeastern Brazil and show consistent morphological differences. To test whether reproductive isolation is driven by mating compatibility, leading to predominantly intralineage fertilization, we sequenced a mitochondrial fragment (COI–Leu-tRNA–COII) from sperm stored in the spermathecae of newly mated queens. We estimated haplotype (Hd) and nucleotide (π) diversity, reconstructed Median-Joining haplotype networks, tested demographic expansion using Tajima's D and population dynamics using Bayesian Skyline analyses, and assessed genetic structuring through Analysis of Molecular Variance (AMOVA). Both lineages showed high haplotype and moderate nucleotide diversity, with multiple male haplotypes per queen, indicating polyandry. Lineage I exhibited slightly higher genetic diversity (Hd = 0.95; π = 0.00585) than lineage II (Hd = 0.83; π = 0.00503). Tajima's D was significantly negative in both lineages (lineage I = -2.06, p = 0.018; lineage II = -2.41, p = 0.002), indicating recent demographic expansion. Bayesian Skyline analyses revealed parallel population growth toward the present, with subtle differences in timing and magnitude between lineages. Combined analyses showed extremely strong genetic structuring: AMOVA indicated that 83.8% of variation occurred between lineages, yielding a very high ΦST (ΦST = 0.838, p = 0.001), and haplotype networks revealed two deeply divergent, non-overlapping clusters, with no haplotypes shared between lineages. These results indicate largely independent male genetic pools, supporting strong prezygotic isolation and ongoing sympatric speciation.

Asymmetrical physiological cost of reproduction shapes caste-specific resource allocation in a queenless ant

Yasunari Tanaka[1]; Yusuke Ishizuka[2]; Yu Matsuura[1]; Jilin Pan[2]; **Hiroyuki Shimoji[1]**

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In eusocial insects, queens combine exceptionally high reproductive output with long lifespans, exemplifying a fundamental trade-off in resource allocation. Workers, by contrast, perform non-reproductive tasks such as brood care and foraging, thereby reducing the energetic demands placed on queens. Because queens devote most of their lives to reproduction, this alleviation of energetic costs allows them to live longer while producing large numbers of eggs. Despite this, the physiological specialization of queens differs markedly from that of workers.

Here, we examine the trade-off between reproduction and immunocompetence across castes in the ant Diacamma cf. indicum from Japanese that lacks a morphologically distinct queen caste. First, gamergates (functional queens) exhibited higher expression levels of innate immune genes than workers. Second, to experimentally bias resource allocation toward immune function, gamergates and reproductive workers were subjected to an immune challenge. As a result, expression of the antimicrobial peptide gene Hymenoptaecin increased in gamergates without reducing the expression of reproduction-related genes such as Vitellogenin. In contrast, reproductive workers showed decreased expression of genes associated with reproduction. In addition, we found that gamergates possessed remarkably low fat content, comparable to those of non-reproductive foragers.

Taken together, these results suggest that gamergates can mitigate the trade-off between immunity and reproduction, whereas reproductive workers are constrained by the physiological costs of reproduction.

SYMPOSIUM 06 · From founding to function: early-stage dynamics in the life cycle of social insects
ORAL · Thu 20 Aug · 10:15 · K8 · Session 52 · Abstract ID 149763

Turtle ants undergo an unexpected pattern of caste investment and colony development to function in the arboreal realm

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Castes are one of the main innovations in the adaptive evolution of the colony phenotype in social insects. Yet a major knowledge gap remains in our understanding of how and why caste structure changes during colony development. I explore the diversity of caste structure development in ant colonies, and complement it with analyses of novel turtle ant (Cephalotes) datasets. The iconic caste system of the turtle ants includes discrete worker, soldier, and queen female castes, and each has distinct armor traits that are engaged in different functional aspects of colony life. The novel datasets capture the colony development of turtle ant caste structure from founding queens through to reproductive maturity, and integrate associated data from the multi-nest ecology of the same colonies. Analyses reveal active nest defense by founding queens and the unusual pattern of immediate soldier production in the queen's first cohort of nanitic offspring. Caste size frequency distributions then shift substantially in early colony life, yielding a mixture of size cohorts at intermediate colony sizes, before stabilizing at reproductive maturity. In contrast, proportional caste investment is remarkably stable across all colony sizes, with high soldier investment, and as colonies grow by adding new nest units. Broadly, these results show a developmental pattern for caste structure that challenges classic theoretical expectations while being highly consistent with modular colony growth in the arboreal realm. They further highlight the potential of evolutionary innovation in the development of caste structure across diverse ecological contexts.

SYMPOSIUM 06 · From founding to function: early-stage dynamics in the life cycle of social insects
ORAL · Thu 20 Aug · 10:30 · K8 · Session 52 · Abstract ID 146259

The reversible specialization of ant queens allows them to start a new colony again

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In eusocial insects, the only function of queens is to produce eggs. This specialization is typically considered as being independent of environmental conditions. However, founding queens express non-reproductive behaviors to establish their colony, and it is the presence of workers that induces their specialization in egg production. Furthermore, in ants, isolated established queens lose their specialization and revert to expressing brood care. Our objective is to understand why established queens retain the ability to express brood care. We propose that its benefit would be that ant queens may start a new colony again if they lose all their workers. This hypothesis makes two predictions. First, some environmental perturbations should lead to the loss of all workers, for example because queens and workers differ in resistance to stressful conditions. We are in the process of subjecting young Lasius niger colonies to multiple stress to monitor the survival of queens and workers. The second prediction is that once isolated, queens would manage to produce new workers. To test it, we isolated 82 queens either with 5 larvae or completely alone. We found that within 5 months, 84% of the queens isolated with larvae succeeded in producing a new worker, while 53% of the fully isolated queens managed to do so. Our results support the hypothesis that the behavioral flexibility of ant queens may allow them to start a new colony again. This study provides important information to better understand colony founding, queen specialization and division of labor in ants.

Colony Foundation and Symbiont Transmission in an Ant-Plant Farming Mutualism

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When a social insect species is dependent on a symbiotic partner for survival, the already risky business of dispersal and colony foundation gains additional complications. Any new colony must identify and associate with suitable and reliable symbionts to be successful.

Across many symbioses, these challenges are avoided when beneficial partners are transmitted vertically. The fungus-farming attine ants and ambrosia beetles load reproductives with fungal propagules and associated microbial consortia, facilitating co-dispersal. In almost all cases of myrmecophytism however, associations must be re-established between each new colony and host plant generationally. One key exception might be the reciprocally obligate ant-plant farming mutualism of Fijian Philidris nagasau ants and their Squamellaria cultivars. The foundation of new colonies and associated “plantations” has not been observed, but a form of “opportunistic’ dependent colony foundation is proposed.

A fission/budding system where new colonies arise in maternally cultivated host plants would provide a mechanism for co-establishment including both partners. Whole genome analyses at individual and population levels suggest a pattern of spatial genetic structure and male biased dispersal consistent with this hypothesis. Co-phylogenetic approaches complicate this however, suggesting surprisingly frequent horizontal transmission of plant symbionts between colony lineages.

The role of early colony life-cycle stages on the maintenance of social polymorphism in ants: a population genetic model

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The suppression of recombination in large inverted genomic regions is important for preserving co-adapted gene complexes. A class of such inversions, known as supergenes, consist of linked loci controlling complex phenotypes. By promoting the co-segregation of adaptive mutations, supergenes play a central role in the evolution of alternative phenotypes maintained by balancing selection, sustaining adaptive polymorphism. An emerging example of a social supergene occurs in several ant species in which colonies are polymorphic in queen number; some nests harbour a single queen (monogynous), whereas others contain multiple queens (polygynous). Despite a range of phenotypic differences and an established genetic basis for the two discrete morphs, the forces maintaining this polymorphism remain poorly understood. Several interacting processes; including recessive lethality, selfish genetic elements, and strong assortative mating; have been implicated in its maintenance. Given the complexity of the selective forces involved, existing theory has understandably struggled to explain how the persistent coexistence of the alternative morphs is achieved. Here, we address this gap by developing a comprehensive population genetic model that captures the social interactions associated with the social supergene, particularly during early colony life-cycle stages. We explicitly focus on colony joining and budding by polygynous queens, as well as dispersal and independent founding by monogynous queens, and test whether the downstream effects of these processes on colony productivity interact with genetic and ecological factors to shape the relative frequencies of the alternative morphs. We will then synthesize and discuss the factors that promote balanced polymorphism within this framework

From mate choice to colony founding: supergenes control reproductive dynamics in the ant, Formica cinerea

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Colony foundation in ants is a critical life-history stage, requiring queens to successfully mate, disperse, and establish new colonies. Reproductive success, therefore, depends on coordinated suites of traits rather than single characters. How such trait complexes are maintained across generations remains unresolved. Supergenes, chromosomal regions of suppressed recombination, offer a potential solution by physically linking loci controlling multiple traits and preventing recombination from breaking apart coadapted allele combinations. Although supergenes are widespread in ants and known to regulate social organization, whether they coordinate entire reproductive syndromes remains unclear.

We address this question in Formica cinerea, which harbors a complex supergene system associated with alternative colony social organization (monogyne versus polygyne) and body size polymorphism (macrogynes/macraners versus microgynes/micraners). We test whether supergene-associated morphs integrate dispersal ability, mate choice, and colony founding strategy into alternative reproductive syndromes.

Our data show that microgynes and micraners exhibit smaller wing areas and thorax volumes than macrogynes and macraners, indicating reduced dispersal ability. These morphological differences translate into divergent mating strategies: large queens participating in mating flights preferentially mate with similarly dispersing partners, generating assortative mating, whereas small queens predominantly mate with small males. Queens attempting independent colony foundation are large and carry monogyne-associated supergene haplotypes. Moreover, when queens mate with males of different genotypes, polygyne-associated haplotypes are transmitted to eggs more frequently than expected, suggesting sperm competition.

Together, these results demonstrate that supergenes in F. cinerea integrate dispersal, mate choice, and reproductive dynamics into cohesive reproductive syndromes, thereby maintaining the social polymorphism.

BumbleMATE – Agent-based modelling of bumblebee mating flights to predict gene flow and delimit populations

Lilian Gornall; Frank Sommerlandt; Anne-Kathrin Schneider-Hohenbrink; Jens Dauber; **Wiebke Sickel**

Monitoring genetic diversity in bumblebees is crucial, as its loss poses a significant threat to populations and compromises their resilience and adaptability to changing environmental conditions. Due to their high agility and widespread distribution, the delimitation of bumblebee populations remains a major challenge for genetic diversity assessments and has so far only been possible by means of complex and expensive genetic analyses. Alternative strategies for delimiting bumblebee populations that do not rely on genetic data are required.

To remedy this issue, we have developed BumbleMATE, an agent-based model. BumbleMATE depicts dispersal capabilities of bumblebees by modelling sex-specific behavioural patterns such as flight and dispersal trajectories during mating season and outputs mating networks, which cannot be produced through DNA-based methods at a sufficient scale and resolution. Based on a generic bumblebee ecotype, we ran nine scenarios with ten repeats each, that differed in nest densities and distributions.

Overall, all mating networks exhibited a dominant gene flow cluster that encompassed the majority of colonies, indicating sufficient gene flow. Reducing nest densities increased network modularity and the number of unmated agents. Differences in spatial distribution had a smaller effect on mating networks, but local nest clusters led to shorter distances between colonies of mating partners, indicating an increased probability of population sub-structuring. As these patterns align well with literature, BumbleMATE has the potential to become a powerful tool to model gene flow and establish a basis for in silico genetic diversity monitoring of bumblebees.

SYMPOSIUM 06 · From founding to function: early-stage dynamics in the life cycle of social insects
ORAL · Thu 20 Aug · 11:45 · K8 · Session 52 · Abstract ID 146395

Prolonged maternal care and rudimentary division of labour in facultatively social small carpenter bees

Sandra Rehan
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Facultatively social bees exhibit behavioural plasticity in response to maternal care and social environment, providing a natural experiment to compare solitary and social behaviours within a single species, offering empirical insights into the evolution of eusociality. The small carpenter bees (genus Ceratina) are of special interest because they exhibit rich behavioural plasticity. Species range from solitary to eusocial and benefit from detailed behavioural research and well-established phylogeny. As such, small carpenter bees are poised to further comparative early-stage dynamics in understanding the relative roles of maternal care and division of labour underlying social phenotypes and organizational complexity. Mothers have complete control of order of eclosion, sex, size, and division of labour through manipulating pollen provisions and social environment. Worker-like daughters ensure the overwintering survival of siblings at the cost of any direct fitness. Here, I present development, nutritional and behavioural data in a facultatively social bee, highlighting the importance of simple societies to examine the evolution of social traits.

SYMPOSIUM 06 · From founding to function: early-stage dynamics in the life cycle of social insects
ORAL · Thu 20 Aug · 12:00 · K8 · Session 52 · Abstract ID 148540

One dose does not fit all: Species-specific and dose-dependent responses of bumble bee queens to insecticide exposure

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Bumble bee queens are critical to colony survival, acting as the bottleneck for generational establishment. However, there is limited knowledge about how they respond to agroecological stressors such as pesticides. Regulatory risk assessments often rely on honey bee data as a proxy, despite known key biological differences that may lead to inaccurate predictions for bumble bees. Compounding this, bumble bee species respond differently to environmental stressors, with some experiencing sharp declines while others remain stable or expanding, likely due to species-specific traits. Together, these knowledge gaps highlight the need to better understand both taxonomic and caste variation in pesticide responses.

Our study examines how varying levels of dimethoate exposure affect queen health and nesting success, using Bombus impatiens (commercial and wild) and Bombus griseocollis (wild) as models. We housed and monitored queens for up to 45 days or until successful colony establishment or mortality. We measured survival, diet consumption, nesting initiation, colony establishment, and reproductive output under control and treated conditions.

The results reveal species-specific and dose-dependent patterns in queen responses to dimethoate exposure. At high concentrations, B. griseocollis queens experienced mortality more rapidly than B. impatiens. At the lowest exposure level, queens of both species showed increased early activity relative to controls, indicating sublethal responses. These findings can inform pesticide risk assessments, refining risk models, and guide strategies to reduce queen exposure. Ultimately, this work offers valuable insights to support conservation efforts and the sustainability of native pollinator populations.

Reproductive Traits of Honey Bee Queens Predict Colony Growth Trajectories

Zhaorigetu Hubhachen; Heaven Strachan; Rameshwor Pudasaini; Xaryn Cleare; Danielle Kroh; **Hongmei Li-Byarlay**

Central State University

Queen reproductive performance is a central determinant of honey bee (Apis mellifera) colony growth, resilience, and long-term persistence. Despite its importance, variation in queen fecundity among different genetic stocks—and its consequences for colony dynamics—remains poorly resolved. Here, we compared egg-laying performance and colony demography of queens from three genetic stocks: Russian, feral, and commercially reared honey bees, across 3 years. Queens of the same age were reared from a single mother colony per stock, open-mated within the same year, and established under standardized colony conditions. Across years, Russian and feral queens consistently exhibited higher egg-laying rates than commercially reared queens, indicating substantial stock-dependent differences in reproductive capacity. In 2024, these differences translated into divergent colony trajectories: worker populations in Russian and feral colonies increased over time, whereas colonies headed by commercial queens declined, suggesting reduced colony sustainability. While pollen storage and brood area did not differ significantly among stocks in earlier years, patterns of brood production closely mirrored differences in queen fecundity. These results suggest that queen reproductive traits, shaped by genetic background and selection history, play a critical role in mediating colony-level outcomes. Our findings highlight the ecological and evolutionary significance of queen quality and underscore the potential value of locally adapted and naturally selected stocks for enhancing colony performance and resilience under ongoing environmental pressure.

Altered colony initiation enabled the evolution of fully asexual lineages in termites

Simon Hellemans; Toshihisa Yashiro; Nobuaki Mizumoto

Termite societies are usually composed of immatures of both sexes, and new colonies are initiated by a male-female pair. In most species, the pair searches for a nest site via a distinctive coordinated behavior referred to as tandem running. One may wonder whether tandem running would be maintained in asexually-reproducing lineages since (i) pair formation entails costs as individuals are more likely to be lost to predation, and that (ii) a single female could theoretically initiate a colony alone. We compared mate-pairing processes in the sexual and asexual lineages of the termite Glyptotermes nakajimai. In both lineages, tandem running is rare and ephemeral, but colonies are initiated by more than two individuals. By contrast, closely-related species exhibit both male- and female-leader tandem runs, and colonies are initiated by one opposite-sex pair. Our results suggest that modifications of the mate-pairing process are likely preconditions for the evolution of asexuality in species with biparental care. While pair formation may not be an obligatory step for colony initiation, the occurrence of more than one individual at the nest site is still required since de-winged individuals die without allogrooming.

Nesting biology drives the stability of tandem movement coordination in mating termites

Elijah Carroll[1]; Nobuaki Mizumoto*[1]; Nathan Lo[2]; Taisuke Kanao[3]

[1] Auburn University; [2] University of Sydney; [3] Yamagata University

The colony foundation process of termites, like many goal-oriented behaviors, is highly order-dependent. In most species, dispersing alates shed their wings before forming tandem pairs, because wings impair movement coordination and tactile communication required for joint nest searching. This conserved sequence reflects the dual demands of mate acquisition and nest-site discovery during colony founding, in which dispersal, partner coordination, and nest searching must be resolved in a specific order. Here we show that differences in nesting biology can relax these constraints and favor alternative behavioral priorities. In the Australian termite Microcerotermes nervosus, we discovered a reversed mating sequence in which tandem running occurs prior to wing shedding, and tandem running facilitates dealation. Using automated video tracking, we found that wing shedding improves tandem stability, yet M. nervosus exhibits exceptionally stable coordination even while winged. Comparative analyses across sympatric termite species revealed that M. nervosus displays greater tandem stability than all others examined, even though those species perform tandem running only after dealation. We propose that this flexibility arises from the nesting ecology of M. nervosus. This species constructs abundant, broadly distributed mound nests, reducing constraints on immediate nest-site discovery during mating. Under these conditions, selection may favor rapid partner acquisition and retention over early nest searching. Enhanced movement coordination appears to mitigate the typical costs imposed by wings, allowing reordering of a functionally integrated behavioral sequence. Together, our findings demonstrate that ecological context can reshape mating priorities, enabling rare but consequential changes in order of socio-sexual behaviors.

First experimental evidence of social parasitism in termites

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Nestmate recognition is the primary defense mechanism maintaining the integrity of eusocial insect colonies. While social parasitism is widespread in Hymenoptera, it is rarely documented in termites, and the behavioral boundaries preventing interspecific infiltration remain poorly understood. Here, we investigated the potential for interspecific integration between two closely related termite species under laboratory conditions. We introduced Reticulitermes labralis workers and reproductives (queens and kings) into orphaned groups of R. aculabialis. We found that host workers exhibited caste-dependent aggression: introduced workers were immediately attacked and eliminated, whereas alien reproductive were partially tolerated. Surviving alien reproductives successfully integrated into host group, receiving allogrooming and trophallactic care from host workers. Crucially, these integrated pairs produced viable eggs and larvae. Molecular analysis confirmed that the brood reared by the host workers were the genetic offspring of the introduced R. labralis pair, demonstrating successful “cuckoo-like” reproduction. These findings reveal that termite colony recognition is sufficiently flexible to permit the acceptance of heterospecific reproductives when native royals are absent. While field evidence remains to be discovered, our results demonstrate that the behavioral and physiological prerequisites for social parasitism exist in termites.

SYMPOSIUM 06 · From founding to function: early-stage dynamics in the life cycle of social insects
ORAL · Thu 20 Aug · 15:30 · K8 · Session 58 · Abstract ID 149741

Flexible cognitive switching allows economical early stage nest defense.

Lorenz Mammen; Weelo Ghamra; Michael Sheehan
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Managing all the tasks on early social insect nests is cognitively challenging. One such task is to defend the nest against predators and conspecifics, but constant vigilance has energetic and opportunity costs. Understanding how foundresses manage these costs is important for understanding adaptive behavioral strategies during the founding stage. Being able to flexibly adapt vigilance to acute defensive needs would be a solution. Due to the open nests and a clear indication of defensive postures, paper wasps are an excellent model to investigate flexible cognition for nest defense. Here we tested foundress-stage Polistes fuscatus nests. We built an immersive 3D virtual environment to control the visual stimuli surrounding a wasp nest. Foundresses reliably responded to moving stimuli presented on the screen. Responses were more likely when foundresses were in aggressive postures, indicative of increased motivation to defend the nest. We reliably induced aggressive posturing by vibrating the nest. Wasps in aggressive states responded to smaller moving objects, demonstrating increased visual acuity (1.4° instead of 2.1° visual angle). These findings imply that there is a distinct behavioral state of arousal in P. fuscatus wasps that might modulate motivation as well as early motion vision pathways. This state switch allows single foundresses to economically defend their nests by remaining in a low arousal state most of the time, and entering into a state of higher vigilance and arousal when necessary.

SYMPOSIUM 06 · From founding to function: early-stage dynamics in the life cycle of social insects
ORAL · Thu 20 Aug · 15:45 · K8 · Session 58 · Abstract ID 146505

Natural History observations of a population of social wasp, Polistes arizonensis: colony survival and productivity in relation to the number of foundresses

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[1] Arizona State University; [2] Arizona State University

Wasps in the genus Polistes, paper wasps, have long been subjects of biological research and inspired generations of researchers interested in their sociobiology. The high visibility of colony life (in contrast to many species of social insects) – wasps building a paper nest without an outer covering – has made them a valuable model organism for the study of colony foundation, division of labor, dominance hierarchies, among other questions in sociobiology. Colonies can be founded by either a single female (haplometrosis) or a group of cooperating females (pleometrosis). In many species, pleometrotically founded colonies generally outperform haplometrotic colonies. But the presence of multiple potentially fertile females on the same nest introduces questions of reproductive conflict and how this might be managed in a proximate (regulatory) sense or why it might work in the ultimate (evolutionary) sense. Why should Polistes females cooperate or go it alone when founding a nest? For the last four years, we have been documenting colony foundation in the species Polistes arizonensis. Using a telephoto lens, we have photographed colonies from March to September in their naturally chosen nesting sites in Tempe, Arizona (in the Sonoran Desert). Colonies can be founded by a single female or by multiple females. By analyzing these photos we are able to compare the survival and growth rate of colonies – a first pass in what will be a long-term study of the sociobiology of this species. In this presentation, I will describe our initial findings from four years of observation.

Behaviourally different foundresses initiate two types of nests in the primitively eusocial wasp Polistes wattii

Ruchira Sen
Sri Guru Gobind Singh College

Polistes, one of the most widely distributed social wasps, typically employ solitary and multiple-founding strategies to establish nests. While most Polistes species use a mix of these methods, some species only initiate solitary nests. P. wattii, however, exhibits a unique season-specific biannual strategy where, in spring, overwintered females found small nests individually, while in summer, multiple foundresses collaborate to initiate nests and build much larger nests. In an attempt to understand why P. wattii needs to initiate nests twice, we compared the morphophysiological and behavioural parameters of foundresses from these two nesting phases. Our findings reveal a compelling paradox: while solitary foundresses resemble the reproductively dominant foundress in body size and mating status, their behaviour more closely aligns with that of the unmated workers seen in multiple-foundress colonies. Despite the clear ecological advantages of multiple-foundress nests, our data suggest an evolutionary trade-off. We propose that natural selection maintains the solitary strategy because a few of these early nests produce the females who eventually become the dominant foundresses of the more successful summer colonies.

SYMPOSIUM 06 · From founding to function: early-stage dynamics in the life cycle of social insects
ORAL · Thu 20 Aug · 16:15 · K8 · Session 58 · Abstract ID 149952

Climate shapes wasp foundress cooperation across Africa

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Cooperation correlates with climate, but we do not fully understand why. Within-species studies of cooperation across climatic zones are powerful but rare. Here, we investigate one of the planet's most climatically cosmopolitan cooperative breeders: foundress groups of Africa's most widespread social wasp (Belonogaster juncea). Using field surveys, low-coverage genome resequencing, a behavioural experiment, and simulations, we compare foundress cooperation in three climate zones: the humid tropics (Congo Basin and contiguous forests), semi-arid tropics (margin of the Sahel), and temperate highlands (southern Africa). Climate exerts strong and unpredicted effects. First, dry climates constrain populations: over the past million years, two collapses in effective population size coincided with intensified aridity. Second, the 'hard life' hypothesis (predicting that challenging abiotic conditions promote cooperation) may break down at extremes: there was an unexpected lack of foundress cooperation in the extremely dry Sahelian margin, but extensive cooperation elsewhere. Third, indirect fitness drives foundress cooperation where it evolves. Relatedness was high in the humid tropics and temperate highlands, and helpers typically rejected direct fitness opportunities. Finally, our evolutionary simulations predict that seasonal rains determine social structure. Our results are among the most geographically wide-ranging comparisons of a cooperative breeder to date, and indicate that climate shapes cooperation in ways that differ from current theoretical expectations.

Repeated evolution of dispersal and reproductive patterns in East Asian Monomorium

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Dispersal and reproductive strategies in ants are essential for understanding the evolution of social systems and invasion biology. The ant genus Monomorium, comprising approximately 300 species, includes several well-recognized tramp species and exhibits remarkable diversity in dispersal traits and reproductive modes, making it a useful model for studying the evolution of these traits. Here, we analyzed the phylogenetic distribution of dispersal and reproductive modes in East Asian Monomorium, including a newly discovered species with short-winged queens. From the southern part of Japan, we discovered a Monomorium species whose queens have markedly reduced wings. Together with the absence of small incipient nests in its natural habitat, this suggests intranidal mating and colony fission. Phylogenetic analyses based on mitochondrial genome protein-coding genes, including known East Asian congeners, showed that this species is most closely related to M. intrudens. Although the two species have overlapping distributions, they are clearly distinguishable by queen wing morphology. DNA barcoding using the mitochondrial COI region further supported their separation into distinct lineages at all sampled localities. Based on these results, we describe this species as M. brachypterum. Phylogenetic relationships among East Asian Monomorium species also suggest that reduced dispersal and alternative reproductive modes such as thelytoky have evolved independently multiple times. We further discuss phylogeographic scenarios for M. intrudens and M. brachypterum in relation to their contrasting vertical distribution patterns.

Queen number and early colony growth in the desert leafcutter ant Acromyrmex versicolor

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Siena University

Nest-founding is an intensive period of the ant colony life cycle for queens, and a period where mortality rates are high and selective pressures are strong. We put newly mated queens of the desert leafcutter ant Acromyrmex versicolor into pairs or groups of six to evaluate how group size influences nest-founding success and early colony growth (n=20 and 22, respectively). By day 65, only 14 colonies remained alive (9 pairs, 5 groups of six). Out of these, nests with groups of six queens initially contained more eggs. However, by the time of worker emergence and growth (days 50-188), worker numbers were equivalent across both nest types. Thus, there appears to be no clear added benefit to larger group sizes within this species, at least in the studied context. Future work will evaluate these findings relative to the extent of pleometrosis/polygyny observed in colonies in the wild.

The intrusive behavior of new queens into mature colonies observed in the Japanese harvester ant, Messor aciculatus

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The post-flight behavior of new queens of ants is crucial to determine regional population genetics, colony life history, and genetic structures within the colony. However, in many polygynous species that engage in nuptial flights, the post-flight behavior of new queens remains unclear. Japanese harvester ant Messor aciculatus shows nuptial flight in spring season (Onoyama 1981), and dealate queens establish colonies by haplometrosis or pleometrosis (Maekawa 1986, Taki 1976). Concomitantly, the number of the queen(s) in the mature colonies is reported to be one to three (Mizuno and Abe 2007). But it remains unconfirmed whether pleometrosis is responsible for the polygyny of this ant.

We observed the post-flight behavior of new queens of M. aciculatus in Japan. Following the nuptial flight, the dealate queens started to establish the colonies by haplometrosis or pleometrosis. While some queens persistently attempted to intrude into mature colonies. Some intruded queens were immediately removed by workers, while others were not. The removal behavior of workers was not fatal to the queen.

The ecological significance of the intrusive behavior remains unclear. To our knowledge, similar behavior has not been reported in either Messor or Veromessor. We currently consider three possibilities to explain this behavior; 1) the new queens successfully intrude and cause polygyny, 2) the new queens intrude according to their homing instinct, but are eliminated eventually, 3) the new queens are attracted to conspecific cues as the mechanism of pleometrosis but are eliminated eventually. To confirm these hypotheses, genetic, chemical and behavioral examinations are indispensable.

Behavioral Interactions in an Ant Social Parasitism System and Evidence for a Native Supercolony

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Ants exhibit diverse nesting strategies, from single-nest colonies to expansive networks spanning thousands of nests. In the southeastern United States, two native species, Dorymyrmex bureni and D. smithi, represent opposite ends of this spectrum. While D. bureni typically occupies a single nest, D. smithi can utilize hundreds to thousands of nests. Notably, D. smithi is a temporary social parasite of D. bureni, and the two species can form mixed nests without interspecific aggression. This study provides a preliminary behavioral investigation of these species by assessing interactions between workers from nests collected across three sites (3–35 km apart). We conducted pairwise aggression assays within and between nests for each species, as well as between species. Our results reveal that D. smithi workers from different nests exhibit extremely low levels of aggression regardless of geographic distance, suggesting a potential supercolonial structure. Conversely, D. bureni displays high aggression between all non-nestmate pairs. Furthermore, both species interact aggressively with each other across all sites when not part of a pre-existing mixed parasitized nest. We will also present preliminary behavioral results of artificial mixed nests that mirror D. smithi colony founding. These findings enhance our understanding of ant colony structure and provide a foundational framework for future research into the mechanisms of social parasitism between these two species.

Manipulation of exploited host workers via social fluid exchange in social parasite colonies

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Social species, including humans, use social fluid exchange not only for feeding but also for the transfer of immune factors and information. In antagonistic interactions, such exchange can influence recipient behaviour and lifespan and can lead to overexploitation of their resources. Trophallaxis occurs regularly in insect societies. In ants, the transfer of social fluid primarily serves the exchange of liquid nutrients. However, trophallactic fluid also contains cuticular hydrocarbons involved in communication, as well as proteins and hormones that affect larval development and immune function.

In social parasite colonies, the care behaviour of host workers is exploited. This system forms a social fluid exchange network across species, castes, and developmental stages. In our study using the model system of the obligate social parasite Temnothorax americanus and its host Temnothorax longispinosus, we test whether the parasite uses social fluids to manipulate host worker behaviour. We also examine whether exploited host workers adjust the composition of their trophallactic fluid depending on the interaction partner, including its species, caste, and developmental stage.

Both mouth to mouth trophallaxis and proctodeal trophallaxis occur in these interactions. We quantify both types of fluid exchange with respect to frequency, interaction partners, fluid composition and consequences. This study provides the first systematic analysis of the social fluid network in a dulotic ant species.

SYMPOSIUM 07 · Nutrition and insect health, from single individuals to colonies
ORAL · Tue 18 Aug · 10:15 · K10 · Session 18 · Abstract ID 144785

Nutritional niches reveal mutualism resilience mechanisms in urban leafcutter ants

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While most organisms engage in mutualisms, mutualism stability is often threatened by environmental degradation. Since mutualism stability often depends on nutritional trade, I propose that nutritional niches can used to predict the risks of mutualism breakdown under environmental stress. This framework tests: 1) if the realized nutritional niche (RNN) of symbiotic provisioning optimally targets the fundamental nutritional niches (FNN) of symbiont need and 2) if environmental degradation causes nutritional provisioning mismatches. The fungus-farming mutualism of Panamanian Atta colombica leafcutter ants is a model system to test this hypothesis as colonies live in both rainforest and urban areas. By nutritionally analyzing plant fragments selected by free-ranging foragers, I show that RNNs of urban leafcutter colonies have lower %C (but not %N) than rainforest RNNs. In contrast, intake targets for protein and total non-structural carbohydrates (starch and sugar) within these RNNs showed similar macronutrient selectivity between these habitats, and thus no systematic nutritional provisioning mismatch. Moreover, the cultivar's nutritional yield was stable across these habitats, highlighting mechanisms of mutualism resilience when ants navigate nutritionally degraded foraging landscapes. Although measuring the strength and dimensionality of nutritional limitation remains challenging, doing so is essential since nutritionally explicit niches offer a powerful lens for applying niche theory to predict ant community structure and ecological resilience.

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ORAL · Tue 18 Aug · 10:45 · K10 · Session 18 · Abstract ID 149513

Answering the garden's call: Fungal cues inform nutritional decision-making in leaf-cutting ants

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Anthropogenic pressures reshape plant nutrient composition, altering the nutritional ecology of key herbivores, including leaf-cutting ants (LCA). LCA maintain a tripartite mutualism with a cultivated fungus and microbiome to access plant resources. Because fungus garden growth depends on food-plant quantity and quality, nutritional deprivation or imbalance may pose particular challenges to this system. To assess LCA responses to such deficiencies, we asked two questions: (1) do nutritionally deprived gardens emit cues that influence worker orientation, and (2) how does colony starvation shape responses to these cues during foraging and resource allocation across the fungus garden? We worked with paired subcolonies whose gardens exhibited differing nutritional states. When testing whether gardens emit cues, we olfactometrically measured worker orientation toward starved versus nourished fungus. To examine how starvation-induced cues influence ant behavior, we assessed preference for sugar-enriched leaves (mimicking drought-associated carbohydrate shifts) and tracked fragment deposition across the gardens. Workers from both starved and nourished colonies showed preferential orientation towards starved fungus, suggesting that starved gardens emit attention-attracting cues. Colony nutritional state also shaped foraging decisions: nourished colonies significantly preferred sugar-enriched leaves, while starved colonies were indifferent. Regarding resource allocation, foragers prioritized deprived sections, while gardeners more evenly redistributed fragments. Nutritional stress reshapes how colonies respond to garden-derived cues. Specifically, food plant deprivation resulted in a disruption of nutrient discrimination following the detection of starvation-induced volatiles. We conclude that the capacity to evaluate the garden state is an essential component of foraging decisions in LCA under fluctuating food qualities through anthropogenic pressure.

Dynamic nutritional strategies in ants: exploring the role of plant in combating pathogens

Danae Nyckees

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Animals modulate their nutritional intake to combat pathogens, and this behaviour is extremely dynamic. In insects, it is common to observe ingestion of antimicrobial chemicals as defence mechanism against pathogenic threats. Plants secondary metabolites (PSM) have been shown in multiple studies to help prevent infection or fight off pathogens in multiple insect's species including ants. We explored how ants interact with plants through eDNA in their gut in relation to the pathogenic pressure in their nest. We also explored whether Formica fusca ants exposed to a fungal pathogen use an artificial diet spiked with PSM. While the DNA metabarcoding approach is currently being executed, we already tested multiple parameters such as foraging behavior, survival, gene expression and conidia germination assays using two plant alkaloids: caffeine and aconitine. We observed that the presence of the pathogen increases contact with food and that caffeine is slightly deterrent when ants are healthy. However, these compounds alone might not have a strong effect on survival, even though they did have antifungal properties. We observe a stronger benefit in survival when having access to a varied diet including those alkaloids and non-spiked food. Finally, we unravelled the differently expressed genes under infection, and they were only altered by the pathogen. We observed genes related directly to the immune system and indirectly such as symbiotic relationship and feeding behaviour. Overall, our observations suggest that these PSM are potentially beneficial against infection, but as part of a complex nutritional system where costs and benefits must moderate.

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ORAL · Tue 18 Aug · 11:15 · K10 · Session 18 · Abstract ID 148111

Hints of self-medication? Foraging decisions of bumblebees with different health status

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Self-medication - selective consumption of compounds reducing infection - is increasingly discussed in pollinator–pathogen ecology. We tested whether bumblebee colonies (Bombus terrestris) modify nectar choice under pathogen challenge, focusing on quercetin, a common nectar secondary metabolite with antimicrobial activity. Colonies were maintained as healthy controls or challenged with Ascosphaera apis or Serratia marcescens, and allowed to forage in a flight cage with robotic flowers offering either control or quercetin-supplemented nectar.

A. apis–challenged colonies increasingly preferred quercetin, expressed as higher visitation and longer probing-time attributed to quercetin flowers, hinting towards self-medication. Healthy colonies and S. marcescens–challenged colonies showed no significant preference, with trends toward reduced use of quercetin.

This disparate reactions might be a result of the basic differences in the pathogen's life histories and the potential metabolic cost of quercetin. A. apis primarily affects brood, so increased quercetin foraging could reflect social medication. S. marcescens is an opportunistic gut pathogen of adults; if quercetin imposes metabolic or detoxification costs, challenged foragers may not benefit from increasing quercetin intake.

These results indicate that pathogen identity could shape behavioural plasticity in nectar foraging, and illustrate the value of robotic flowers for deciphering complex changes in behaviour and their impact.

Changes in gene expression linked to foraging choices in self-medicating Lasius platythorax ants

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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.

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From individual digestion to colony nutrition: microbial pre-digestion in the termite Velocitermes heteropterus

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Nutrition and health in social insects emerge from interactions across biological scales, from individual digestive physiology to colony-level organization. In termites, this integration may extend beyond the gut through food storage and nest-associated microbial processes. Here, we examine how nutritional functions are partitioned between individual termites and the colony as a whole in the Neotropical mound-building termite Velocitermes heteropterus. We analyzed nest architecture, carbon and nitrogen content of stored food, gut contents of workers and soldiers, and the taxonomic and functional profiles of microbial communities associated with termite guts and nest substrates. Mounds exhibited a conical shape with a sponge-like internal structure in which dry grass fragments were stored throughout the nest. The presence of small satellite nests connected to larger mounds suggests a polydomous organization, potentially facilitating spatial allocation of nutritional resources. Stored food displayed significantly higher C:N ratios than fresh plant material, indicating a modification of nutrient stoichiometry at the colony level prior to ingestion. Microbial communities differed markedly between nest substrates and termite guts. Nest-associated microbiota were enriched in Proteobacteria and Actinobacteria and showed a higher predicted abundance of hemicellulolytic enzymes, particularly xylanases, consistent with the grass-based diet of the species. In contrast, gut microbiota were more strongly associated with cellulolytic and starch-degrading functions, reflecting digestion at the individual level. Chitinase-related functions in nest fecal material suggest nutrient recycling within the colony. Microscopic analyses revealed plant fragments and fungal elements in the guts of both workers and soldiers. Together, colony-level and individual digestion jointly shape termite nutrition.

Can agricultural Helianthus annuus cultivar selection influence neighboring Bombus terrestris colony development?

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Sunflower, Helianthus annuus L., is a prominent global oilseed crop with increasing cultivation and bee-friendly appeal as it attracts many pollinators. Despite sunflowers apparent attractiveness, not much is known regarding its' nutritional potential for pollinators. Laboratory studies report inconsistent developmental parameters after bee consumption of sunflower pollen, and field realistic conditions are lacking. We conducted a semi-field study in which Bombus terrestris colonies were housed in flight tents and exclusively foraged on different IFVCNS sunflower hybrids (Duško, NS Konstantin, NS Romeo, and NS Kruna) with variable pollinator favorable traits. Sunflower hybrids were also investigated quantitatively for their pollen (amino acids and fatty acids) and nectar (sugar spectrum) nutritional potential. We found that the colonies that foraged on sunflower hybrids selected based on their nectar characteristics (Duško and NS Romeo), were significantly heavier two to three weeks after sunflower exposure. Furthermore, Duško and NS Romeo had pronounced differences in their pollen protein profile. Hybrids also revealed significant differences in their nectar production. NS Konstantin had significantly lower sugar mass per floret after 48 hours compared to 24 hours of undisrupted nectar accumulation, suggesting quicker nectar reabsorption compared to Duško, NS Romeo, and NS Kruna. Overall, these findings offer new insights into how crop selection can impact pollinator colony development and reproduction, and potentially biodiversity in agricultural landscapes. Floral resource traits should be given consideration when selecting sunflower genotypes for agricultural production, however more research is needed to target which traits could make the difference for pollinator communities and pollinator health.

SYMPOSIUM 07 · Nutrition and insect health, from single individuals to colonies
ORAL · Tue 18 Aug · 14:30 · K10 · Session 24 · Abstract ID 146504

Balancing the fat: how dietary fatty acid composition regulates nurses bee feeding

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Dietary lipids are essential for the growth, physiology, and colony-level functioning of honey bees, yet the mechanisms by which nurse bees regulate the intake of specific fatty acids remain poorly understood. Because nurse bees provision larvae and support other colony members through glandular secretions, their ability to balance dietary lipids may have cascading effects on colony health. In this study, we examined how variation in dietary fatty acid composition influences feeding behavior and physiological development in nurse honey bees. Using a combination of no-choice and choice feeding assays, we tested lipid supplements that differed in their ratios of saturated to unsaturated fatty acids (SFA:UFA) and linoleic acid to alpha-linolenic acid (LA:ALA). In no-choice assays, both daily and cumulative food consumption were significantly influenced by dietary fatty acid profile, indicating that nurse bees modulate intake in response to lipid composition. These dietary differences also affected key physiological traits, including hypopharyngeal gland (HPG) acinus size, total lipid accumulation, and dry mass, all of which are closely associated with nursing function. In choice assays, nurse bees exhibited clear and consistent preferences among lipid sources and concentrations, demonstrating active selection rather than passive consumption. Survival remained high across treatments, suggesting that observed differences in feeding behavior and physiology were not driven by acute toxicity or nutritional stress. Together, these findings provide evidence that nurse bees actively regulate fatty acid intake to achieve specific nutritional targets. This regulatory capacity likely plays an important role in maintaining nurse bee performance and supporting overall colony health.

SYMPOSIUM 07 · Nutrition and insect health, from single individuals to colonies
ORAL · Tue 18 Aug · 15:00 · K10 · Session 24 · Abstract ID 147986

You Are What You Don’t Eat: Nutritional Control of Fatty Acids in Bees and Wasps

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Nutrition underpins the ecological success and social organization of insects, yet the physiological mechanisms by which social insects manage dietary variation remain poorly understood. In bees and wasps, carbohydrates fuel immediate energy demands, while lipids play central roles in energy storage, membrane structure, and signaling. Fatty acids de novo from carbohydrates must be balanced with essential polyunsaturated fatty acids (PUFAs) obtained from diet, primarily pollen in bees and prey or carrion in hornets. However, natural diets vary widely in lipid composition, and optimal lipid–protein or PUFA ratios are often rare in the environment.

Here we synthesize our recent work on lipid nutrition in social insects, focusing on how bees (Bombus) and hornets (Vespa) maintain remarkably stable tissue lipid profiles despite large differences in dietary inputs and energetic demands. Using stable-isotope tracers and lipidomic approaches, we show that dietary PUFAs, such as linoleic and α-linolenic acids, are rapidly oxidized and, in part, recycled into saturated fatty acids, thereby limiting their accumulation in membranes and storage lipids. This tight regulation occurs even in species that experience extreme metabolic transitions, from prolonged diapause to sustained flight, suggesting that lipid homeostasis is a key adaptation in social insects.

We propose that selective oxidation and carbon recycling of excess dietary PUFAs represent an underappreciated nutritional strategy that protects membranes from instability and oxidative stress while allowing dietary flexibility. Understanding these mechanisms provides new insight into the nutritional physiology of social insects and has implications for pollinator health in changing environments.

SYMPOSIUM 07 · Nutrition and insect health, from single individuals to colonies
ORAL · Tue 18 Aug · 15:15 · K10 · Session 24 · Abstract ID 147877

Nutritional Ecology of Ant-Aphid Interactions

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A classic example of an insect mutualism, ant-aphid interactions often span the breadth of the mutualism-antagonism continuum. While primarily studied from the perspective of the ant, aphids (as another social insect) present an opportunity to examine the effects of interactions between both individuals (ant-aphid) and groups (aphid colony-ant colony)of social insects. In this project, I supplemented Chaitophorous aphid-tending Crematogaster torosa populations on Populus trees in the Sonoran Desert with protein and carbohydrate sources across 6 months to assess how this change in resource availability would affect the interaction outcome through identifying aphid population growth and number of winged-reproductives produced within the population. Simultaneously, I conducted a morphological trait analysis of both tended and untended Aphididae populations (genus Chaitophorini), to compare and contrast different functional traits involved in the interaction, and identify whether ant tending catalyzes change in trait expression across generations. Results will contribute an aphid-focused perspective on the maintenance of mutualisms across a season, with implications for how ant-nutrition can indicate the outcome of an interaction.

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ORAL · Tue 18 Aug · 15:30 · K10 · Session 24 · Abstract ID 148856

Metabarcoding reveals dietary shifts and resource partitioning of urban paper wasps (Genus: Polistes)

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Paper wasps (Genus: Polistes) are generalist predators and pollinators that provide ecosystem services along urban gradients worldwide. Moreover, the globally invasive European paper wasp (Polistes dominula) is hypothesized to have a distinctly generalized diet compared to other Polistes, which facilitates its nesting success in urban zones. Thus, characterizing the diet diversity of paper wasps across urban gradients can not only indicate biodiversity turnover with disturbance and increase our understanding of social wasp ecosystem services, but also decipher what contributes to P. dominula's invasion when coupled with nest success data. These factors, however, remain vaguely characterized due to a lack of diet and nesting data at landscape scales. Therefore, we are characterizing the dietary taxa and quantifying nesting success of three co-distributed paper wasp species (P. dominula, P. exclamans, and P. metricus) along an urban gradient in St. Louis, Missouri, USA. We are using sequencing data from the metabarcoding of larval feces and honey to test three hypotheses: 1) that the diversity of Polistes dietary taxa and nesting success covary with urbanization, 2) that Polistes study species each provide unique pest control and pollination services, and 3) the generalist advantage hypothesis, whereby P. dominula is assisted by diet flexibility. Preliminary data from four P. dominula nests identified 74 unique taxa in seven arthropod orders. We will identify taxa in our remaining 225 sampled nests and test our three hypotheses using generalized dissimilarity models (GDMs), phylogenetic analyses (UniFrac), and redundancy analysis (RDA).

SYMPOSIUM 07 · Nutrition and insect health, from single individuals to colonies
ORAL · Tue 18 Aug · 15:45 · K10 · Session 24 · Abstract ID 149293

Do infected bumblebees forage differently? Feeding responses to an antiparasitic compound

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Pollinator decline threatens the ecological stability of ecosystems. Various factors drive pollinator health, with pathogens playing a key role. The trypanosome gut parasite Crithidia bombi is a widespread pathogen affecting bumblebees (Bombus spp.), and previous studies show that the plant secondary metabolite callunene found in heather nectar (Calluna vulgaris) can act against this parasite by preventing an infection from establishing. Our study tested whether Bombus terrestris infection status influences feeding preference for callunene. We conducted two five-day choice experiments with two groups of bees: infected vs uninfected. In the first experiment (conducted in two blocks), caged bees had access to a feeder with plain sugar water and another with heather honey extract (a natural callunene source) diluted in sugar water. In the second experiment, bees had access to plain sugar water and a feeder with synthetic callunene diluted in sugar water. In both experiments, solutions contained the same sugar and callunene concentrations, and pollen was available ad libitum. In the first experiment, infected bees consumed more food overall, and uninfected bees preferred the natural callunene source, consuming a higher proportion than infected bees. This suggests infection status alters foraging behavior toward this natural compound source. In the pure callunene experiment, infection status did not significantly affect food intake or the proportion of callunene-containing food consumed; neither group preferred the synthetic compound. These results suggest that bees forage to minimise future infections, but this is only possible when callunene is part of a complex, natural nectar profile.

SYMPOSIUM 07 · Nutrition and insect health, from single individuals to colonies
ORAL · Tue 18 Aug · 16:00 · K10 · Session 24 · Abstract ID 148237

The taste of flowers: how bees assess the nutritional quality of pollen and why it matters

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Bees, like most animals, need diets that provide all required micro- and macro-nutrients in appropriate amounts and ratios in order to thrive and reproduce. However, apart from some 'model' bee species, little is known about the nutritional requirements of bees. Bees obtain most nutrients from two resources: floral pollen and nectar – with pollen playing a particular important role, as it provides most nutrients. However, in particular pollen is often not produced by plants for bees, but serves the plants' very own reproductive interests. This dual function results in a food source that can strongly vary in nutritional composition and therefore needs a proper "quality check" to ensure safe consumption.

We have developed a unique behavioral assay to assess (taste) perception in bees, i.e. chemotactile conditioning of the proboscis extension response (PER), which we combine with classical feeding experiments using manipulated pollen diets to understand the connection between nutrient perception, consumption, survival and fitness. Our ultimate aim is to better understand the nutritional requirements of wild bees.

Our results point to a "perceptional hierarchy", suggesting that bees, i.e. presented by our main model species Bombus terrestris, are particularly sensitive to those nutrients where they can tolerate little variation in concentration. This finding is confirmed by observations of nutritional niches occupied by bees in the field.

(Sea) salt of the earth: Coastal Scottish machair plant communities retain environmental sodium to attract bumblebee pollinators

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One of the rarest habitats in Europe, machair supports several species of endangered pollinators, including the great yellow bumblebee (Bombus distinguendus). Once found throughout Great Britain, this species is now restricted to the machair of north Scotland and its islands. Previous investigations into what makes this habitat suitable for these rare bees have focused on food plant abundance and diversity. But the underlying nutritional landscape of the machair has gone unexplored. This research combines plant physiology and bumblebee foraging ecology approaches to explore the ‘Salty Nectar Hypothesis’, which describes a mechanism of pollinator attraction mediated by sodium (Na) reward. We measured plant uptake of Na and four other mineral salts – calcium (Ca), potassium (K), and magnesium (Mg) –in plant tissues, pollen, and nectar as well as bee preference for these elements through analysis of pollen forage and foraging behaviour. Our findings suggest machair plants maximize low quantity elements beneficial to their growth and development (i.e., K), while restricting uptake of Ca and Mg. But they retain environmental levels of Na – an extraneous nutrient for most plants that can stunt growth in large quantities – tentatively supporting the ‘Salty Nectar Hypothesis’. These findings might explain why several species of rare bumblebees in the UK tend to be confined to coastal sodium-rich environments and provide insight to help forecast future distributions.

Factors shaping wound care dynamics in the army ant Eciton burchellii

Jakob Jansen; Juan José Lagos-Oviedo; Erik Frank

Open wounds pose a high risk of infection. In many social insects, individual and collective adaptations evolved to prevent the spread of infectious diseases or to mitigate their effects. In the Neotropical army ant Eciton burchellii, injured workers receive first aid wound care during the hunt and prolonged wound care in the nest. But it remains unclear how first-aid care is dynamically prioritized during their hunts. We therefore tested whether first aid propensity varies with worker size and the phase of the hunt. In over 66 hours of field observations, we quantified the occurrence and duration of caring behaviors such as allogrooming and wound licking toward 207 injured individuals.

First-aid behavior increased with worker size and was more pronounced at the raid front. In addition, first aid propensity declined towards the end of the raid. Together, these patterns suggest context-dependent allocation of care: larger workers may receive more care due to the greater investment in their production by the colony, while first aid during early raid stages may be more beneficial due to the greater delay until nest-based wound care can be conducted. Our findings highlight how individual investments and temporal dynamics during a hunt shape wound care decisions in an army ant.

Functions of trophic eggs in the ant, Plagiolepis flavescens: Insights from their production and storage patterns

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Ants exchange nutrients among colony members by trophallaxis or direct solid food transfer. However, some species are known to exchange nutrients by “trophic eggs”—unhatched eggs used as food. Trophic eggs are considered to require more time and energy for production than other methods, but their advantages remain unclear. Furthermore, the presence of trophic egg laying remains unclear in many species, and studies elucidating the significance and function of trophic eggs are limited. We discovered that the ant Plagiolepis flavescens uses trophic eggs for nutrient exchange, in addition to trophallaxis and solid food transfer. These trophic eggs are primarily laid by workers and consumed by queens and larvae. Furthermore, while trophic eggs in many species have thin shells and tend to be consumed immediately, Plagiolepis trophic eggs have thick shells and are stored in the nest for extended periods. Based on these findings, we hypothesized that the trophic eggs of this species function as a “reserve food” to buffer the balance between food demand and supply within the colony. We tested this hypothesis by experimental manipulation of the amount of trophic eggs. In experiments altering larval demand, the number of trophic eggs stored decreased in the presence of larvae. Conversely, in experiments reducing both food supply and stored trophic eggs, larval growth rates slowed; however, providing colonies with more trophic eggs did not improve growth rates. These experiments suggest that trophic eggs are consumed and stored according to larval demand, but their effect on promoting larval growth appears limited.

Let’s speak about un-royal jelly - the larval food of ordinary Western honey bees (Apis mellifera)

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Western honey bees (Apis mellifera) do not feed their larvae directly with pollen and honey, but with a special food jelly that is produced in two head glands of the feeding workers. Although all larvae - queen, worker & drone - receive food jelly up to a certain age, almost all our knowledge concentrates so far on queen larvae food jelly (royal jelly). Furthermore, royal jelly research is so far limited to Europe, where A. mellifera has been subjected to selective breeding since the middle of the 19th century - or to regions where it is not native (the Americas & large parts of Asia). Particularly in view of the poor genetic diversity of European A. mellifera, this calls for the inclusion of African A. mellifera, especially when it comes to basic Western honey bee biology such as food jelly characteristics and larval rearing. Otherwise, we may miss the full variation in traits that may no longer be present in highly bred European A. mellifera bees. For this purpose, food jelly samples from the natural range of A. mellifera are investigated and their protein (e.g. major royal jelly proteins) and lipid (fatty acids & sterols) composition is compared. Perhaps the small quantitative differences in the macromolecular composition between royal and worker jelly found in Europe become irrelevant when the variation across the natural range is considered.

Collective nutritional choices in infected ant colonies

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Nutrition in social insect colonies has additional complexities when compared to solitary insects. Not only must foraging workers acquire resources that meet their own nutritional needs but also that of other colony members. In ants, foragers can adjust their food choices depending on their individual nutritional state and they can recruit nestmates via trail-laying to supply resources that match colony-level demands. In infected colonies, foragers preferentially collect protein rich diet, likely to meet the increased protein demands associated with an immune response (1). However, a protein-rich diet preferred under infection drastically decreases survival of healthy ants. Here, we use colonies of the Argentine ant, Linepithema humile, infected with the fungal pathogen Metarhizium, to ask whether the observed protein-biased foraging reflects the infection status of the foragers themselves or the health status of other colony members. If foraging decisions are driven primarily by the foragers' individual needs, we will further test whether a diet change imposed on healthy nurses by infected foragers may, despite a possible long-term survival cost, lead to a preemptive protection of the nurses in case of later disease spread through the colony. Together, this study advances our understanding of how collective and individual nutritional decisions interact in ant colonies under pathogenic stress.

1. Csata, E. et al. Fungal infection alters collective nutritional intake of ant colonies. Curr. Biol. 34, 902-909.e6 (2024).

Lab-to-field risk assessment of the biopesticide Bacillus amyloliquefaciens in bumble bees

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The increasing use of microbial biopesticides in sustainable agriculture requires a deeper understanding of their potential impact on non-target pollinators, particularly wild species such as bumble bees. Although biocontrol agents are generally considered safer than synthetic pesticides, they may still cause subtle but ecologically relevant effects that are often largely overlooked in current risk assessment frameworks. In this study, we investigated the sensitivity of Bombus terrestris to the biopesticide Bacillus amyloliquefaciens QST713 using a multi-scale approach that combined laboratory assays and semi-field experiments. In the laboratory, we evaluated oral toxicity in the context of nutritional stress by exposing workers to sugar diets of optimal and suboptimal quality. Sublethal effects were quantified using a classical Pavlovian conditioning paradigm to assess learning and memory at both short- and long-term intervals. While no significant mortality was observed, exposed individuals exhibited impairments in cognitive performance. Building on these findings, we conducted a semi-field experiment to assess whether the laboratory-observed sublethal effects translate into alterations of ecologically relevant behaviours. Individually marked workers were monitored over several weeks to record foraging activity and resource collection, providing insight into the functional consequences of exposure under more realistic environmental conditions. Overall, our study highlights the importance of integrating laboratory and field evidence to achieve a more comprehensive and ecologically meaningful evaluation of biopesticide risks.

Do periodical cicada emergences alter ant foraging behavior?

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The highly predictable emergence of billions of mature Brood XIII periodical cicadas (Magicicada spp.) in the midwestern U.S. in the spring of 2024, together with the second pulse of their offspring later the same summer, provide excellent opportunities to explore the ecological impacts of landscape scale pulsed biomass resources on ant foraging. We hypothesized that ants will opportunistically adapt their foraging to capitalize on abundant cicada prey, both during the adult emergence and again when the next generation of cicadas hatches later in the summer. We used a combination of direct foraging observations on cicadas and dead fruit flies, and stable isotopes to quantify the impacts of these cicada biomass pulses on ant foraging in five different forest/savannah communities in Lake County Illinois. The relationship between the status of the cicada emergence and the rate at which foraging ants would remove prey items were quantified. Ant foraging on fruit flies had both a faster rate of removal and a greater total percentage of fruit flies removed after the spring periodical cicada emergence compared to the later summer hatchling emergence. Removal rates and percentage removal of fruit flies was also greater at sites with lower cicada density. Over the course of two periodical cicada pulses ant foraging on cicadas was consistently high. But, the dramatic increase in resources due to the cicada emergences did not appear to strongly alter ant foraging patterns within that year.

The characterization of reproductive and trophic eggs of the black cocoa ant (Dolichoderus thoracicus)

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National Taiwan University

The black cocoa ant (Dolichoderus thoracicus) is a notorious pest in Taiwan. Recent studies have revealed that the trophallaxis nutrient transfer of D. thoracicus within colonies occurs exclusively through trophic eggs. While only queens are capable of producing reproductive eggs, both queens and workers can lay trophic eggs, as workers possess developed and functional ovarioles. This study examines the structural and compositional differences between reproductive eggs and trophic eggs produced by queens and workers of D. thoracicus. Electron microscopy reveal that unlike reproductive eggs, trophic eggs lack a complete eggshell, and possess only a thin and fragile yolk membrane. Histochemical staining showed that reproductive eggs are rich in yolk, lipid droplets, and carbohydrates. In contrast, queen-produced trophic eggs although containing yolk and lipid droplets, do not contain significant amounts of carbohydrates. Worker-produced trophic eggs contain only small amounts of yolk, but exhibit abundant lipid droplets and carbohydrate components, consistent with the results of chemical composition analysis. Without feeding on the queen's trophic eggs, the larvae cannot successfully develop into pupae. Based on this finding, we speculate that trophic eggs produced by queens of D. thoracicus mainly primarily provide the protein required for development, whereas trophic eggs produced by workers mainly supply carbohydrates as an energy source for larval activities.

Unbalanced dietary omega-6:3 ratio increases the duration of orientation flights but not foraging flights in honey bees

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Imbalances in the consumption of essential fatty acids affect the ability of animals to perform tasks necessary for survival and reproduction, with excess consumption of omega-6 relative to omega-3 fatty acids negatively impacting learning and memory in mammals and invertebrates. Honey bee adults that consume an unbalanced omega-6 to omega-3 diet (ratio = 5) show impaired associative learning ability and nursing behavior relative to bees that consume a balanced omega-6:3 diet (ratio = 1) when tested within 1-week following diet consumption. In this experiment we tested whether an unbalanced omega-6:3 diet consumed during the first week after emergence has a negative impact on ontogeny and learning that persists into later life stages. Using a common garden design, we placed barcodes on 1-day old bees and fed them either a balanced or unbalanced diet in separate cages for 7-days, after which bees were released into a shared hive. Transits in and out of the hive were monitored to determine the age at first orientation and first foraging flights, and lifespan, along with the duration and number of flights performed. Bees which consumed an unbalanced diet had longer orientation flights relative to bees fed a balanced diet, but with no difference in the duration of foraging flights, nor in the number of orientation or foraging flights, or age at task transitions. These results suggest that an unbalanced omega-6:3 diet impairs the rate of information acquisition and processing in honey bees, and that this impairment will persist for the lifetime of the bee.

The impact of pesticides on wild bee health

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Martin-Luther Universität Halle-Wittenberg

Numerous studies have shown that bees are increasingly threatened by anthropogenic pressures such as agricultural intensification, including exposure to pesticides. In ecotoxicology, honey bees and bumble bees have been widely used as test surrogates to assess the effects of these stressors on bees. However, many crops rely primarily on wild, often solitary, bee species for effective pollination, raising questions about the extent to which social (and frequently commercial) bee species can serve as reliable proxies for all bee species.

To address these open questions, we used adult males and females of two solitary bee species to test the effects of exposure to one or more pesticides via two different exposure routes: contact and oral. In addition to mortality, we quantified behavioural changes and sugar consumption, allowing us to infer potential long-term consequences of non-lethal effects at the individual level. This dataset also allowed us to explore how ecological specialization (specialist vs. generalist) impacts pesticide sensitivity. Our results suggest that wild bees are not only more sensitive to commonly used pesticides, but also better reflect complex interactions following exposure to multiple plant protection products.

By integrating our results with previously reported responses of social bee species, our findings highlight the importance of incorporating diverse pollinator taxa into risk assessment frameworks and emphasize the need for broader, more inclusive conservation and management strategies to reduce the impact of pesticides on bees, social and solitary.

Oxidative stress responses in honey bee (Apis mellifera L.) exposed to neonicotinoid pesticides

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Neonicotinoid pesticides present similar properties with nicotine and highly toxic in small quantities to many invertebrates, including beneficial insects such as bees. These compounds act on the central nervous system and can lead to mortality even at low doses. Oxidative stress biomarkers are increasingly used to evaluate the physiological and cellular effects of neonicotinoid exposure in bees.

In this study, Apis mellifera individuals were divided into four groups of ten bees each, with experiments conducted in triplicate. One group served as a control and received uncontaminated glucose solution, while the remaining groups were exposed to increasing doses of acetamiprid, imidacloprid, and thiamethoxam via oral and topical routes. Protein concentration and oxidative stress markers, including malondialdehyde (MDA), reduced glutathione (GSH), and superoxide dismutase (SOD), were analyzed.

The results revealed dose-dependent biochemical alterations, notably a significant increase in protein concentration. Exposure to thiamethoxam induced pronounced oxidative stress, as indicated by elevated MDA levels and a significant depletion of GSH, suggesting activation of detoxification pathways.

These findings highlight the cellular toxicity of neonicotinoid pesticides in honey bees and underscore the importance of oxidative stress biomarkers in assessing sublethal pesticide effects. Strengthening collaboration among researchers, agricultural policymakers, and professionals is essential for developing sustainable strategies to protect bee health.

Can an ant heal herself? Exploring Wound-care in Dinoponera

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Insect societies exhibit a division of labor between reproductive and non-reproductive members. In many species, reproduction is monopolized by morphologically specialized individuals, while non-reproductive members perform tasks such as foraging. However, in some species, morphologically similar individuals retain equal reproductive potential. This is the case in Dinoponera grandis, a queenless, predatory ant where workers can mate and lay fertile eggs. Reproduction is regulated through behavior, establishing a dominance hierarchy. In this study, we investigate how this species responds to injured foragers. Our research was conducted in the Atlantic Forest of Argentina, where D. grandis occurs at high colony densities. We found that 19% of foragers sustained injuries and report, for the first time, the existence of social wound-care behavior in D. grandis, which increases the survival of injured ants. However, unlike in other ant species where this behavior has been observed, injured D. grandis workers invested significant time in self-care—tending to their own wounds and sometimes applying metapleural gland secretions. When restricted from accessing their wound themselves, isolated ants showed a higher mortality tendency. Our findings suggest that, while social wound care plays a role in this species, self-care is much more pronounced and likely more important for surviving injures.

From individuals to collectives: Insights into the ethology of hygienic behavior via the BeesBook system

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Hygienic behavior is a key component of social immunity in honey bees and is an effective defense against parasites and pathogens. Yet, the individual decision rules and social dynamics that drive hygienic behavior remain poorly understood. Most tests of hygienic behavior involve colony-level responses, such as the pin-killed or freeze-killed brood assay: Damaged brood is introduced to the colony, and after some time, the number of brood cells cleaned by the workers is determined. This allows one to select colonies for hygienic behavior, but one does not gain insight into the ethology of this behavior. Using the BeesBook automated tracking system, we recorded colony activity over two months continuously to capture the fine-scale behavioral trajectories of individually marked workers. We introduced two standardized manipulations, so-called pin-killed brood assays, at defined intervals to elicit hygienic behavior under natural colony conditions. Continuous tracking and a background-subtraction pipeline enabled us to quantify how workers detect, inspect, and remove compromised brood. Furthermore, we could assess how task allocation shifts across time, and how individual experience shapes subsequent participation in hygienic events. This data set provides unprecedented resolution of hygienic behavior and may reveal the temporal, individual, and collective structure underlying this critical behavior.

SYMPOSIUM 08 · The role of brood in social insect colonies
ORAL · Wed 19 Aug · 14:30 · K10 · Session 42 · Abstract ID 149735

Small bodies, big influence: how brood shapes social cohesion in wasps

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Vespidae wasps represents a key group for studying the mechanisms that maintain social cohesion, as these wasps show a range of behaviours from solitary to highly eusocial species. While social cohesion has been examining through adult interaction, several studies reports have reported that brood (eggs, larvae or pupae) can also act as key social units within the colony. Despite this, wasps remain comparatively understudied relative to ants and bees, and even less is known about the role of brood in wasp societies. For example, brood may act as direct or indirect sources of chemical cues that convey information and regulate social behaviour. Wasp larvae are carnivorous and effectively function as a collective “stomach” for the whole colony, positioning them as active participants in social dynamics rather than passive dependants. As interest has grown in understanding how brood contributes to social organization, in this talk, I want to synthesize these findings for wasps. By integrating recent work with my own research, I will cover the role of brood in wasp's nests across different levels of sociality, with a particular focus on chemical communication and social evolution.

SYMPOSIUM 08 · The role of brood in social insect colonies
ORAL · Wed 19 Aug · 14:45 · K10 · Session 42 · Abstract ID 148981

The Evolution of a Larval Worker Caste

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For decades, both empirical and theoretical research on the eusocial insects has focussed on the role of adult altruism, but the possible importance of larvae as helpers has received surprisingly little attention. Larvae of social wasps (and some other Hymenoptera) act as a ‘communal stomach’, digesting solid food provided by workers and regurgitating it to adults (‘larval-adult trophallaxis’) in a nutritionally rich ‘saliva’. This act of donation is potentially costly to larvae, hindering their future reproductive prospects. In 1916, Émile Roubaud hypothesised that larval–adult trophallaxis is the principal attractant of adults to the nest, placing larval actions at the foundation of eusociality. Despite this claim, larval–adult trophallaxis has received little empirical attention no theoretical attention. Using kin selection methodology and agent-based simulation, we show that the development of an adult worker caste in primitively eusocial insects can occur during larval development. Small differences in larval development (e.g., in provisioning by adults or digestive ability) can drive large differences in larval and adult strategies. By modelling ‘larval altruism’ games in which larvae exhibiting higher levels of altruism (donation of resources to adults by trophallaxis) hinder their own reproductive prospects in adult life, we find a ‘larval altruist caste’ can develop prior to adult workers and that larval altruists are subsequently more likely to be adult altruists. Our results highlight the importance of larvae in social insects, and provide testable predictions for empirical research into the long-neglected role of larvae in the evolution of eusociality.

SYMPOSIUM 08 · The role of brood in social insect colonies
ORAL · Wed 19 Aug · 15:00 · K10 · Session 42 · Abstract ID 146469

Brood-Mediated Regulation of Queen Fecundity in Pharaoh Ant

Allina Win

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Queen fecundity is a key determinant of colony growth and fitness in social insects, yet it may be regulated not only by queen physiology but also by interactions with other colony members. Previous work in ants has shown that late-instar larvae can stimulate queen egg-laying, suggesting a form of bottom-up reproductive regulation originating from the brood. However, the proximate source and behavioral mechanisms underlying this effect remain poorly understood. Here, I investigate the role of larval-derived fluid in regulating queen fecundity in the pharaoh ant (Monomorium pharaonis). Focusing on a molting-associated secretion released by late-instar larvae, I experimentally manipulate larval presence and isolate larval components to test whether larval fluid alone is sufficient to alter queen egg-laying and survival. Queens are monitored longitudinally for reproductive output under standardized laboratory conditions, and behavioral observations are used to document how larvae release the fluid and how queens and workers interact with it. This study combines experimental manipulation and natural history observation to clarify how brood actively shape queen reproduction and colony development, highlighting larvae as dynamic regulators within ant societies.

SYMPOSIUM 08 · The role of brood in social insect colonies
ORAL · Wed 19 Aug · 15:15 · K10 · Session 42 · Abstract ID 149912

Molecular evidence for metabolic division of labor and information transfer through ant social fluids

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Metabolic division of labor, the decoupling of resource acquisition, processing, and use across individuals, is fundamental to most biological cooperation. Private channels of metabolic exchange build evolutionary ratchets, driving increasing interdependence as partners lose independent metabolic capabilities. Social insect colonies, where individuals function as differentiated "tissues" connected through socially transferred fluids, offer an ideal system to test this framework.

Here, we integrated transcriptomics and proteomics across five ant species spanning two major lineages (Formicoid: Camponotus, Myrmica; Poneroid: Stigmatomma, Platythyrea) to map colony-level metabolic networks. By tracing protein production, circulation, and utilization, we highlight two forms of social transfer. Resource-based transfers show lineage-specific directionality: Formicoid adults provision larvae with resources and metabolic enzymes, while Poneroid larvae export storage proteins to adults. Formicoid transfers were enriched for autophagy and longevity-regulating pathways, suggesting adults may mobilize cellular resources with potential costs to their own somatic maintenance. Despite reversed flows, transferred proteins share some orthologous functions, suggesting a small ancestral toolkit repeatedly co-opted for colony integration. We also identify information-based transfers including a newly described route: larval excretion. Adult-derived proteins pass through larvae and return via excretion, potentially conveying larval nutritional status as metabolic feedback. This bidirectional flow transforms larvae from passive recipients into active nodes in colony information networks. Together, these findings reframe the colony as a physiological unit where adults and larvae function as interdependent tissues connected through specialized transfer routes. Larval excretion, carrying adult-derived proteins back to workers, suggests larvae actively participate in colony-level information networks.

SYMPOSIUM 08 · The role of brood in social insect colonies
ORAL · Wed 19 Aug · 15:30 · K10 · Session 42 · Abstract ID 149749

Social modulation of decision-making in Drosophila larvae

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All animals must make appropriate, but also flexible, foraging decisions, especially when food availability is scarce or when facing starvation. Drosophila larvae need to eat throughout their life to pupate, eventually become a fly, and mate. It has been shown that they can even feed and survive on a conspecifics diet when no other food is present. We investigated how fly larvae sense each other and if the same sensory systems are involved in cannibalistic behavior. We find that both alive and dead larvae provide overlapping and distinct multisensory cues, such as chemosensory and mechanosensory cues. We investigated the circumstances under which fly larvae turn to cannibalism and how internal state and social context influence these foraging decisions. A group of fed larvae shows weak attraction towards dead conspecifics; however, this preference can be enhanced by starvation. A single alive larva shows an enhanced attraction towards dead conspecifics even when fed, thus social group context prevents cannibalistic behavior. We hypothesize that a cannibalistic context provides the presence of a potential food source, but also the danger of being eaten. Flexibility in foraging behavior enables fly larvae to optimally weigh food availability vs. threat in a social foraging situation and to expand their feeding choices to overcome starvation.

Larval immunity depends on worker presence in the clonal raider ant

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Social insects live in dense groups and are highly susceptible to disease. To mitigate this risk, they have evolved collective defenses known as social immunity. While most research focuses on social immunity among adult nestmates, the influence of workers on brood immunity remains poorly understood. The clonal raider ant Ooceraea biroi is an ideal model because its genetically uniform, synchronously developing colonies and reliance on chemical communication allow controlled larvae–worker experiments.
To investigate if and how workers influence the brood's immune response, I experimentally wounded larvae with sterile saline or infected them with Pseudomonas entomophila. Larvae were kept isolated or with workers, either with or without physical contact. Larval immune response were assessed using survival assays and image-based wound melanization measurements.
Across treatments, larvae kept in contact with workers survived significantly better than isolated larvae. Melanization analyses revealed a significant reduction of wound melanization in sterile-injured and infected larvae in contact with workers. This indicates that the larval immune response is influenced by worker presence.
However, sterile-injured larvae show similarly increased survival in the presence of dead workers, whereas infected larvae need living workers to enhance survival. These results indicate two distinct mechanisms in social immunity towards larvae, based on larvae detecting worker-presence and workers taking care of the larvae.
Together, larval survival and immunity in the context of wound and infection is influenced by workers, underscoring the importance of social immunity toward brood.

SYMPOSIUM 08 · The role of brood in social insect colonies
ORAL · Wed 19 Aug · 16:00 · K10 · Session 42 · Abstract ID 149771

Brood care and larval behavior in Holcoponera striatula

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The care of immatures affects their survival. However, this care can be influenced by the immatures themselves. The initiation of feeding, for example, can be generated through larval beggings, which influence the distribution of resources by the workers. Through this research, we proposed to address brood care from a perspective that includes both, the caregivers and the brood. For this purpose, the ant Holcoponera striatula was studied, analyzing the behaviors of adults and immatures in the absence and presence of food.

Twenty behaviors were recorded, ten performed by workers and ten by larvae. All behaviors had been previously reported, but their descriptions were complemented.

Regarding food availability, in workers three behaviors showed higher values in the absence of food. Two of these were associated with resource allocation, and one, licking, with an additional investment in this task due to the absence of feeding. As for larvae, five behaviors showed higher values in the presence of food. These differences were associated with food solicitation. Some of these behaviors had previously been dismissed due to their low frequency. Additionally, in larvae a disparity was also found in the terms used to describe behaviors, evidencing a lack of homogeneity.

Through this work, brood care is therefore addressed in an integral manner, complementing previously established descriptions and evidencing the appeal that the larva may have in its own care.

SYMPOSIUM 08 · The role of brood in social insect colonies
ORAL · Wed 19 Aug · 16:15 · K10 · Session 42 · Abstract ID 146779

Transcriptomic signatures of parental and alloparental care in the facultatively eusocial ambrosia beetle Xyleborinus saxesenii

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Social behavior ranges from simple, transient interactions to complex societies with cooperative brood care and division of labor. Early social evolution is often associated with regulatory changes that modify the timing and patterns of gene expression underlying social behavior. In my PhD project, I investigated transcriptomic patterns associated with parental and alloparental care in the facultative eusocial ambrosia beetle Xyleborinus saxesenii (Curculionidae: Scolytinae). This cooperative fungus-cultivating beetle exhibits sibling mating and haplodiploidy, parental care, division of labor between adults and larvae, larval cooperation, and delayed dispersal of some adult daughters that provide alloparental care despite being capable of independent reproduction. We generated head and abdominal transcriptomes from adult females during a solitary phase, three distinct parental care phases, and from adult daughters remaining in the natal nest. In addition, we analyzed transcriptomes from larvae at second and third larval stages. Gene expression profiles differed significantly among all adult female phases and between larval stages. The strongest transcriptomic shifts occurred between post-hatching caring mothers and nest-staying daughters, as well as during the transition from nest-staying daughters to dispersing females. Notably, genes associated with Juvenile Hormone signaling showed elevated expression in dispersing females and caring adults compared to nest-staying daughters. These results suggest that transitions between caregiving, helping, and dispersal states are accompanied by pronounced regulatory changes, supporting the idea that behavioral flexibility in facultatively eusocial species is underpinned by dynamic gene expression rather than fixed caste-like programs.

Decoding social information: How state-dependent larval signals orchestrate the division of labor in clonal raider ants

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Division of labor in parental behavior is linked to evolutionary success across species. In social insects, age-dependent variation in the propensity to nurse and forage among workers is fundamental to colony organization, with larval signals playing a key role in regulating this division of labor. However, the proximate mechanisms and sensory pathways remain poorly understood, as most social insect species lack experimental tractability and tools. Recent progress in ant circuit neuroscience makes the clonal raider ant (Ooceraea biroi) a uniquely powerful model for studying the neural and behavioral basis of alloparental care. Here, we use a novel behavioral assay to examine the microstructure of offspring-directed care across various brood states and worker traits in individual worker–larva pairs. By combining the spatiotemporal resolution of this approach with video-analysis tools for behavioral segmentation, we aim to identify stereotyped behavioral sequences, create a detailed atlas of alloparental behavior, and pinpoint entry points for dissecting the neural pathways that mediate caregiving. Detailed insight into caregiving mechanisms primarily comes from rodent research, as invertebrate models like Drosophila lack parental care. Here, we leverage functional imaging in the clonal raider ant to map neural activity in peripheral sensory pathways and across distributed neuropiles. By comparing activity patterns across workers with known behavioral tendencies, we will identify how larval signals are transformed and integrated across brain networks to bias caregiving decisions. Altogether, aligning behavioral sequences with neural responses will reveal how social cues are encoded in the brain and how colonies flexibly allocate care.

Hidden helpers? Exploring larval trophallaxis as altruism

Ellena Trelfa-Stewart

For primitively eusocial wasps, unequal access to nutrition is a source of power asymmetry. Despite this, paper wasp larvae relinquish a portion of the nutrients they receive by producing protein-rich saliva for adult nestmates - a behaviour that helps to sustain the entire colony. More than a century after larval saliva trophallaxis was first observed, it remains unclear whether the behaviour constrains larval life prospects, and thus whether this donation constitutes altruism. Here, we manipulated saliva production to test whether donation reduces lifetime fitness. We experimentally increased the saliva production of individual Belonogaster juncea larvae in Kenya, evaluating the prediction that the most generous donors would experience physiological costs, such as under-developed ovaries. Further, the post-emergence integration of saliva-depleted individuals was tracked using social network analysis to assess whether they were more likely to prioritise their indirect fitness by assuming subordinate roles. We also investigated whether larvae could buffer against the effects of prolific saliva donation – for example by begging adults for nutritional compensation – using observations of larval behaviour and adult-larva interactions. Collectively, our results present the first test of whether larval helping behaviour shapes adult power asymmetries - and whether wasp larvae represent hidden altruists in the evolution of eusociality.

SYMPOSIUM 08 · The role of brood in social insect colonies
POSTER · Abstract ID 149941

The (underappreciated) contribution of brood metabolic rate to whole-colony metabolic expenditure: Comparing metabolic rate during foraging and statary phases of clonal raider ants (Ooceraea biroi)

Ioulia Bespalova; **Jane Waters**
Providence College

Models of whole-colony metabolic rate have suggested that worker movements are a major component of a colony's energy budget. While worker movement is indeed a cost, the metabolic expenditure of brood activity can be an equally high contributor, especially in small or young colonies with a low worker to brood ratio. In this study, we used the clonal raider ant Ooceraea biroi to study how brood contribute to whole colony metabolic rate. This species lacks queens, and parthenogenic reproduction by workers is highly synchronized, so that brood develop on the same schedule, leading to functionally and compositionally different phases of colony growth. We measured whole colonies of O. biroi and found that colonies in the foraging phase (dominated by workers and larva) had a higher mass-specific metabolic rate than colonies in the statary phase (dominated by workers, pupa, and eggs). We then measured the metabolic rate of small groups of eggs, larva, pupa, and workers, and created an energy budget for the colony during the two phases. We additionally quantified movement in whole colonies, and individual workers, to connect worker movement to metabolic rate. We found that the lower metabolic rate of colonies in the statary phase could be largely attributed to the higher proportion (by mass) of pupa, which had the highest mass and lowest metabolic rate of all colony components. Meanwhile, larvae in the foraging phase contributed almost as much to metabolic rate as workers. Worker movement did not differ between the two phases in our experimental setup.

Nutrient investment in offspring across social organization in cockroaches

Sofia Bouchebti

Ben Gurion University of the Negev

Nutritional interactions among individuals generally increase with social complexity, as social living facilitates resource exchange within groups. While postnatal nutrient transfer has been relatively well characterized in many taxa, far less is known about how it interacts with prenatal parental investment. In particular, investment trade-offs may occur if postnatal feeding reduces the need for prenatal provisioning. Prenatal maternal investment may also vary with mating systems, especially when males can contribute nutrients via nuptial gifts.

This study examines how such investment trade-offs are shaped by social organization and reproductive mode using a comparative framework in cockroaches (Blattodea). The three study species represent distinct levels of social organization: the greenhouse cockroach, a gregarious species forming small aggregations; the American cockroach, a highly gregarious species forming large aggregations; and the lobster cockroach, a subsocial species exhibiting maternal behavior. These species also differ in mating systems and opportunities for parental investment, ranging from exclusive maternal investment under parthenogenesis to sexual reproduction with potential paternal contributions.

Stable isotope labeling was used to track the fate of nutrients in parents and offspring. Newly emerged adults were fed an artificial diet containing ^{13}C-labelled leucine, and isotopic enrichment was measured in multiple adult tissues and in offspring produced subsequently to characterize patterns of nutrient allocation.

Overall, the results reveal distinct patterns of nutrient allocation across species that are consistent with differences in social organization and mating systems, contributing to a broader understanding of the relationship between nutrition and social organization.

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

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Parental care is a major evolutionary innovation that enhances offspring survival but may constrain parents through trade-offs with self-maintenance. Such physiological costs are thought to play a key role in the evolution of family life and sociality, yet they remain poorly quantified, particularly in insects.

Here, we investigated the immune costs of maternal care in the European earwig (Forficula auricularia), an insect in which females provide prolonged care to both eggs and juveniles. Earwig mothers lay eggs in early winter, cease foraging, and provide continuous care until hatching in early spring, including nest defense, egg grooming, thermal regulation, and food provisioning. After hatching, mothers continue caring for juveniles for approximately two weeks before family dispersal. To test whether this sustained investment compromises maternal immunity, we experimentally manipulated caregiving effort by varying brood size at either the egg (0, 55, 110 eggs) or juvenile stage (0, 40, 80 juveniles) in 1,040 mothers. Female immune function was assessed at four key reproductive stages, from pre-oviposition to post-hatching, using measures of encapsulation response, respiration rate, lytic activity, and phenoloxidase activity, under both basal conditions and following immune activation with the heat-killed bacterium Serratia marcescens. Maternal survival following bacterial challenge was also quantified. We predict that increasing caregiving effort reduces immune performance, revealing physiological trade-offs that may constrain parental investment and influence the evolution of parental care and early forms of social life.

Diversity of Social Behavior in Ceratina Bees: A Global Perspective

Michael Mikát
Charles University

Small carpenter bees (Ceratina) bees represent an excellent model for studying social evolution due to their remarkable interspecific and intraspecific variability in parental and social behavior. Most species are facultatively eusocial, allowing direct comparisons of solitary and social nests within single populations. Despite their suitability for comparative analyses, high-quality data on nesting and social biology are available for only a few species, primarily from temperate regions. Here, I analyzed the social biology of Ceratina bees by dissecting approximately 25,000 nests from 30 species across five continents, including tropical regions. I confirm that most species exhibit facultative sociality, although the proportion of social nests varies between species, with solitary nests predominating in nearly all species. Social nests typically contain two females, though up to eight may co-occur. These nests are generally more productive than solitary ones, yet per capita productivity varies across species. Interestingly, wet tropical regions do not exhibit a higher proportion of social nests than Mediterranean climates, whereas species inhabiting dry biomes tend to show increased social nesting. These findings provide a comprehensive framework for understanding the ecological and evolutionary drivers of sociality in Ceratina bees.

The effects of serotonin in modulating behaviour and brain gene expression within a facultatively social bee

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Dominance interactions between nestmates are essential in establishing and reinforcing social hierarchies. Neural modifiers like biogenic amines are a key influence on the neural process behavioural pathway, affecting responses to new stimuli. Serotonin is known to modulate aggression, motor behaviour, sensory processing and social interactions in social insects. The small carpenter bee Ceratina calcarata, is a facultatively social bee species where a dominance hierarchy is established between the mother and her eldest daughter. Mothers establish this dominance hierarchy by provisioning their eldest offspring with less pollen and less protein, resulting in a worker-like dwarf eldest daughter (DED). We posit that this dominance hierarchy is further modulated by biogenic amines, namely serotonin. To explore the influences of serotonin on social behaviours, serotonin was topically administered to C. calcarata dwarf eldest daughters (DEDs), while the mothers were topically treated with the serotonin antagonist cyproheptadine hydrochloride. Mothers and DEDs of the same nest underwent behavioural assays to assess aggressive and avoidant behaviours. We additionally compared brain gene expression profiles between mothers and DEDs across treatment groups. Our findings indicate that the supplementation of serotonin to DEDs stimulated an increase in aggressive behaviours within the typically tolerant DEDs, and were also associated with the upregulation of genes associated with circadian clock and olfactory learning found within treated daughters. These findings provide the foundations to understanding the role of biogenic amines in regulating neural activities for social behaviour to investigate mutual tolerance and social group formation.

Brain development in an allodapine bee aligns with social caste and ecological intelligence

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Social complexity and group size are often posited as important factors driving the evolution of animal brains. Diverse lineages of social insects offer alternate opportunities to assess the influence of group-living behaviour on neurobiology, that do not always conform to emerging hypotheses: social brain; distributed cognition; sensory environment. The facultatively social bee Exoneura angophorae was used to explore intraspecific variation in brain development - comparing individuals from social (queens, workers) and sub-social (single-female) colonies. Brain volumes (mushroom body calyces, optic lobes, antennal lobes, whole-brain) were measured as a proxy for neural investment. Mushroom bodies were reduced in workers, but did not differ between queens and single-females. Workers had larger optic lobes than queens, but did not differ from single-females. There were no significant differences in antennal lobes or whole brain volumes between behavioural categories. This implies that social caste, rather than group nesting per se, influenced mushroom body volume – opposing both ‘social brain’ and ‘distributed cognition’ theories. Results comparatively align with ceratinine and halictine bees that also form small facultatively social colonies. Enhanced optic lobes of workers and single-females is likely associated with foraging behaviour and a response to dietary niche requirements – supporting ecological intelligence hypotheses rather than any social affect. Optic lobe development may be highly plastic, capable of rapid transition in allodapine and ceratinine bees. Results suggest common trends among independently evolved lineages of facultatively social bees that warrant further investigation on the neural circuitry involved in alternate environmental and social-caste contexts.

Variation in ants olfactory system design

Carlotta Martelli

Johannes Gutenberg University Mainz

Odorant receptors (OR) gene families have undergone significant expansion in ants and other social insects. While this expansion might not be strictly tied to the evolution of eusociality, undoubtedly ants rely on a more complex olfactory system in their colony life. On one hand, numerical complexity (i.e. a large number of ORs) is key for the detection and the discrimination of many odors. On the other hand, additional plasticity in the adult, as well as stochastic mechanisms during development might endorse ants with the capability to individualize their behaviors based on social and environmental conditions.

I will discuss our effort to characterize inter-individual variation in the anatomy of the olfactory system of more than 120 worker ants of Temnothorax longispinosus. We have analyzed variation in the anatomy of the main olfactory neuropil, the antennal lobe, which is characterized by glomerular structured formed by the axon terminals of the Olfactory Receptor Neurons and their partners. I will show how size and number of glomeruli depend on colony identity, colony type and environmental conditions discuss and how this anatomical variation relates to underlying genomic and transcriptional properties. This work constitutes a first step in understanding the origins of non-genetic variation that may contribute to division of labor within colonies and shape the evolutionary trajectories of social insects.

SYMPOSIUM 10 · Mechanisms facilitating the evolution of social behavior in insects
ORAL · Wed 19 Aug · 10:45 · K7 · Session 33 · Abstract ID 149990

Mischocyttarus Wasps as a Window into the Origins of Social Cognition and Chemical Communication

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Primitively eusocial wasps of the genus Mischocyttarus occupy a critical phylogenetic and social position for understanding the evolutionary origins of complex insect societies. Here, we integrate behavioral, chemical, and endocrine studies to argue that Mischocyttarus provides a key perspective on how social cognition and reproductive signaling evolved prior to the emergence of morphologically distinct queens.

Our work shows that chemical communication in primitively eusocial species extends across life stages: eggs bear colony-specific cues that enable efficient nestmate recognition and egg policing, indicating that recognition systems operate early in development. Cognitive assays further reveal that learning and memory vary with age and sex, reflecting socio-ecological constraints associated with division of labor rather than fixed caste morphology.

At the colony level, dominance hierarchies and reproductive status correlate with quantitative shifts in cuticular hydrocarbons, and experimental manipulation of hierarchies demonstrates their social plasticity. Importantly, juvenile hormone regulates both reproduction and fertility-linked chemical cues, including egg-associated compounds.

We propose that such hormonally controlled fertility signals represent ancestral mechanisms from which queen pheromones and stable reproductive castes evolved in highly eusocial insects, positioning Mischocyttarus as a bridge between solitary ancestors and advanced eusocial lineages.

Cryptic chemical and genomic differentiation correlates with social complexity in the socially flexible sweat bee Megalopta genalis

Callum Kingwell[1]; Andrew Webb[1]; Olivia Harringmeyer[1]; Sarthok Rahman[1]; Anvita Chaudhary[1]; Eli Wyman[1]; David Cardona[1]; Joanna Shoubaki[2]; William Wcislo[3]; Sarah Kocher[1]

[1] Princeton University; [2] Harvard University; [3] Smithsonian Tropical Research Institute

Understanding transitions between solitary living and obligate eusociality remains a central challenge in evolutionary biology. The sweat bee, Megalopta genalis, is a socially flexible species in which solitary and eusocial nesting strategies coexist within a single population. While M. genalis was previously assumed to be a single species, chemical and genetic data reveal two distinct populations varying in cuticular chemistry, social organization, and physiology. Roughly half of ‘chemotype I’ foundresses establish eusocial colonies, while ‘chemotype II’ foundresses form eusocial nests almost exclusively. Chemotype II eusocial nests are larger and dominance hierarchies are more stable than those of chemotype I. Consistent with increased commitment to eusociality, chemotype II queens exhibit higher titers of juvenile hormone and a queen pheromone promoting worker sterility. Genome-wide association and selection scans indicate a largely polygenic architecture underlying social behavior in the species complex, but also reveal a ~5 Mb region of suppressed recombination centered around an array of near-identical odorant binding protein (OBP) genes. Variation within this structural variant resolves distinct haplogroups biased toward eusocial nesting in highly social chemotype II, but not chemotype I. Phased, long-read assemblies show extensive variation in OBP copy-number across haplotypes, and antennal transcriptomes reveal that the same OBP is the most strongly female-biased gene expressed. Together with ligand binding assays, this expression bias supports a role in sociochemical signal processing. Our results suggest that evolutionary transitions from flexible to obligate eusociality can arise through genomic changes that bias how social information is perceived by the peripheral nervous system.

SYMPOSIUM 10 · Mechanisms facilitating the evolution of social behavior in insects
ORAL · Wed 19 Aug · 11:15 · K7 · Session 33 · Abstract ID 140628

Behavior and chemical signaling facilitate the social dominance of reproductive workers across contexts in queenless groups of Indian jumping ants (Harpegnathos saltator)

Benjamin Pyenson[1]; Christopher Albin-Brooks[2]; Majid Ghaninia[3]; Juergen Liebig[3]

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The evolutionary ecology of social insects relies on an understanding of how dynamic contexts influence multiple traits of individuals. Without an obvious queen, reproductive individuals often retain their social dominance over subordinates through different strategies. Here, we find that reproductive Indian jumping ant workers (Harpegnathos saltator) in queenless groups adjust their ovarian activity, strength of chemical signaling, and frequency of behavioral dominance in response to artificial manipulations of their social context. Social context influenced neither the reproductive workers' brain size nor their sensitivity to many hydrocarbons, however. In different contexts, then, modifications of either behavior or signaling are sufficient for these reproductives to maintain their social dominance.

Genetic, behavioral and chemical data give discordant information about population structure in Formica exsecta

Anu Halonen
University of Oulu

Formica ant supercolonies are unique social systems, but we do not fully know how they form. In order to understand dispersal mechanisms and how supercolonies spread it is important to gain a better understanding of the current state of supercolonies. Recent work has shown that Formica supercolonies may be more complicated than thought, with complex internal structures, rather than large homogenous populations. However, such complexity is poorly understood: Are supercolonies in large continuous habitats homogenous, or do they split into smaller units over time? Or do neighboring and expanding supercolonies fuse when they come to occupy the same area?

We investigate the relationships between the aggression or lack thereof within supercolonies, the pattern of cuticular hydrocarbons (CHCs) i.e. the odors on which nestmate recognition and possible aggression towards intruders is based, and the underlying relatedness between workers.

Behavioral data revealed some unexpected aggression within the populations, without any clear geographic patterns. In contrast, GC-MS analysis showed no within-population CHC substructuring, suggesting unified identity in both populations. Furthermore, DNA microsatellite analysis suggests that both populations have lower than expected levels of polygyny, with high within-nest relatedness, and that most structuring is between nests.

Overall, our findings show that chemical and behavioural coherence in these populations does not necessarily reflect high polygyny or genetic homogeneity, underscoring the complexity of social structure in Formica ants.

Evolutionary transitions in social behavior are associated with convergent and partially reversible expansions of transcription factor binding sites

Savanna Ploessl; Beryl Jones
University of Kentucky

The evolution of sociality involves shifts in physiology and behavior, but most notably the emergence of a reproductive division of labor. Within social colonies, these distinct behavioral phenotypes arise from differential regulation of a shared genome. Changes in transcription factor (TF) binding motifs are one potential mechanism underpinning this plasticity, with prior studies suggesting that social species exhibit expansions in TF binding sites. However, it remains unclear whether motif expansions are reversed when sociality is lost. Here we analyze predicted TF motif occurrences across gene promoters in 42 bee species spanning millions of years of evolutionary divergence and multiple independent gains and losses of sociality. We compare motif presence across species to test whether motif expansions are a convergent feature of social evolution and whether their presence secondarily decreases when social behavior is lost. Our findings are consistent with previous research, demonstrating an expansion of TF motifs in lineages which have gained sociality. However, contrary to expectation, we do not observe genome-wide motif contractions in lineages which have secondarily lost social behavior. Despite this overall pattern, we still identify several motifs, promoter regions, and specific motif-promoter pairs which exhibit complementary changes with both gains and losses of sociality. These regulatory targets are enriched for similar organismal functions, providing strong candidates for further study. Overall, our results provide new insights into transcriptional control points involved in the evolution of sociality.

SYMPOSIUM 10 · Mechanisms facilitating the evolution of social behavior in insects
ORAL · Wed 19 Aug · 12:00 · K7 · Session 33 · Abstract ID 149744

The Pace-of-Life syndrome as a potential mechanism underlying the evolution of sociality in Arthropods

Violette Chiara[1]; Tristan Robineau[2]; Magdalena Witek[2]

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Over recent decades, the pace-of-life (POL) hypothesis was introduced to explain the existence of variations in a suite of phenotypic traits. The POL hypothesis posits that differences among individuals involve a suite of intercorrelated traits and that animals can be ranked along a slow–fast continuum merging behavioral, physiological, and life-history traits. Along this continuum, species at the “slow” extreme are, for instance, characterized by slow development and long adult lifespan. The POL hypothesis has been particularly validated in ectotherms; arthropods are therefore an interesting model.

Arthropods can also be distributed along a social gradient, ranging from solitary to eusocial species. Interestingly, higher levels of sociality are characterized by slower life-history traits. Despite those observations, the relationship between POL and sociality remains unresolved.

In this presentation, we first summarize the numerous clues found in the literature suggesting that POL traits and social level are intrinsically correlated. We will also discuss the limits and exceptions to this idea.

When studying the evolution of sociality, it is generally assumed that the social component is the main selected trait, while physiological and life-history traits co-evolve as a form of “support” for sociality. In a second part, we propose a refreshing framework that approaches this question from a different perspective, treating sociality as one component of the POL rather than as an independent leading trait. We will also review the current state of the literature supporting this view and discuss the implications this idea would have for the mechanisms underlying social evolution in arthropods.

SYMPOSIUM 10 · Mechanisms facilitating the evolution of social behavior in insects
ORAL · Wed 19 Aug · 14:30 · K7 · Session 39 · Abstract ID 149838

Wing polyphenism and eusociality during the origin of ants

Ehab Abouheif
Zhejiang University

Major evolutionary transitions occur when individuals unite to form a single organism with a division of labor between its constituents. Programmed Cell Death (PCD) has been proposed to play a role during major transitions at different scales of organization, such as the transition to multicellularity and to eusociality. Yet, this proposal has not been tested rigorously using phylogenetic comparative methods. We therefore use ancestral state reconstruction to test if PCD was involved in the major transition to eusociality in ants. Wing polyphenism, where wings develop in queens but not in workers in response to environmental cues, evolved once and is a general feature of ants. Wing polphenism evolved at approximately the same time as, and is thought to have facilitated, the origin of eusociality in ants. Here we show that PCD, mediated by apoptosis, plays a role in the degeneration of wings in the worker caste across the ant phylogeny, and infer a role for PCD in regulating wing polyphenism in the last common ancestor of all extant ants. Our findings therefore provide evidence that PCD played a role in the major transition to eusociality in ants, and raises the possibility that PCD facilitates major transitions at different scales organization.

SYMPOSIUM 10 · Mechanisms facilitating the evolution of social behavior in insects
ORAL · Wed 19 Aug · 14:45 · K7 · Session 39 · Abstract ID 146484

Larval social fluids modulate caregiver feeding drive in ants

orli snir
The Hebrew University

.Communication underpins the cooperation of ant societies, enabling their evolutionary success and ecological dominance across terrestrial ecosystems. Yet, the fundamental modalities of communication remain poorly understood. We previously showed that pupal molting fluids—a developmental byproduct—function as a communication modality supporting a dense interaction network. Here, we address a critical gap in understanding communication across development: how larvae signal their needs to caregivers. Isolating larvae revealed that, like pupae, they secrete social fluids consumed by adults in a colony context. Whereas pupal fluids originate from molting exudates, larval fluids derive from hemolymph, establishing a second chemical communication channel intrinsically linked to developmental physiology. Blocking larval secretion abolishes food provisioning without disrupting general care, indicating that these fluids convey hunger state. Thus, developmental dynamics are mirrored in their secretions, which act as real-time information channels enabling caregivers to fine-tune feeding decisions. We propose a general principle of social communication: developmental processes generate chemical cues that integrate offspring state into caregiver responses and colony-level cooperative care.

SYMPOSIUM 10 · Mechanisms facilitating the evolution of social behavior in insects
ORAL · Wed 19 Aug · 15:00 · K7 · Session 39 · Abstract ID 150045

Gut Microbiota Regulation of Social Behaviour in Honeybees

Gregorio Calderoni; Maria Holzmann; Chrystelle Perruchoud; Joanito Liberti
University of Geneva

The molecular determinants of social behaviour remain poorly understood, yet elucidating them is key to understanding the evolution of sociality in insects. Social behaviour is shaped by internal physiological states and external cues, with the gut microbiome emerging as a key internal regulator across animal models. Previous research has shown that honeybees possessing a gut microbiome exhibit more frequent and specialized social interactions compared to gut microbiota-depleted bees. Following up on these findings we used an automated behavioural tracking system, quantifying the social interactions of separate bee subcolonies over 6 days after mono-colonisation with 5 core honeybee gut bacteria, in order to disentangle the effect of each bacterial genus on honeybee social behaviour. Each treatment was compared against a group of microbiota-depleted bees and one of bees conventionally colonised by their native hive gut microbiota. Doing so, we identified the gut microbiota symbionts inducing significantly higher social interactions. To reveal molecular mechanisms underlying microbiota-driven social behaviour, we will perform brain metabolomic analyses and relate metabolite abundance to social interactions. Candidate metabolites will then be experimentally manipulated to test their causal effects on behaviour. Together, this work will provide mechanistic insight into how gut microbes shape social behaviour and contribute to the evolution of insect sociality.

SYMPOSIUM 10 · Mechanisms facilitating the evolution of social behavior in insects
ORAL · Wed 19 Aug · 15:30 · K7 · Session 39 · Abstract ID 149772

Pace of life and sociality: variations of behavioral and physiological traits among four Anelosimus species.

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The transition from solitary to social lifestyles is one of the seven most important evolutionary transitions. While the benefits and costs of social life have been deeply studied, the mechanisms supporting the adaptations arising with sociality are still 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. In social species, we often observe life history traits characteristic of a slow POL, theoretically favoring the maintenance of social life. Despite those observations, the relationship between sociality and POL has not been assessed yet.

In spiders' evolutionary history, sociality emerged independently 18 times. These numerous transitions suggest that the emergence of sociality in spiders is a relatively straightforward process. Here, we propose that the spiders' rapid adaptation to sociality results from a slowdown of their POL traits, which we predict to favor the maintenance of social life. We therefore expect social spiders to exhibit, besides slower life-history traits, behavioral and physiological traits characteristic of a slower POL.

We measured behavioral traits (exploration, activity, and boldness) and physiological traits (metabolic rate) of four species of Anelosimus collected in Serra do Japi (Brazil), ranging from social species to nearly solitary ones.

As predicted by our hypothesis, we found a switch toward slower POL characteristics in all measured traits as the sociality level increased.

This comparative study provides new insights into the relationships between POL and sociality, offering a better understanding of the mechanisms supporting the emergence of sociality.

Context-dependent intruder recognition and aggression in a subsocial cockroach

Haruka Osaki; Kensei Kikuchi

Stable social associations require mechanisms that allow individuals to selectively tolerate partners while excluding non-partners. Context-dependent regulation of aggression is one such mechanism, as it prevents misdirected aggression that would otherwise destabilize social relationships.

Aggressive behavior enhances fitness by securing access to mates, offspring, and other critical resources. In social animals, aggression toward outsiders often depends on the ability to discriminate between social partners and non-partners. In pair-living systems, such discrimination may be expressed cooperatively, with both members jointly directing aggression toward intruders while maintaining tolerance toward each other.

Although recognition-based aggression has been well studied in vertebrates, its expression and flexibility in insects remain poorly understood.

The subsocial wood-feeding cockroach Salganea taiwanensis forms stable mating pairs that cohabit within decaying wood. Within established pairs, both partners engage in coordinated aggression against conspecific intruders, while never directing aggression toward their partner, suggesting selective recognition of social partners and outsiders.

Here, we tested whether aggression toward intruders functions as a consistent pair-defense response or a context-dependent outcome of intruder recognition. We introduced conspecific intruders to established mating pairs and quantified aggressive responses by both partners. Aggressive responses varied markedly among intruders, ranging from immediate joint attacks to weak or absent aggression.

These results demonstrate that aggression toward intruders in S. taiwanensis is not an automatic response to conspecific presence, but a flexible, context-dependent behavior. Our findings highlight regulated aggression as a behavioral mechanism stabilizing pair-based social associations and provide insight into early-stage mechanisms underlying the evolution of social behavior in insects.

The enemy of my enemy is my friend: intergroup conflict and cooperation in the Pacific dampwood termite (Zootermopsis angusticollis)

Jasmine Lowe[1]; Michael Cant; Faye Thompson

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Intense conflict between groups is thought to drive the evolution of cooperation within them. However, intergroup interactions aren't always aggressive: in many species, groups tolerate or even cooperate with rivals, but little is known about what drives this variation. Here, we test the hypothesis that a 'common enemy' promotes cooperative intergroup interactions, using laboratory colonies of the dampwood termite, Zootermopsis angusticollis. Wild Z. angusticollis colonies live in rotting logs and interactions between colonies within logs can vary from lethal fighting to peaceful fusion. To test our hypothesis, we placed two size-matched 'focal' colonies (of varying pairwise relatedness) side by side and kept them separated by a mesh barrier. After 2 days we introduced a 'common enemy' colony of varying size and removed the barrier separating the focal colonies to observe their intergroup interactions. Rates of affiliative, agonistic, and alarm behaviours between the pair were measured. Our preliminary findings suggest that: 1) the presence of a common enemy presence may increase rates of affiliative behaviour between focal colonies, and decrease rates of agonistic and alarm behaviours; 2) affiliative behaviours vary with genetic relatedness between colonies; 3) affiliative behaviours may increase with the size of the common enemy group; 4) reproductive castes are particularly vulnerable during intergroup interactions. Our study suggests that a common enemy may promote fusion between colonies, likely because joining forces offers a size advantage against a shared threat. These results contribute to our understanding of intergroup behaviour and how intergroup cooperation and conflict shape the evolution of societies.

When social signals disappear: cannibalism among siblings in a solitary spider

Antoine Lempereur[1]; Raphaël Jeanson

[1] *University of Toulouse*

Tolerance among conspecifics is essential to social life, which implies that dedicated mechanisms have evolved to inhibit aggressive behaviours. Sociality in many taxa may be transient, adding a layer of complexity, as individuals of the same species may exhibit variable responses to social signals throughout their development. Spiders are a relevant model for studying these mechanisms, as juveniles are social early in their development, then become solitary and aggressive towards conspecifics after dispersal. Previous research has shown that social isolation induces cannibalism towards siblings, while those raised in groups remain tolerant. In many species, intraspecific aggression is often modulated by the nutritional status of individuals. In the solitary spider Agelena labyrinthica, we found that the social context did not affect the fat reserves of juveniles, suggesting that the nature of social interactions is not influenced by differences in energy reserves. We then examined whether the tolerance expressed in spiders raised in groups disappeared when they were confronted with the corpses of their siblings, whether freshly killed or 24 hours old. We found that, regardless of age, most sibling corpses are consumed within an hour of first contact. These results suggest that tolerance towards conspecifics is induced by a signal that disappears after death, exposing corpses to cannibalism by siblings.

Analysis of molecular bases underlying the increase in the number of Kenyon cell subtypes during the evolution of hymenopteran insects

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In hymenopteran insects, the number of Class I Kenyon cell (KC) subtypes, which constitute the mushroom bodies (MBs), an insect higher-order brain center, has increased in association with the behavioral evolution. To clarify the molecular developmental bases that have led to the increase in the number of KC subtypes, we conceived an interspecific comparison of the KC subtype development between the European honey bee and the turnip sawfly, whose MBs comprise three and one KC subtypes, respectively. We first identified pupal stages when each KC subtype is produced from MB proliferating cells in each species by labeling proliferating MB cells, at various pupal stages with EdU. The results indicated that three KC subtypes are produced sequentially at different pupal stages in the honey bee, while one KC subtype is produced until about 40 hours after pupation in the sawfly. Next, to investigate the molecular basis for differentiation of each KC subtype in the honey bee, we performed single-cell RNA-seq analysis of MBs of pupae at stages when each KC subtype is produced. Some genes encoding transcription factors were preferentially expressed in the MB proliferating cells in a pupal stage-specific manner, implying their functions in the differentiation of each honey bee KC subtype. Based on these results and the ongoing identification of genes involved in the differentiation of one KC subtype in the sawfly, we propose a model of the cellular and molecular basis underlying the increase in the number of KC subtypes during the evolution of hymenopteran insects.

Sociality and pollen usage of New Zealand's Little Sweat Bee (Lasioglossum sordidum)

Tovah Kashetsky[1]; Jessica Forrest[1]; Nigel E. Raine[2]; Jenny Jandt[3]

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Bees are a diverse clade of animals that exhibit the entire spectrum of sociality and demonstrate a considerable range of diet breadth. The sweat bee Lasioglossum sordidum, one of only 28 bee species native to New Zealand, is thought to be primitively eusocial; however, little is known about the extent of their sociality. Further, this species collects pollen from numerous plant families, but individual preferences through time have yet to be characterized. We investigated L. sordidum sociality through behavioural observations, quantified the dynamics of pollen usage by repeatedly sampling and identifying pollen from marked females, then compared how diversity of collected pollen was related to sociality. Between 15 and 42% of nests were social, with at least 2 females undertaking nest care, but relatedness between caretakers was unclear. Individuals varied in plant fidelity across foraging trips, as some females collected from the same plant families over multiple trips while others collected from new plant families. We found no relationship between nest sociality and pollen collection diversity. Our research provides insight into fundamental knowledge about the ecology of L. sordidum and contributes to our wider understanding of social evolution by investigating species that represent extant examples of what is hypothesized to be an early transition.

Individual variation in the organization of the olfactory system in workers of the ant Temnothorax longispinosus

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In social insects, particularly ants, the olfactory system supports chemical communication and behavioral specializations through an expanded Odorant Receptor (OR) repertoire. Olfactory Receptor Neurons (ORNs) expressing the same Odorant Receptor (OR) project to a specific glomerulus in the antennal lobe (AL), the primary olfactory neuropil. This highly conserved one-OR:one-ORN:one-glomerulus model implies a fixed number of glomeruli that are species-specific, and caste-specific in ants. The genome of Temnothorax longispinosus encodes ~450 OR genes, half of which are differentially expressed between nurses and foragers, suggesting a molecular basis for behavioral specialization. However, it remains unclear whether anatomical variation in the AL occurs among monomorphic workers within a species, and whether such variation may influence behavioral specialization.

Quantification of glomerular variation in 115 workers across six colonies and two age classes yielded on average 438 glomeruli per AL. However, counts varied by 37 glomeruli (8%) across and within colonies, indicating inter-individual variation independent of colony-related factors. While AL hemispheres develop independently in ants, only 33% of workers exhibited asymmetry (>±3) in glomeruli numbers between the hemispheres, suggesting the presence of robust developmental mechanisms that maintain structural symmetry. While glomeruli counts did not markedly differ between young and old, glomeruli volumes significantly increased with age, consistent with age and experience-related growth of specific brain neuropils in other ant species. Taken together, our results indicate the presence of anatomical variation in the olfactory system within a monomorphic species. This variation may arise from developmental or environmental conditions and may contribute to the division of labor.

SYMPOSIUM 11 · The organismal social insect colonies
ORAL · Tue 18 Aug · 14:30 · K8 · Session 22 · Abstract ID 149392

Major transitions in evolution and insect eusociality: new developments

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The study of the major transitions in evolution seeks to address a key topic neglected by the Modern Synthesis. This is the organisation of living things into a nested hierarchy (e.g. of cells within organisms and organisms within societies). This presentation considers new developments in the study of the major transitions, especially as regards insect eusociality. Its standpoint is that major transitions represent higher levels of individuality that evolve through the coincidence of inclusive fitness interests of the constituent units. A recent review proposes that insect eusociality is not a major transition in individuality and that only direct fitness effects on queens, not inclusive fitness, are required to understand its evolution. However, these arguments seem to deny agency to workers, in contrast to much empirical evidence, and overlook the point that inclusive fitness incorporates direct fitness effects. Other recent work proposes, on an inclusive fitness basis, that irreversible worker castes evolve only under conditions of colony closure (lack of remating by founding queens and lack of queen replacement). This work has the benefits of clarifying existing concepts and proposing the novel hypothesis that obligate eusocial colonies (superorganisms) do not evolve from open societies lacking closure. However, the evolution of irreversible worker castes itself potentially contributes to closure, implying closure may not be an essential precondition. In contrast to the (super)organismality concept, the concept of individuality recognises a wider class of social groups as major transitions and in so doing arguably addresses potential difficulties in alternative views.

SYMPOSIUM 11 · The organismal social insect colonies
ORAL · Tue 18 Aug · 14:45 · K8 · Session 22 · Abstract ID 149337

A formal theory of group-level adaptation for obligate eusociality

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Darwin argued that natural selection leads organisms to appear as if they are striving to maximise their fitness. This idea is readily recognised at the individual cell or body level, but such adaptive design may also manifest at some higher levels of biological organisation. Previous work has formalised the idea that social groups can be viewed as adaptive individuals in their own right—i.e., 'superorganisms'—under the assumptions that within-group selection is absent and that there is no class structure. However, the original and most common biological use of the term 'superorganism' is in reference to insect colonies in which members exhibit striking class structure in the form of reproductive division of labour. Accordingly, although obligately eusocial colonies are regularly conceptualised as having the capacity for colony-level adaptation, current formalisms are unable to support this idea. Here, we develop a formal theory of group-level adaptation for obligately eusocial colonies by establishing mathematical correspondences that connect the dynamics of natural selection—as described by Price's equation—to the mathematics of optimisation—wherein the colony is considered a fitness-maximising agent—under a range of assumptions as to which members of the colony control its phenotype and the degree to which they are genetically related.

SYMPOSIUM 11 · The organismal social insect colonies
ORAL · Tue 18 Aug · 15:00 · K8 · Session 22 · Abstract ID 148870

The Wheeler superorganism: recent advances highlighting its conceptual relevance

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Social insect research reached a pinnacle of synthesis when William Morton Wheeler's first book was published in 1910, entitled Ants: their structure, development and behavior. Conceptually, Wheeler's early (1910/1911) work completed tentative explanations by Darwin and Weismann for how neuter (worker) castes could evolve via family selection, by emphasizing the close foundational and developmental analogies between superorganismal colonies and metazoan bodies. Some decades later Julian Huxley (1930) and Suzanne Batra (1966) independently coined the term true sociality (eusociality) to characterize non-caste-differentiated families consisting of a nest-founding female with daughter helpers. Inclusive fitness theory (Hamilton, 1963, 1964) then explained how and why helper- or worker-caste altruism are in reality self-interested behaviors to maximize the indirect component of inclusive fitness. If only the field had retained Huxley's clear distinction between (1) parental care, (2) true sociality expressed as conditional sibling care, and (3) caste-societies in which offspring are transformed to unsexed neuter workers, we would have continued along transparent "Narrow Hamiltonian Roads" (https://academic.oup.com/book/51226) towards more advanced understanding of social evolution. However, the clear terminology by Wheeler and Huxley was rendered opaque during half a century of Wilsonian (1971, 1975) sociobiology, which erroneously proposed that these distinct social categories merely represent some kind of smooth continuum. The resurrection of the Wheeler superorganism (Boomsma & Gawne, 2018) rectified this broad-brush eusociality confusion. As I will summarize in this presentation, substantial recent work has corroborated how the ensuing conceptual clarity helps to reach better understanding of social evolution from first kin-selection principles.

SYMPOSIUM 11 · The organismal social insect colonies
ORAL · Tue 18 Aug · 15:15 · K8 · Session 22 · Abstract ID 140514

A unifying framework for the evolution of metazoa and social insects, two major evolutionary transitions

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The evolution of life is characterized by major transitions, the evolution of new targets of selection (e.g. prokaryotes, eukaryotes, multicellular organisms, social insect colonies). They arose when pre-existing lower level units began to cooperate and gave up the capability to reproduce so that reproductive success can only be achieved at the new, joint, higher unit. Currently, increasing confusion exists about major transition in evolution (MTEs) that hampers progress in this fundamental research field. Misconceptions arose due to inadequate evolutionary reasoning. In addition, pivotal recent work shows considerable organismal diversity in metazoan and social insect systems that make clear-cut distinctions of transitions more difficult and that challenges our classical understanding of MTEs. Applying rigorous evolutionary thinking, we develop three categories that all metazoan and social insect systems can be grouped into. The categories are defined by the reproductive potential of altruistic level units and how they can realize it (i.e., via independent reproduction as dispersing propagules or only through reproduction within the higher-level unit). Reproductive potential is a key parameter defining the organismal complexity that is crucial when analyzing potential major transitions, but was always hard to grasp. This common conceptual framework advances our understanding of MTEs. It will allow comparative analyses within as well as across MTEs to answer fundamental questions about the evolution of life.

SYMPOSIUM 11 · The organismal social insect colonies
ORAL · Tue 18 Aug · 15:30 · K8 · Session 22 · Abstract ID 150039

Shutting the door: irreversibility and the superorganism transition in ants

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Ant colonies are considered the classic superorganisms, yet worker reproductive potential persists across several lineages where workers have and use functional ovaries and spermathecae. Are these ants superorganisms? I argue yes—but like hydra, which maintain cellular totipotency rather than segregating an early germline, they live with ongoing reproductive conflict between lower-level units. This flexibility represents a form of bet-hedging that constrains evolutionary potential.

I propose that a significant transition occurred at the root of the Formicoid clade where persistent monogyny and monandry and sufficiently stable ecology created conditions where worker reproductive potential was finally lost. Building morphological reproductive division of labour (queen and worker morphologies) as seen across nearly all ants, was not sufficient to become the thriving superorganismal ant colonies we know today. Lineages also had to shut the door behind them. Abandoning reproductive bet-hedging enabled formicoid diversification and several elaborations of complexity found only in this clade.

Recent comparative work shows that in multicellular organisms, early commitment to the collective through early germline segregation, and not necessarily high relatedness through single-cell bottlenecks, predicts the evolution of cell-type diversity. A parallel principle may apply to superorganisms: that the irreversible loss of lower-level autonomy, not high relatedness alone, that ratchets lineages into new evolutionary regimes.

SYMPOSIUM 11 · The organismal social insect colonies
ORAL · Tue 18 Aug · 15:45 · K8 · Session 22 · Abstract ID 145838

The honey bee as model organism for superorganismality

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The honey bee, Apis mellifera, represents a model organism for a wide range of studies and a prime example of social insect colonies, which are considered as superorganisms. Here, the intricate life history of the honey bee superorganism is used as a vantage point to take the analogy between insect colonies and animals further and to contextualize superorganismal traits in a new light. By recognizing unique genotypes for individual superorganisms, notions of potential immortality and bypass of reproductive bottlenecks can be refuted. A refined colonial life cycle is presented, from which an image of the honey bee superorganism emerges as viviparous with strictly sexual reproduction. Zygotic, embryonic, fetal, juvenile and adult stages are identified during superorganismal ontogeny. Since swarming precedes fertilization, it can be viewed as superorganismal autotomy rather than reproduction. While the prime swarm serves the function for maternal superorganisms to survive reproduction, afterswarms are means to produce more than one offspring per reproductive cycle. Based on the insights gained from the honey bee, a general life cycle for insect superorganisms is drawn. While criteria for the beginning of superorganismality on the sociality spectrum have been proposed, here, an attempt is made to narrow in on the concept's upper boundary with a view towards higher levels of biological organization.

SYMPOSIUM 11 · The organismal social insect colonies
ORAL · Tue 18 Aug · 16:00 · K8 · Session 22 · Abstract ID 149308

Defining social complexity in arthropods: a consensus from expert elicitation

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Quantifying social complexity (SC) across arthropod societies has long been constrained by categorical definitions and taxon-specific biases. Although SC is widely theorised as a key adaptation shaping ecological performance—such as facilitating colonisation and long-term persistence—broad comparative tests remain limited by the lack of a consistent, cross-taxon metric.

To characterise how arthropod specialists conceptualise SC, an essential step toward quantification, we surveyed nearly 300 arthropod specialists worldwide. Participants scored SC for a set of species archetypes, including real anchor taxa (e.g. Apis mellifera) and fictional archetypes defined by eight core traits (e.g. queen–worker dimorphism, richness of communication), using a 0–20 scale. The results reveal a striking consensus among experts. While researcher age showed a small negative effect on absolute scores, respondents strongly agreed on the relative importance of key traits. Queen–worker dimorphism, richness of communication, division of labour (DoL) among worker, and reproductive DoL were consistently prioritised, whereas colony size, brood-care system, generational overlap, and loss of totipotency were judged less informative.

This convergence of expert opinion bridges continuous and threshold-based perspectives on SC and provides a validated empirical basis for a standardised, multidimensional measure of social complexity. Such a framework will enable robust, phylogenetically controlled tests of how SC relates to invasion success, resilience to environmental change, and ecological dominance. Although our study does not resolve longstanding theoretical debates, it shifts the focus from definitional disagreements toward developing an empirically grounded, coherent framework able to generate testable predictions about the ecological and evolutionary consequences of social organization in arthropods.

One mother for two species: obligate cross-species cloning in ants

Jonathan Romiguier

Living organisms are assumed to produce same-species offspring. 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 parasitism that evolved into a natural case of cross-species cloning 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. Besides revealing a reproductive mode under which one species needs to clone another, such a 'two-species superorganism' challenges the usual boundaries of individuality. Major evolutionary transition in individuality occurs when distinct entities evolve into an integrated, higher-level unit. As two species have become sexually interdependent in such an integrated entity, evolution towards xenoparity exemplifies how such transitions can occur through a sexual domestication process.

SYMPOSIUM 11 · The organismal social insect colonies
ORAL · Tue 18 Aug · 16:45 · K8 · Session 28 · Abstract ID 145577

Superorganisms, hologenomes and phylosymbiosis of fungus-gardening ants

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Hosts and their microbiomes can be extensively integrated so that they behave across evolutionary scales as a single unit or as a ‘hologenome’. Eventually symbiotic organisms become so entangled that they may exhibit a unique sets of emergent traits and represent a ‘super-organism’. Alternatively, the interactions between hosts and symbionts may exhibit traits more associated with communities where individuals in the interaction retain some independence. A feature of a superorganism would be similar evolutionary histories, which can be quantified using a 'phylosymbiosis' approach, which is a method that examines phylogenetic concordance between hosts and symbionts. Here we apply experimental and phylosymbiosis approaches to tease apart the components of five species of fungus-gardening ants. The obligate symbiosis of fungus-gardening ants represents a complex symbiotic system as there are two macroscopic hosts (ants and fungi) that each have associated bacterial microbiomes. The strongest evidence of phylosymbiosis (i.e., congruent topologies between host phylogenetics and microbiome structure) was found between ants and ant-associated microbiomes. While fungal phylogenies and microbiome dendrograms were correlated, these correlations were not topologically congruent. Cross-fostering experiments demonstrated that bacterial communities of the fungus gardens were altered by ant hosts when forced to grove distantly related fungi. We conclude that phylosymbiosis is present between the ant hosts and their ant-associated microbiome and this would be the strongest evidence of the hologenome concept within the attine symbiosis, whereas much of the microbiome is more consistent with an ecological community that is characterized extensive horizontal exchange and incomplete lineage assortment.

SYMPOSIUM 11 · The organismal social insect colonies
ORAL · Tue 18 Aug · 17:00 · K8 · Session 28 · Abstract ID 145708

Elevated developmental robustness of ant queen germlines in a colonial superorganism

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Major transitions in evolution have repeatedly shifted selection from lower-level entities to higher-level organisms and, in some lineages, to colonial superorganisms. Within these “fraternal” transitions, multicellular organisms and insect superorganisms are nested yet analogous cases, both built on high relatedness, irreversible division of labor, and integrated development that aligns fitness interests across levels. We tested whether superorganismal colonies truly parallel multicellular bodies by building on Weismann’s germ-plasm theory, which separates a protected germline from a more expendable soma. In turn, queens (as the colony’s germline) should be more robust to perturbation than workers (as the colony’s soma) during development, reflecting stronger protection of the hereditary lineage. Waddington’s canalization concept, with Hsp90 as a key molecular buffer, offers a concrete mechanistic link between germ-plasm theory and measurable developmental robustness. Using the ant Cardiocondyla obscurior, which has irreversibly sterile workers and reproductively specialized queens, we inhibited Hsp90-mediated buffering during late larval development and quantified caste-specific changes in morphology and gene expression. Our results show that queens proved more developmentally canalized and less responsive to perturbation than workers, supporting an extension of Weismannian germline insulation to the colony level within the major-transitions framework.

SYMPOSIUM 11 · The organismal social insect colonies
ORAL · Tue 18 Aug · 17:15 · K8 · Session 28 · Abstract ID 147924

Ant queen specialization is flexible and controlled by the social environment

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The superorganism analogy posits that social insect colonies are analogous to multicellular organisms: queens monopolize egg production (similar to germ cells), and workers perform all non-reproductive tasks (similar to somatic cells). Most discussions on the topic focused on the worker analogy to the soma, but Wheeler (1911) emphasized the queen aspect as well, for example stating "the fecundated queen of the ant colony [...] corresponds to the fertilized egg of the personal organism". We use this analogy to contextualize our study of ant colony foundation from a single queen, which is akin to the development of a multicellular organism from a single zygote. In both cases, investigating the ontogeny of the (super)organism is critical to understand the emergence of specialization and division of labor. Using the ant Lasius niger, we produced experimental evidence that the presence of workers induces the behavioral specialization of founding queens from performing non-reproductive tasks to focusing solely on egg production. We also demonstrated that the queen specialization is reversible -even after several years - and continuously maintained by the presence of workers in established colonies. We found evidence for such flexibility and social control of queen specialization in more than 20 species across the ant phylogeny, showing that queen specialization is usually not constitutive. However, queens in a few ant species did show true specialization, unaffected by manipulations of the social environment. Our findings have important implications for the queen analogy to the germline and the defining criteria of superorganismal insect societies.

SYMPOSIUM 11 · The organismal social insect colonies
ORAL · Tue 18 Aug · 17:30 · K8 · Session 28 · Abstract ID 146616

Conserved regulatory architecture enables stable yet plastic caste differentiation across 150 million years of ant evolution

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The evolution of insect social colonies represents a major evolutionary transition where colonies function as superorganisms, with caste-differentiated individuals arising from identical genomes. While conserved signaling pathways regulating caste differentiation have been identified, the regulatory mechanisms enabling both evolutionary stability and developmental plasticity—key to superorganismal function—remain unclear. Here, we performed comprehensive analyses of ultra-conserved elements (UCEs) across 163 ant species spanning 12 subfamilies, integrated with developmental epigenomics and transcriptomics in the pharaoh ant Monomorium pharaonis. We identified 3,537 UCEs that exhibit caste-specific chromatin accessibility and regulate 729 genes with caste-biased expression patterns, which are significantly enriched for canalized expression and located within conserved microsyntenic blocks. These UCE-regulated genes are involved in transcription factor networks, metabolic regulation, and MAPK signaling essential for caste differentiation, a core feature of superorganismal organization. We further show that specific UCE losses in independently evolved queenless lineages disrupt wing development gene regulatory networks, providing a genomic mechanism for social innovation that shapes superorganismal structure. Our findings establish that UCEs constitute the stable regulatory foundation underlying ant superorganism evolution, resolving the conservation-plasticity paradox by showing how deeply conserved elements maintain robust developmental programs while enabling caste-specific responses through differential chromatin accessibility, linking genomic regulation to superorganismal structure.

SYMPOSIUM 11 · The organismal social insect colonies
ORAL · Tue 18 Aug · 17:45 · K8 · Session 28 · Abstract ID 148883

Common principles of disease defence in insect colonies and individual organisms

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The colony-wide immune system of insect colonies shows remarkable parallels to the individual immune system of organisms. These similarities across biological levels arise from common organisational principles, since both show a strict germline-soma separation into reproductive and non-reproductive body cells resp. colony members, requiring full cooperation between the distinct tissues or castes for the success of the whole reproductive unit. Notably, social and individual immunity do not only resemble each other in their high level of specialisation and complexity; in both, we also find infected body cells or colony workers actively signalling their infection, which induces their own removal, yet protects the health of the whole entity. Such altruistic disease signalling evolves under high relatedness, where it allows the infected to pass on the own genes indirectly via supporting kin. Their underlying organismal structure therefore explains well, how cooperative disease defence evolved and functions in social insects with a permanent caste fixation and full worker sterility. However, not all social insects show this transition to organismality. Instead, their social structure resembles that of cooperative breeders, where own reproduction may only transiently refrained from when helping in the maternal nest. Here, I will discuss, which components of social immunity are expected to be inherent to the unconditionally-cooperating organismal social insects, and which defence lines should also evolve in non-organismal insect colonies, where cooperation is condition-dependent.

The roads to superorganisms: an evo-devo perspective from termites

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Major transitions in evolution are often associated with the loss of independent reproduction by formerly autonomous units. Termites provide a powerful system for studying this process because they exhibit diverse social systems in which worker developmental and reproductive potential declines with increasing colony-level organismality. However, the evolutionary sequence and developmental genetic basis of these transitions remain unresolved. Here, using comparative developmental transcriptomics across seven termite species that differ in worker reproductive potential, we reconstructed the evolutionary history of termite social systems. We found that linear caste development, in which workers retain full reproductive potential, represents the ancestral state of termites, whereas bifurcated caste development, in which workers partially lose reproductive potential early in development, evolved independently multiple times, with two origins subsequently giving rise to superorganisms with unipotent, sterile workers.

Ancestral gene regulatory network (GRN) reconstruction reveals that linear caste development evolved through retention of a juvenile-like worker state and co-option of a conserved developmental GRN for hemimetabolous insect nymphal development, in which juvenile hormone, ecdysone and TGF-β signaling pathways play central roles. In addition, the convergent evolution of bifurcated caste development repeatedly co-opted the GRN underlying linear caste development, heterochronically shifting its activity to earlier developmental stages. Finally, we found that the evolution of termite superorganisms involved somatization of the worker caste and co-option of a conserved endocrine GRN for terminal differentiation. Together, these findings reveal repeated routes to reduced worker reproductive potential through GRN co-option and highlight striking parallels between superorganism evolution in social insects and organismal evolution in metazoans.

What ends a social insect colony: accumulation of uric acid increases infectious disease risk in termites

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In social insect colonies, the high reproductive output of kings and queens is supported by non-reproductive castes. This division of labour allows for the rapid recovery of individuals, often including those of the reproductive castes. However, these seemingly permanent colonies eventually face collapse. Studying the mechanisms of colony death is crucial for understanding the maintenance of insect social systems. Here, we show that the accumulation of uric acid (a major product of nitrogen metabolism) in workers increases their infectious disease risk in the Japanese subterranean termite Reticulitermes speratus. In this species, king replacement has been associated with colony decline, and we found that king replacement increases the uric acid contents in worker bodies in the field. The accumulation of uric acid, which has antioxidant activity, reduced in vivo levels of reactive oxygen species (ROS) in workers. Considering ROS is a key player in innate immunity, we then conducted infection assays. Workers with decreased ROS levels were more susceptible than those with normal ROS levels to an opportunistic pathogen that causes disease to immunocompromised termites. Our results indicate that regulating the individual oxidant/antioxidant balance via interactions among colony members plays a pivotal role in the immunity of social insects.

EXPLORING THE ATTINI–MICROORGANISM SYSTEM : A STUDY OF ATTA SEXDENS (L.)

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Leaf-cutting ants of the genus Atta are important ecosystem engineers that influence soil structure and microbial communities. We investigated this influence by characterizing the bacterial and fungal communities associated with the body of the leaf-cutting ant Atta sexdens, its fungus garden, and the surrounding soil at 0 or 5 m from the nest entrance. We integrated 16S rRNA and ITS metabarcoding with soil physicochemical properties. Both bacterial and fungal communities form distinct clusters associated with ants, fungus gardens, and soils located at 0 or 5 m. Soil adjacent to nests showed higher relative abundance of microbial lineages commonly associated with biological nitrogen fixation, phytohormone production, and antagonism against phytopathogens and nematodes. Bradyrhizobium was the only bacterial genus detected across all samples, constituting the core microbiota of the system and showing particularly high relative abundance in the fungus garden and nest-adjacent soils (~10%), suggesting a central role in nitrogen cycling and availability. In contrast, the fungal community exhibited strong compartmentalization, with Leucoagaricus almost exclusively dominant in the fungus garden (~99,9%). Ant activity was associated with changes in soil physical and chemical properties, including reductions in macro- and micronutrients and a significant increase in soil moisture near the nest entrance (~15%). These changes are related to microbial spatial distribution, favoring plant-growth promoting bacteria and repealing ant-antagonistic fungi. Leaf-cutting ants offset low soil nutrient availability and the effects of herbivory by increasing soil hydration and promoting microbial-mediated fertilization, potentially contributing to sustainable soil management.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Wed 19 Aug · 10:15 · Halle 4 · Session 31 · Abstract ID 148061

Stress is social: brain-level gene expression and physiological evidence from the honeybee

Rachael Halby; Megha Majoe; Chelsea Cook
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The physiological stress response is a widely studied phenomenon. Across taxa such as birds, fish, and mammals, the social environment has been shown to buffer stress, while adverse social conditions such as isolation or overcrowding can themselves act as stressors. These findings suggest that stress is socially modulated. However, the potential mechanisms or pathways through which social context alters stress physiology remain unclear. Here, we investigate the physiological underpinnings of the social modulation of stress by i) exploring gene expression changes across heat-stressed and control honeybees (Apis mellifera) experiencing varying social conditions (isolated versus group setting). ii) Additionally, we confirm and correlate proteins such as Hsp70, typically associated with various stress conditions. By comparing individuals who experienced heat stress or control conditions across social contexts, we identify molecular targets and gene networks associated with both stress buffering and social stress conditions. Our results build a framework for utilizing social insects as a model organism for studying the social regulation of stress. We anticipate that our results will help broaden the understanding of stress in social organisms and clarify how access to social feedback shapes individual stress responses.

Faster liquid flow under greater resistance: Red Queen dynamics in honey bee trophallaxis networks

Tim Gernat; Deisy M. Gysi; Gene E. Robinson

In honey bees, efficient foraging depends not only on the acquisition of resources but also on how they are handled once inside the hive. Liquid resources such as nectar are distributed via trophallaxis, a mouth-to-mouth exchange that generates a dynamic social network. If group-level selection favors efficiency, this network should facilitate rapid transport and reorganize during nectar influx to accelerate spread.

We tested this prediction using automated behavioral monitoring to continuously track trophallaxis among ~10,800 individually barcoded workers across nine colonies for two weeks, while experimentally separating pollen foraging from nectar foraging. This effort yielded 1.9 million trophallaxis interactions. Analysis of this data set showed that nectar influx triggered a strong increase in trophallaxis frequency, involving both returning foragers and hive bees. This increase accelerated liquid flow.

However, network structure (how trophallaxis interactions are arranged in time and across individuals) consistently restricted liquid flow. This structural resistance strengthened specifically during nectar influx, even as interaction rates increased. Thus, colonies simultaneously increased throughput by elevating trophallaxis frequency while reinforcing network-level constraints that limit dissemination speed.

Our results reveal a dual regulatory strategy: behavioral modulation of interaction rates controls throughput, while network organization acts as a brake on liquid spread that buffers hive workers from rapid exposure to incoming liquid. We speculate that this regulatory architecture has evolved as a colony-level mechanism to balance efficiency of food acquisition and storage with the risk posed by environmental hazards, such as pathogens and toxins.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Wed 19 Aug · 10:45 · Halle 4 · Session 31 · Abstract ID 148541

Soldiers boost colony defense by enhancing information flow and modulating minor behavior

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Ants coordinate complex defense strategies through self-organization, yet the broader functions of specialized soldiers beyond direct combat remain poorly understood. By tracking Pheidole megacephala during intercolonial battles, we show that soldiers enhance group defense through two key mechanisms, the optimization of information flow within social networks and by adaptively regulating the behavior of minor workers. Using network analysis and individual behavior quantification, we found that increased soldier proportions enhanced information transmission efficiency within groups and promoted minors' flexibility in switching between battlefields, while suppressing death-feigning behavior. At the individual level, Minors adjusted their fighting decisions based on the cumulative numerical imbalance between nestmates and opponents encountered, reflecting a dynamic, context-dependent assessment process. We developed a multi-agent combat model incorporating the observed behavioral rules and was parameterized using individual fighting strength assays. This model not only replicated the experimentally observed mortality patterns and network structures but also demonstrated that these soldier-modulated behavioral modulation enhances collective combat performance, with context-dependent effects across environmental conditions. These findings advance our understanding of how individual-level interactions scale into emergent collective defense in social insects.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Wed 19 Aug · 11:00 · Halle 4 · Session 31 · Abstract ID 149876

Honeybee foragers discriminate between safe and dangerous resources at the flower-level but not at the patch-level

Natalie Lemanski; Allison Lozano
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All animals must balance resource acquisition with avoidance of dangers. In social animals, individuals can often improve foraging success or minimize risks by utilizing social information. In honeybees (Apis mellifera), foragers communicate about resource location and quality using the waggle dance language. Previous work has indicated that waggle dances can also convey information about flower danger. However, given the waggle dance's limited spatial resolution, the use of social information to avoid dangerous flowers should also decrease visitation to nearby "safe" flowers within the same patch. While previous work has shown that honeybees avoid dangerous flowers, most previous studies did not distinguish between flower-level and patch-level avoidance. In this study, we examined how the presence of predators on specific flowers affected honeybee visitation patterns both within and between patches. Our results confirmed that honeybee foragers reduce visitation to dangerous flowers. However, contrary to our expectations, we found no evidence of patch-level avoidance; “safe” flowers within dangerous patches received similar visitation rates as flowers in entirely safe patches. Because the waggle dance lacks the precision to distinguish individual flowers, these findings suggest that the observed avoidance was based primarily on personal information rather than information from waggle dances. This study highlights the nuances of honeybee collective decision-making, suggesting foragers sometimes prioritize personal rather than social information when navigating fine-scale risks. Future work is needed to untangle the factors influencing honeybees’ use of personal vs. social information to balance safety with collective foraging success.

Organisational immunity in ants: the importance of socio-spatial structure in mitigating epidemic risk

Nathalie Stroeymeyt
University of Bristol

Group living offers favourable conditions for the spread of infectious diseases, because high population densities and frequent social contacts facilitate pathogen transmission. To mitigate that risk, social animals have evolved a variety of defence mechanisms to prevent the entry and propagation of pathogens within the group, ranging from a raised investment in personal immunity to highly coordinated collective sanitary actions known as social immunity. Recent studies have shown that social groups can also adopt organisational features, such as the subdivision into socially and spatially separated subgroups, which reduce epidemic risk through transmission bottleneck effects, and may enhance collective resilience to disease. However, the importance of organisational immunity features in disease risk management by real animal groups is still poorly understood. In this talk, I will present multi-threaded evidence for the existence of organisational immunity in the black garden ant Lasius niger, from division of labour in healthy colonies to the adoption of anti-epidemic nest architecture following disease challenge. Furthermore, I will discuss the complex interplay between organisational immunity, personal immunity and sanitary care in different conditions, showing how ants flexibly switch between different tools in their disease defence arsenal to achieve effective protection against pathogens in a broad range of situations.

Pathogen Spread and Removal in Multilayer Ant Social Networks

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Social insect colonies face a trade-off: dense interaction networks enable sophisticated coordination but also facilitate rapid disease spread. Ants have evolved allogrooming as a form of cooperative defence, where individuals mechanically remove fungal spores from nestmates, thereby reducing infection risk for recipients but potentially increasing helper exposure. Through the use of marker-based tracking of individuals in social insect colonies, we can obtain social networks based on proximity, to model and experimentally confirm disease spread. Since such networks aggregate multiple behaviours that differ in their likely effect on transmission and removal of pathogenic particles, we here use a multilayer approach to split up traditional proximity networks into different layers. Using garden ants and their natural fungal pathogen, Metarhizium, as an experimental study system, we identify interacting ants with individual markers. We also observe their grooming interactions to obtain a two-layer network based on spatial proximity and their dyadic grooming interactions. We quantify pathogen load on all ants at the end of the experiment. In parallel, we model how pathogen spread is affected by spatial ant-to-ant contact and their grooming interactions, with the latter contributing to both the transfer and removal of pathogens. To capture the natural transmission mode of the fungal pathogen, we model spore spread using diffusion dynamics on two-layer networks, while incorporating a novel degree-dependent negative term to capture grooming-mediated removal. We hereby study disease dynamics in systems where social interactions both transmit and eliminate pathogens, as under social immunity.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Wed 19 Aug · 11:45 · Halle 4 · Session 31 · Abstract ID 144987

Social and Spatial Affinity Drive Wound Care by Ants

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In group-living animals, open wounds pose a risk not only for the injured individual but also for the entire group, especially when the risk of infection transmission is high. To mitigate this danger, different species have developed diverse strategies – with ants representing one of the few taxa beyond humans that engage in social wound care. Yet, who provides this care and what determines its allocation remains unclear. To answer these questions, we combined controlled injury experiments with automated behavioral tracking across six colonies of the ant Camponotus fellah. Our results reveal that wound care is primarily provided by a non-specialized subset of individuals whose behavioral traits align with a transitional phase between the nurse and forager roles. Among these transitioning ants, care provision was best predicted by their prior spatial and social proximity to the injured individuals in the hours before the injury, indicating that pre-existing social affinity influences caregiving behavior. These findings offer the first empirical evidence of how caregivers are integrated into the colony's social structure and highlight the role of social interactions in shaping the organization of wound care in ants.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Wed 19 Aug · 12:00 · Halle 4 · Session 31 · Abstract ID 149783

Nest-level phase transition drives synchronized activity bursts in ant colonies

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Many natural complex systems exhibit synchronization, characterized by temporal coherence among the dynamics of their units. In ant colonies, synchronization manifests through activity bursts: sudden, sharp spikes of concurrent motion by a significant portion of workers throughout the nest. These activity bursts have been studied for over three decades; yet, how they emerge in a spatial context and as a function of nest density remains elusive. In this study, we present a novel model of ant activity that integrates both the motion of individuals within the nest and the transitions between behavioral states, and compare its predictions to experiments on colonies of Aphaenogaster fulva ants. In the model, we identify a nest-level phase transition from unsynchronized to synchronized activity and test for its existence through laboratory experiments. Our model offers two key insights: (i) activity bursts emerge as a balance between the responsiveness of the colony to the first ant that activates and the ability of the colony to completely deactivate before the onset of the next burst, and (ii) the timescale of the motion of individuals through the nest is faster than that of the burst, suggesting that ants operate in a high-speed interaction regime where new behaviors are near-instantaneously transferred through the nest. Tested against laboratory experiments, our results hint that ant colonies that exhibit activity rhythms live near the critical point of a phase transition, drawing important connections to the broad literature of life near criticality.

Form, function, and evolutionary origins of architectural symmetry in honey bee nests

Michael Smith
Auburn University

Symmetry is pervasive across the tree of life, and organisms (including humans) build symmetrical structures for reproduction, locomotion, or aesthetics. Symmetry, however, does not necessarily span across levels of biological organization. If and how symmetry exists in structures built by social insect collectives, where there is no blueprint or central organizer, remains an open question. Here, we show that honey bees actively organize nest contents symmetrically on either side of their double-sided comb; 79% ± 7% of cell contents match their backside counterpart, creating a mirror image inside the nest. Experimentally restricting colonies to opposite sides of comb, we find that independent colonies will symmetrically mimic each other's nest organization. We then examine the mechanism by which independent colonies can indirectly coordinate nest symmetry, showing that 100% of colonies (n = 6) perfectly co-localize their brood nest with a randomly positioned heat source, indicating that heat drives nest site initiation and early brood production. Nest symmetry also has adaptive benefits: two-sided nests grow more quickly, rear more brood, and have a more stable thermal environment than one-sided nests do. Finally, examining the evolutionary origins, we show that symmetry persists in three-dimensional (3D) nests of Apis mellifera and across multiple Apis species, coinciding with the onset of double-sided combs, which made it possible to symmetrically stockpile nest contents. This work shows that, similar to molecular mechanisms that create symmetry in multicellular organisms, there are behavioral processes that create functional symmetry in the collective organization of animal architecture.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Wed 19 Aug · 14:45 · Halle 4 · Session 37 · Abstract ID 147646

Gene networks and the pathway to honeybee fanning

Kerrigan Tobin[1]; Megha Majoe; Chelsea Cook

[1] *Marquette University*

Collective thermoregulation is a crucial social response to changing environmental conditions. Social insects coordinate group responses to changing conditions such as during warming events. Honeybee fanning behavior, where workers face the entrance of the colony and rapidly flap their wings to circulate cool air into the hive, increases as temperature increases. Thermoregulation is critical because developing brood must be kept near constant temperature or suffer physical defects, learning deficits, or in extreme cases mortality leading to colony level consequences. Fanning is also context-dependent; for example larger groups, bees in the presence of larvae, and bees allowed physical contact with one another are more likely to fan in laboratory experiments. Genetic backgrounds, brood-rearing conditions, age, and other physiological factors could explain the discrepancy in fanning behavior amongst workers. This study controls for many possible confounding factors to investigate genetic pathways to fanning. We sequenced the brain transcriptomes of age-matched fanner and guard bees, two behaviors performed primarily by middle-aged workers at the entrance of the colony. Here we show differentially expressed genes of the fanner brain and explore the genetic and neural basis of fanning. We conducted weighed gene co-expression network analysis to identify hub-genes and genes of interest involved in the pathway to fanning. We also highlight genes that should be functionally tested or investigated across social organisms in future evolutionary comparisons. This work identifies proximate mechanisms that ultimately orchestrate colony-level thermoregulatory behavior crucial to survival and resilience in the face of climate change.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Wed 19 Aug · 15:00 · Halle 4 · Session 37 · Abstract ID 150048

Cooling down and heating up: Thermal history dependence in acorn ants

Kendrick Nakamura[1]; Grant Doering[2]; Timothy Linksvayer[1]; Theodore Pavlic[1]

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What ants can or cannot do is innately tied to the ambient temperature; however, the capacity for activity does not necessarily translate to activity. We tested how the path of the temperature change affects the activity of the acorn ant Temnothorax rugatulus and found a striking difference between cooling and heating cycles; at a single temperature, ants will exhibit different activity responses depending on thermal history. We then investigated whether this behavioral plasticity is the additive sum of the individuals or an emergent property of the colony. Our findings show that individuals will exhibit activity in a temperature history-dependent manner, but with high variation between individuals.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Wed 19 Aug · 15:15 · Halle 4 · Session 37 · Abstract ID 146628

Collective survival during floods in Solenopsis invicta fire ants

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Georgia Institute of Technology

Understanding how membership affects group success is a vital step towards unraveling the mechanisms coordinating collective behavior. The fire ant Solenopsis invicta is an excellent model to study collective survival behavior. Whole colonies can form living rafts of their own bodies to withstand flooding conditions for days. We build on our understanding of how membership affects collective behavior in S. invicta by investigating the explicit roles of worker sizes, castes, and developmental stages. Specifically, we altered raft membership based on presence of larvae, reproductive castes, or worker body size under experimental, flooding conditions to measure how raft composition impacted collective survival. We paid special attention to the behavior and senescence of rafts and analyzed data from video recordings to estimate the size and activity levels of these living structures. Control rafts lasted roughly thirty hours on average, and rafts were not different when larvae or males were added; however, large worker rafts persisted longer than control rafts, sometimes for weeks. In contrast, rafts containing a queen failed more quickly on average. Additionally, rafts of smaller workers show lower activity levels than large-worker or control rafts. Last, we constructed a model based on prior ant rafting research to compare with our results. In general, our model overpredicted early raft failures when compared to experimental outcomes, suggesting that our current understanding of fire ant rafts is incomplete. Our results highlight the ways individual qualities impact collective behavior as well as specific roles of larger castes on collective survival.

Making balls out of leaves, with weaver ants.

Gadi Trocki

Weizmann Institute of Science

Weaver ants (Oecophylla smaragdina) construct their nests by gluing together leaves in tree canopies. They accomplish this by forming joining their bodies into tools which they use to bend the leaves into place. We studied this phenomenon in the lab using carefully arranged artificial leaves, where the ants built viable nests by bending the leaves either upwards or downwards. Leaf thickness and initial placement were major factors in determining the configuration adopted by the ants. We look at the dynamics of ants' tools and how they affect the leaves, and show that local ant-scale rules operating under geometric constraints explain why some nests bend downwards while others bend upwards; we also compute the transition angle. Finally, we use differential geometry to suggest why, in our experimental conditions, nests are constrained to be convex, architecturally stable, sphere-like surfaces. Our findings provide insights into the interplay of geometry, biomechanics, and local-ant-scale rules in complex collective construction.

The role of individual learning in weaver ant collective self-assemblages

Rob Boddington[1]; Christos Ioannou[2]; Sabine Hauert[2]; Chris Reid[3]

[1] Macquarie University, University of Bristol; [2] University of Bristol; [3] Macquarie University

Individual information can influence behaviours at a collective level. In social insects, self-assemblages are a collective behaviour that can be costly as they divert workers away from essential colony tasks. To mitigate these costs, social insects may integrate individual level information into the decision to form an assemblage by adjusting individual behaviours as a result of experience. To explore this, we examine how learnt information influences chain formation behaviour in weaver ants (Oecophylla smaragdina). We associatively conditioned colonies of ants to blue or yellow stimuli with a sugar reward or aversive quinine using Y-mazes in a foraging context. Colonies were then presented with a choice of forming a chain towards either the rewarded or aversive stimuli in the absence of any reward or aversive quinine in an exploratory context using a T-maze. We examine if colonies preferentially form chains toward rewarded stimuli (avoiding aversive stimuli), and how individual-level behaviours such as joining and leaving rates, time spent within, and recruitment into chains guide the group-level decision. In our setup, conditioning occurs in a foraging context, while the self-assembly behaviour occurs in a non-foraging context. Therefore our study will not only provide insight into how individual-level information can shape collective-level decisions, but also explore the weaver ants' ability to generalise information between contexts. Should we find evidence to support our hypothesis, this may indicate a mechanism that weaver ants may use to mitigate decision costs.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Wed 19 Aug · 16:00 · Halle 4 · Session 37 · Abstract ID 145804

Detecting the failure of the honeybee’s decentralised thermoregulation system

Theotime Colin

Macquarie University

Honeybee colonies maintain brood temperature within a narrow range through decentralized worker behaviours such as fanning, evaporative cooling, shivering, heat-shielding and clustering. These simple, local rules generate a robust collective homeostasis that is essential for colony survival—yet this resilience can fail rapidly under environmental stress. Here I show that breakdowns in thermoregulatory dynamics reveal early, quantifiable signatures of colony-level instability before collapse occurs. Using three independent datasets (96 colonies), I analysed internal hive temperature time-series and found that colonies destined to fail exhibited altered fluctuation patterns, reduced stability, and shifts in minima and maxima days to weeks before death. Simple summary statistics derived from temperature traces were sufficient to classify colony health using a ROC framework, with clear sensitivity–specificity trade-offs relevant to real-world management. These results demonstrate that complex collective systems can show detectable early warning signals even when individual agents follow minimal behavioural rules and when the transition to failure unfolds rapidly. More broadly, this work links mechanistic individual behaviour—particularly worker thermoregulation—to emergent resilience, offering a tractable model for understanding tipping points and robustness in other decentralized biological systems.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Wed 19 Aug · 16:15 · Halle 4 · Session 37 · Abstract ID 146390

From individual thermal limits to collective resilience through plasticity and microclimate use

Jelena Bujan; Lina Bajić; Antonia Smolić; Marko Bračić
Ruder Boskovic Institute

Global warming poses a significant threat to insects, whose body temperatures closely track habitat temperatures, and whose ecological roles are essential. In social insects, responses to thermal stress emerge from decentralized decisions made by workers, yet the consequences of these decisions and worker physiology scale to colony-level resilience. We examined how physiological plasticity and behavioral thermoregulation jointly shape collective responses to fine-scale temperature variation in the Mediterranean seed-harvester ant Messor wasmanni from two climatically distinct localities which differ by 2°C in their mean annual temperature. To test this, we measured thermal tolerance which closely aligns with ant activity windows, as well as the relevant microclimates. Seasonality was the best predictor of thermal tolerance indicating that temporal temperature variation currently drives most of the observed thermal plasticity in this biodiversity hotspot. Such physiological thermal plasticity may allow resilience in a varying climate; however, behavior is the first line of defense against overheating. An ant can escape to a cooler microclimate if such microclimate is available. These individual responses to habitat heterogeneity contribute to colony level activity patterns and regulate resource acquisition. Using thermal imaging, we test how nest microclimate governs activity patterns of ants, highlighting the interplay between collective behavior and habitat heterogeneity. By integrating physiological and behavioral responses with relevant climatic data we can better understand insect resilience to thermal stress and predict their responses to climate change.

Exploring mechanisms of cooperative prey transport and nest construction from weaver ants to robots and back again.

Chris Reid

Macquarie University, New South Wales, Australia

Weaver ants (Oecophylla smaragdina) are masters of collective behaviour, working together to move large prey items in teams, and constructing elaborate nests from leaves and silk. This teamwork is coordinated in a self-organised manner, based only on local communication without centralised decision making. This method requires no overseers, blueprints or prior environmental knowledge, and may be crucial for future swarm robotics platforms in exploration, search-and-rescue or space habitat construction. I will present recent work from my lab on weaver ant collective prey transport and silk nest construction, and will showcase our new swarm robotics platform, 'Myrm-X', designed to directly test ant-inspired algorithms for swarm behaviour. We used a tethered-object protocol to show that weaver ants pool together the opinions of all group members to increase their navigational accuracy – the first report of a 'wisdom of the crowd' strategy in ant collective transport. We have also quantified the 3D structure of the ants' silk nests, using photogrammetry and CT-scanning, to understand how the ants essentially 3D-print functional structures as a decentralised swarm. I will describe our efforts to translate these empirical findings into control algorithms for the Myrm-X robots, to both interrogate the ant system, and provide inspiration for future swarm engineering approaches.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Thu 20 Aug · 10:30 · Halle 4 · Session 49 · Abstract ID 146927

Frequent errors are the worst: robustness to individual failures in collective foraging

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Social insects perform foraging in a self-organized fashion, where individual workers discover and collect resources, and may communicate the resource location to their nestmates. During this process, workers can make several kinds of errors that could then get amplified through communication, possibly affecting the whole colony. Here, using an agent-based model in NetLogo, we investigated what effects different error types have on collective foraging performance, whether communication mitigates or exacerbates the effect of these errors, and how increasing error levels affect the robustness of foraging under different error and communication types. We found that the errors that had the highest chance of occurring (i.e., false positive and forgetting errors) were the most detrimental to both resource exploration and exploitation. In contrast to what we expected, communication increased spatial exploration. Moreover, communication dramatically improved resource collection in the presence of errors, indicating its role in mitigating rather than exacerbating the effect of errors. Furthermore, different errors showed varying amounts of decay in resource collection with increasing error probability. Overall, our model shows that the evolution of different communication systems in social insects may have been shaped not only by selection on improved exploitation but also by selection on error mitigation.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Thu 20 Aug · 10:45 · Halle 4 · Session 49 · Abstract ID 149465

Innovative Approach to Delimit Foraging Areas of Hundreds of Termite Colonies in the 3D Space

Rebecca Lessler[1]; Aleš Buček[2]; Thomas Bourguignon[3]; David Sillam-Dussès[1]; Jan Šobotník[2]

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Termites are Earth's most important macroscopic decomposers of dead vegetal matter, with the Congo Basin supporting their highest diversity and abundance. Termite feeding niches span the full decomposition gradient from wood to soil, with niche availability increasing among soil-feeders. Prior research on termite spatial organization focused on single-colony nest structure and foraging gallery mapping, or broad delimitation of individual above-ground nests. These methods explore foraging territories and inter-colony interactions but fail to capture the vertical complexity of spatial coexistence across termite trophic groups, particularly among subterranean soil feeding taxa. We applied a multi-layer approach to visualize how termite foraging behaviors generate collective territorial organization across termite assemblages in Afro-tropical forests. Using a systematic sampling scheme, an entire 5 x 5 meter plot was excavated in soil cubes of 1 liter by volume. All termites encountered in each cube were grouped by morphospecies and confronted with similar-looking termites from neighboring cubes to determine colony affiliation. The 3D reconstructions of subterranean termite assemblages captured soil-feeder foraging arrangements, revealing how species-level adaptation to environmental gradients gives rise to stratified niche occupation. By integrating the results of excavation sampling, behavioral assays, and genomic analysis with spatially explicit digital 3D mapping, we could see how particular termite colonies function in response to resource heterogeneity and competitive interactions with other termites. This innovative study design transforms previously elusive ecological data into intuitive visual 3D representations, showing community-wide relationships and patterns of space exploitation among multiple termite species in a highly diverse tropical ecosystem.

Quantification of territory marking and territorial behavior in weaver ants

Stefan Popp
Free University Berlin

Weaver ants, Oecophylla smaragdina, can live in large colonies, are very aggressive, and defend their nesting trees as territories against other colonies. Since territorial fights can be costly, these ants have been hypothesized to use their excrement as territorial markings serving as cues or signals to their own and competing colonies. However, little is known about the spatial patterns of potential mark deposition, how ants decide when and where to defecate, and how ants react to these spots. We let colonies of weaver ants explore an empty arena in the lab and recorded ant positions and mark depositions every 10 seconds over 9 hours, and in 24 frames for 2 hours. We find that 1) ant numbers peak after about 2 hours after which they slowly decline to a stable level, possibly due to an active colony-level exploration behavior, 2) mark deposition slows down after an initial phase after which the rate stays constant, which means that ants do not reduce their marking activity on highly marked areas, 3) marks tend to be laid less in areas with high ant density, indicating that ants favor marking less occupied regions, though they do not strictly avoid laying marks on top of preexisting marks, 4) ants lay marks relatively early in their exploration bout. These results suggest that ants have a strong drive to mark novel areas but do not finely regulate the position and density of marks.

SYMPOSIUM 12 · From simple rules to collective resilience in a changing world
ORAL · Thu 20 Aug · 11:15 · Halle 4 · Session 49 · Abstract ID 146480

Food for thought – Food type drives cooperative transport performance in the arboreal weaver ant, Oecophylla smaragdina

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Cooperative transport of food items by social insects is a key example of collective decision-making, yet transport behaviors vary widely among species that engage in this behavior. We aim to understand what causes variations in collective transport behaviors among ant species. While group dynamics during cooperative transport have been studied primarily in relation to food size and weight, the role of food properties has been comparatively less explored. We hypothesize that food type, morphology and physical properties of the food influence collective navigation. The arboreal Oecophylla smaragdina is a compelling system to explore this question with an added level of complexity through polydomous nests – spatially separated, but socially connected nests in a colony – and vertical and horizontal group transport to their nests. Previous work has examined how O. smaragdina navigates environmental challenges such as inclines during cooperative transport, and it is the first ant species formally reported to use a 'wisdom-of-the-crowd' strategy in choosing its transport direction. In a natural setting, however, these ants face more complex navigational choices among multiple nests in heterogeneous landscapes. Using video recordings of cooperative transport in O. smaragdina colonies in Townsville, Australia, we examine how food properties and landscape variation shape collective navigation. Preliminary analyses suggest that the food type and food length impact group transport trajectories. This work highlights the importance of food properties in shaping collective foraging behavior and provides insight into how social insects adapt group-level strategies to variation in both resources and environments.

Investigating the mechanisms of information sharing and conflict resolution during collective decision making in Weaver Ants

Asser Loutfi
Macquarie University, New South Wales

Cooperative transport in ants is a remarkable example of collective behaviour in the animal world. Decentralized teams of ants can work together to transport large prey items along flat or inclined surfaces. Weaver ants of the genus Oecophylla are particularly adept at exhibiting impressive levels of coordination when transporting loads much larger than themselves. My research investigates how private and social information are utilised by weaver ants during cooperative transport. Colonies were tested in a Y-maze to determine whether transport groups could detect and respond to pre-laid pheromone trails. Despite having access to these trails, pheromone information had little influence on navigation, whereas the density of freely moving foragers affected the direction chosen by transport groups. These results suggest that visual or local movement cues play a more dominant role than chemical information in guiding collective transport.

Building on this, my current experiments explore how groups of Oecophylla smaragdina resolve conflict when two sub-colonies from the same source colony are provided with opposing directional information. The experiment positions nest boxes of the sub-colonies on opposite sides of an experimental arena with a prey item at the centre. As the groups meet, they are forced to integrate conflicting navigational cues to establish a unified direction of movement during transport. This study aims to uncover the behavioural mechanisms underpinning consensus formation under informational conflict. I will present findings regarding the individual-level behavioural rules that lead to group-level decision making, providing broader insights into collective decision making and conflict resolution in social insects.

Time evolution of wavy pheromone trails reveals a minimal decision rule for ant trail following

Oran Ayalon
Weizmann Institute of Science

Pheromone trails provide a tractable way to link individual sensory rules to collective, macroscopic dynamics. We investigate how the geometry of an established trail changes under continuous traffic by Tapinoma ants. Using a temporary corridor, we imprint trails whose centerlines follow prescribed wavy shapes (sinusoidal or triangular) between nest and food. After a steady bidirectional flux is established, the corridor is removed and the subsequent free-motion evolution is quantified by extracting time-resolved trail centerlines from occupancy ridges. We observe two robust signatures: the trails produced by the two opposite fluxes accumulate a relative phase shift, while their amplitude concurrently decreases.

We propose that these macroscopic signatures arise from a minimal, biologically plausible trail-following rule. Ants are assumed to compare pheromone signals between the left and right antennae using normalized contrast (Weber’s law), maintain a single short-term memory of this contrast, and steer in response to changes in the perceived signal. We show how these microscopic rules give rise to an effective trail-rewriting operator which, when coarse-grained, yields a governing macroscopic differential equation for the trail shape. Its solution predicts a quantitative relation linking drift and decay rates across different wavelengths. Our results demonstrate that a remarkably simple, history-dependent decision rule can account for the observed evolution of trail geometry, providing a direct bridge between microscopic sensing and memory and emergent trail dynamics.

Cooperative Hunting in Weaver Ants: The Spread-Eagle Strategy and the Transition to Transport

Xiaohui Guo

Cooperative hunting is a hallmark of social animals---such as chimpanzees, wolves and lions---underpinning their success in the prey-predator arm races. Unlike strategies requiring high-level cognition, the cooperative hunt in ants usually employ "spread-eagle" technique to immobilize preys tens to thousands of times larger than themselves, followed by transport to the nest. The immobilization phase and its subsequent shift to transport constitute an organized, collective process emerging from individual-level coordination. Weaver ants, Oecophylla smaragdina, a spread-eagle hunting species that is particularly sensitive to force mediation, offer an ideal model to investigate the mechanisms underlying this process. Here, we experimentally decouple the immobilization from transport phases and combine prey movement tracking with individual posture analyses to show how hunting participants interact directly and indirectly to establish the spread-eagle formation and subsequently collapse it to initiate the transport via a set of simple rules. A theory and simulation framework grounded in these rules reproduces the observed variation in hunting duration.

Investigating the effect of nest architecture on colony fitness in Temnothorax albipennis

Freya Gill; Nathalie Stroeymeyt
University of Bristol

Spatial architecture is a major determinant of collective processes in social groups, shaping the movement of individuals, resources, and information. In social insects, nest shape and connectivity influence recruitment efficiency, and spatial complexity is thought to promote colony success by facilitating spatial division of labour and improving local task efficiency. However, the long-term effects of nest architecture on colony fitness remain largely unexplored, and the mechanisms linking spatial complexity to collective performance are still poorly understood. Here, we investigate the short- and long-term effects of nest architecture on colony performance in the ant Temnothorax albipennis. We designed three nest geometries inspired by natural nest sites: flat crevices within shale rock, hollow acorns, and multi-cavity decomposing tree branches. Over several months, we will quantify multiple fitness indicators and conduct tracking experiments to compare information and food flow, as well as division of labour across nest types. Finally, we will test whether colonies collectively select the nest geometry that maximises their short- and long-term performance. By linking nest architecture to both behavioural mechanisms and colony-level outcomes, this work will provide new insights into how spatial structure shapes collective behaviour and colony success in social insects.

Trade-offs and selection for genetic diversity in adaptation to biotic and abiotic stresses in Pognomyrmex occidentalis.

Kaylee Bond
Utah State University

Genetic diversity is adaptive in resilience to abiotic and biotic stressors in agricultural systems. Previous work in ants suggests that colonies with greater genetic diversity have greater fitness via effects of division of labor (such as by increasing foraging time) and greater resistance to pathogens. Pathogen incidence often increases with precipitation. In this study we ask if there is an increase in pathogens across a precipitation gradient in a desert environment, and if genetic diversity within an ant colony varies predictably across the gradient. A positive correlation would indicate that genetic diversity plays a greater role in fitness when faced with biotic stress from pathogens (assuming there is a higher pathogen load with increased precipitation), while a negative correlation would suggest that abiotic stress from drought is a stronger driver in selection for genetic diversity and that drought tolerance and pathogen resistance may trade-off. Pogonomyrmex occidentalis is an ideal system to test these predictions because they exhibit natural variation in genetic diversity (via polyandry) and occupy a wide range of environmental variation. Using sampling sites along a precipitation gradient, we are measuring diversity, pathogen load, activity level, and water retention ability. This observational study will be followed by an experimental stress challenge (pathogens and drought). Our results will help inform how a society’s genetic diversity is adaptive in response to different environmental stressors. Furthermore, our results would link insights on the role of genetic diversity’s role in stress resistance across levels of biological organization, from societies to populations to communities.

Collective decision-making during raiding in the clonal raider ant

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Social insect colonies can make rapid and effective decisions, yet the sensory cues and interaction rules that generate these collective outcomes remain poorly understood. Integrating analyses of sensory perception, local interactions, and colony-level decisions offers a powerful method to uncover the mechanisms of collective decision-making. The clonal raider ant Ooceraea biroi is well-suited to this approach; colonies reliably conduct coordinated raids on prey in laboratory settings. During these raids, colonies may choose to retrieve the prey item to their nest or instead relocate their nest to the prey. Here, we show that colonies integrate multiple cues to collectively make this decision. Colonies are more likely to emigrate when encountering larger prey items, but the prey size threshold that triggers emigration depends on the quality of the location as a potential nest site. Our results suggest that colonies perform a cost–benefit evaluation that integrates food size and nest quality. Building on these findings, we are using artificial food to precisely quantify the food properties and sensory mechanisms underlying this decision. Furthermore, we are combining individual-level tracking with colony-level analyses to resolve the behavioral dynamics that give rise to collective choices. This work advances a mechanistic understanding of how sensory information is integrated to produce adaptive collective decisions.

Balancing resource flow and infection: Adaptive nest architecture in Lasius niger ants

Ioana Mateescu[1]; Nathalie Stroeymeyt[1]; Chris Reid[2]

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Nest architecture plays a central role in the collective behaviour of social insects, shaping social interactions and mediating trade-offs between effective colony functioning and protection from environmental threats. Recent work suggests that Lasius niger ant colonies can flexibly adjust excavated nest architecture in response to pathogen risk, potentially limiting epidemic spread. However, the functional consequences and potential costs of such architectural responses remain poorly understood, largely because individual behaviour and within-nest movements are difficult to observe in underground nests. In this project, we will take advantage of L. niger ants' ability to construct above-ground architectural structures, including galleries supported by pillars and arches, which are accessible to direct observation. We will characterise differences in the morphology and organisation of these structures between control and pathogen-exposed colonies, and test whether these differences reflect a trade-off between disease mitigation and competing colony needs, such as maintaining resource flow. Using 3D scanning, network-based analyses, and tracking of within-nest flows, we will quantify nest organisation and relate architectural differences to patterns of resource and pathogen transmission across treatments. This study will help reveal how nest architecture reflects colony-level decisions, balancing the conflicting attributes of resource flow and pathogen spread.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 10:15 · K9 · Session 53 · Abstract ID 145800

Floral environment and cognition affect individual foraging patterns

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The environment in which animals develop can influence their behaviour as adults. We compared the performance of bumble bees (Bombus terrestris) raised in florally simple or florally diverse environments inside a glasshouse. We tested associative learning of over 100 bees raised in either environment using the Free-Moving Proboscis Extension Response (FMPER). In the glasshouse, we also recorded individual and colony-level foraging effort using RFID tunnels at the nest entrance. We show that individuals raised in simple floral environments that exhibit greater capacity for learning take, on average, shorter foraging trips. On the other hand, those raised in diverse floral environments do not exhibit this pattern as strongly. Our results provide an important step in understanding the extent to which bumble bee health, cognition, and foraging behaviour is influenced by the diversity of the floral environment.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 10:30 · K9 · Session 53 · Abstract ID 145852

Fine-scale navigation: searching ants use multiple guidance mechanisms

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Navigation is of crucial importance for the survival of many species. To guarantee the successful completion of a journey, insects engage in very efficient systematic searches to pinpoint their target. The resulting search patterns are highly structured – systematic – while retaining strong levels of adaptive flexibility. It remains unclear how this sophisticated behaviour is generated by the insect central nervous system. I examine the involvement of several candidate guidance mechanisms in the expression of searching behaviour in the desert ant Cataglyphis nodus. Restricting the ability of ants to form visual memories around the nest entrance results in nest searches that retained their systematic structure but suffered from reduced precision. Interestingly, asymmetrical restriction led to asymmetrical searches. This indicates that searching ants employ visually guided steering mechanisms, in which the perceived environment is matched to visual memories. Where such memories are lacking, the steering mechanism is impeded. Further experiments in an entirely featureless visual environment reveal that ants can still perform systematic, area-restricted searches in the absence of meaningful visual input. These results suggest the involvement of innate movement routines. A further mechanism, guidance by path integration, has previously been identified in the literature. In the natural context, all three mechanisms are most likely active and integrated in the animal to give rise to sophisticated systematic searching behaviour. More broadly, the outcomes allow us to ask questions of fundamental importance about how brains work to produce adaptive behaviour.

Magnetoreception in two Cataglyphis ants species

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Many animal species use the geomagnetic field (GMF) for orientation and navigation. Magnetoreception is the ability of animals to detect and use the GMF. Cataglyphis ants are experimental models for insect navigation. They use magnetoreception for spatial orientation at the beginning of their foraging life. Indeed, in the first two to three days of their outside life, Cataglyphis ants perform learning walks (LWs), explorative excursions around the nest, with pirouettes (partial or complete turns about the ants' body axes). During a pirouette, they gaze to the nest entrance, an invisible hole in the ground. Previously, Cataglyphis nodus has been the only desert ant species shown to use the GMF for a navigational task. In the present study, we show that another Cataglyphis (C. aenescens) species possesses a magnetic sense. C. aenescens is phylogenetically distant from C. nodus and their colonies are smaller than C. nodus colonies, but they inhabit the same environment and perform similar LWs. In the present study, we exposed C. aenescens ants to an experimental alteration of the GMF (alteration of the horizontal component about 180° and +120°). During the magnetic alteration, they gaze to the fictive position of the nest entrance. This study demonstrates that C. aenescens ants use the GMF to gaze back to the nest entrance, confirming the presence of magnetoreception in a second Cataglyphis species, in addition to C. nodus. This suggests that the use of the GMF for path integration is more common than unique in Cataglyphis species.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 11:00 · K9 · Session 53 · Abstract ID 149151

Effects of experimental heatwaves on visual memory in bumblebees

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Bumblebees can be negatively influenced by extreme weather events which are intensifying with climate change. The cognitive abilities of bees are crucial for colony survival – to forage efficiently, bees need to learn, memorise, and recognise flowers containing nectar and pollen, based on floral cues (e.g. colour, scent). However, to our knowledge, learning and memory have not been examined separately in the context of extreme temperatures. In our study, we trained bumblebees (Bombus terrestris) to distinguish a pair of colours in an absolute learning paradigm using a free-moving, proboscis extension reflex-based system. We then exposed the bees to either an experimental heatwave (32°C, 60% RH) or experimental cold snap (4°C, 60% RH) for a period of 2h and assessed their memory. Exposure to an experimental heatwave eradicated memory if bees were exposed to the heatwave temperature within 1h of completing training. By contrast, memory was consolidated when bees were exposed to coldness and when heat exposure was delayed by one hour. We use immunohistochemistry, exploring glutamate signalling within the mushroom body, to provide a mechanistic explanation for heat-induced effects on memory. Our results demonstrate that impact of temperature exposure on bee memory is dependent of both the type and timing of exposure.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 11:15 · K9 · Session 53 · Abstract ID 149262

Information or Imprecision? Patch signaling in the honeybee waggle dance

Renzhuang Xie; Lars Chittka; Mathieu Lihoreau

A century ago, Karl von Frisch discovered that honeybee foragers communicate the location and profitability of resources to recruits via the waggle dance. While the meaning of direction angles and durations of the waggle dance have been well explained, the high level of variability observed among waggle dances performed by the same individuals and among dancers visiting the same resources is puzzling. Here, we hypothesize that this variability is driven by the spatial conditions experienced by the forager within a resource patch. To test this hypothesis, we manipulated food patch size and structure using multiple feeders in a large experimental field. We tracked the feeder visitation sequences of individual bees and analyzed their subsequent dances. Our results show a significant relationship between the divergence angle and the spatial distribution of resources visited along the forager's path. Prominent landmarks in the landscape have no influence on the dances. We conclude that after a complex foraging trip involving visits to patches containing multiple feeding locations, the honeybee waggle dance does merely signal a single point location, but also the spatial extent of the patch.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 11:30 · K9 · Session 53 · Abstract ID 149883

Honey bees (Apis mellifera) learn rules to better solve spatial tasks and these are affected by diet

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We tested whether nutrition affects spatial cognition, which is crucial for social insects. Unbalanced nutrition, specifically omega-6:3 fatty acids ratio, impairs associative learning in mammals and in bees. It also impairs spatial cognitive performance in rats and humans. We kept colonies in netted enclosures and fed them balanced or unbalanced diets, omega-6:3 ratio = 1 or 5, respectively. Foragers from these colonies were tested in an 8-arm radial maze and in a flight arena in which landmark cues led to a rewarding feeder. Unbalanced-diet bees performed less well in both tasks. Compared to rats, which rely on working memory to solve a radial maze very efficiently, bees are less efficient, and mostly rely on stereotypical movement rules. Monte Carlo simulations showed that the adopted rules improve maze performance. Interestingly, balanced-diet bees were quicker at adopting these rules, and thereby also performed better than those on an unbalanced diet. Over trials, bees increased their tendency to make more turns specifically to the left or to the right, though this does not affect maze solving. This superstitious behavior, automating a motor routine that is rewarded, was stronger in bees on the balanced diet. Balanced-diet bees also performed better in the landmark-learning task, increasing their approach to the rewarding feeder from the direction of the landmarks at the center of the arena. Thus, nutrition affects the decision rules that bees use to solve spatial tasks, affecting their performance, and thereby affecting colony strength.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 11:45 · K9 · Session 53 · Abstract ID 149970

Time-space memory in honey bees: from behavior to brain processes

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A hundred years ago Karl von Frisch and his students were the first to demonstrated that animals have a sense of time training honey bee foragers to visit artificial feeders at different times of the day. Moreover, foragers naturally restrict their flower visits to the times these provide highest nectar rewards. Today, there is growing evidence that honey bees and other insect central place foragers evolved the capability to form multiple time-space memories which are likely based on elaborate interactions between memory centers and the circadian clock. We combined feeder-time training with state-of-the-art time-series RNAseq and RNAscope labeling to explore molecular connections between the mushroom bodies, central complex and the clock in honey bees. Our studies showed that the majority of the mushroom body Kenyon cells (KC) and selected central complex neurons express the receptor for pigment dispersing hormone indicating a direct modulatory input from the clock’s central pacemaker. Moreover, some of the KCs even co-express Cry2 and period suggesting that KCs might exhibit the capability to function as local clocks independent of the central pacemaker. These findings indicate a much more complex interaction between the clock and memory centers than previously assumed for insects. The RNAseq and RNAscope labeling studies of mushroom body KCs indicated that the time-trained foraging activity is associated with an anticipatory gene expression including major learning and memory genes. We propose that these internally regulated expression changes are regulated by the clock and prepare the neurons for updating memory contents during foraging.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 12:00 · K9 · Session 53 · Abstract ID 149418

Precise, individualized foraging flights in honey bees revealed by multicopter drone-based tracking

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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 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 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 waggle dance variability does not reflect limits 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 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.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 14:30 · K9 · Session 59 · Abstract ID 149471

Consequences of a sleepless brain: A sleep-restricted dancer sends different messages to her honey bee followers

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Brains and behavior both operate in light of an animal's ability to sleep. A honey bee forager performs waggle dances that can, under normal conditions, direct naïve followers to a distant site, and she dances even after losing sleep—but her dances change, and responses by her followers change as well. Her dances are shorter, and directionally less precise. Followers switch dancers when the dance is imprecise, and follow fewer iterations of the dance when their dancer suffers sleep loss. Following fewer iterations means acquiring less information, posing a risk of degrading flight accuracy. A follower rarely follows a complete dance, so the brevity of the dances alone should not affect a follower bee's behavior. It's possible that she responds to a cue other than directional (im)precision when following a sleep-restricted dancer, but what stimuli inform her decision?

We trained foragers to a feeder at two different distances, individually marked the foragers and added shellac + ferrous nickel to treatment bees, and nonferrous copper to control bees. Using a motorized "insominator" laden with rare earth magnets to perturb the subset of treatment bees at night, we monitored their foraging and dancing, as well as the behavior of their followers before and after sleep restriction. We recorded dancers' surface body temperature with a thermal camera as they danced, and the acoustic emanations of their dances using a mini directional microphone to see if either thermal emissions or near-field sound signatures could serve as cues to a follower wary of wayward dancers.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 14:45 · K9 · Session 59 · Abstract ID 145368

The evolution of communicative complexity across acorn ants

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The cognitive capacities of insects underlie communication systems that vary greatly in their complexity. Understanding the traits that promote evolutionary transitions to more sophisticated cognitive abilities and communication systems is a major research goal of evolutionary biology. Acorn ants (genera Temnothorax and Leptothorax), which utilize a communication method known as tandem running, are uniquely valuable as a model clade for studying the evolution of animal communication and cognition. Tandem running involves a leader ant directing a follower ant to either a food source or a potential nest site. This communication system relies on bidirectional feedback between leaders and followers, is mediated through physical contact, and can vary in complexity as followers can occasionally form groups of several interacting individuals that pursue the leader. In the current study, we observed recruitment behavior across 32 different acorn ant species and obtained high resolution trajectory data from tandem run participants. Using this trajectory data, we quantified information flow between leaders and followers and assessed the interaction patterns within tandem groups. We show that acorn ant species exhibit interspecific differences in their tandem running traits, and we assess if species that exhibit more complex tandem interaction rules exhibit faster rates of evolution in their communication traits.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 15:00 · K9 · Session 59 · Abstract ID 144955

Impact of social isolation on socially selective neurons and high-order visual processing in a social wasp

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Polistes fuscatus wasps possess individually distinctive color patterns on their face, which they can use to visually recognize and discriminate each other. The development of this ability is dependent upon social experience. Previously, we found a localized physiological population of neurons in Polistes fuscatus that are selective to forward-facing wasp images in the lateral protocerebrum. Additionally, the synaptic volumes of high-order visual centers in these same brain areas are differentially impacted by social experience. We now perform multichannel extracellular electrophysiology recordings in the brains of P. fuscatus wasps that have been isolated for their entire adult lives and have never seen another adult wasp. We find a striking difference in the relationship between the selectivity for forward-facing wasp images with and without color across the brains of these animals. In normally reared animals there is a very tight relationship between a unit's selectivity for wasp shape with and without wasp internal features present. Here in isolated animals this relationship is almost entirely gone. However, we do still find units that are selective for forward facing wasp images with and without internal wasp features. This suggests that there is a developmental program in Polistes fuscatus that produces wasp cells in appropriate regions of the brain and experience is not necessary for social image selectivity to develop in these circuits. However, the proportion of selective units and their degree of selectivity across wasp features is impacted. This finding suggests that connectivity between these circuits may be what is shaped by social experience.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 15:15 · K9 · Session 59 · Abstract ID 146361

Leaf-cutting ants learn from their efforts: foragers recall olfactory memories to avoid plants they previously experienced as hard to cut

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Leaf-cutting ants reject previously-accepted plants if they prove to be unsuitable for their symbiotic fungus, a phenomenon that involves olfactory avoidance learning. We asked whether olfactory memory also underlies the avoidance of suitable plants that were previously experienced as hard to cut. Would ants associate an odor with a high cutting effort and would the odor be sufficient to recall such a negative association, leading to subsequent plant avoidance? In the laboratory, naïve workers of the leaf-cutting ant Acromyrmex lundii were initially tested for their spontaneous preferences for different odors in a binary-choice olfactometer. Then, colonies were offered pseudo-leaves (of inert material) of two different toughness, i.e., easily and hard to cut, scented with specific odors, to allow workers to gain experience with them over three days. One day later, putative experience-dependent changes in odor preferences were quantified both as individual responses using the binary-choice assay, and as a colony-wide foraging response when the two odors were offered on soft material, to reveal odor-guided preferences irrespective of the mechanical properties of the material actually cut. After their experience with the two scented materials of different toughness, single workers developed a marked learned preference for the odor associated with the soft material. In addition, colonies foraged more material scented with the odor paired with the low cutting effort, indicating that ants learned to olfactorily recognize, and to avoid, only those leaves they previously experienced as hard to cut.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 15:30 · K9 · Session 59 · Abstract ID 146406

Deciphering Ant Antenna Use Patterns for Exploration

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Ants use their antennae as active sensory organs to gather tactile and chemical information as they move through complex, heterogeneous environments. Yet the principles governing how antenna motion relates to navigation and decision-making remain poorly understood. In this work we employ high-resolution video tracking of ants in controlled laboratory experiments to characterize how the antennae are used during exploration of an arena under various environmental conditions. By quantifying antenna kinematics, wall and obstacle contact events, and spatial sampling strategies, we aim to describe patterns in how individual ants gather and integrate sensory information during movement.

Preliminary analyses suggest the presence of state-dependent antenna motion patterns that vary with ambient conditions, locomotor state, behavioral context, and proximity to boundaries or obstacles. These observations indicate that interactions between environmental features, spatial sampling, and locomotion may form a sensorimotor feedback process, in which changes in sensory input are associated with shifts in antenna use and movement patterns. Such interactions may help ants adjust the balance between exploration, information gathering, and efficient movement.

Together, this work outlines an initial framework for exploring how antennal behavior reflects and potentially shapes navigation and decision-making processes in ants.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 15:45 · K9 · Session 59 · Abstract ID 148545

Innate visual attraction before, during, and after experiencing adversity in the ant Camponotus japonicus

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Insects are not only capable of responding directly to ongoing external stimuli, but can also regulate their behaviour according to internal states induced by recent experience and accumulated exposure to stimuli. In this study, we examined how an innate visual attraction, beacon-aiming, is regulated in response to dynamically changing conditions. This behaviour is a spontaneous approach towards a conspicuous visual landmark, typically a dark vertical stripe. Beacon-aiming has been observed in many insect species, including ants, but we found that workers of the Japanese carpenter ant, Camponotus japonicus, do not exhibit beacon-aiming on a standard dry substrate. In stark contrast, when C. japonicus workers fell onto the water surface, they approached a landmark while swimming or wading across the surface. Beacon-aiming was also exhibited under other adverse conditions, including falling onto a non-aqueous liquid surface (a glycerol–2-propanol mixture), walking upside-down on a dry substrate, or being exposed to strong upward airflow. Furthermore, C. japonicus workers isolated on a small platform surrounded by water initially did not orient to a landmark. However, their preference for the landmark gradually increased during exploration on the platform, and finally they started to swim towards it. Moreover, C. japonicus workers that had swum across the water surface continued to orient towards the landmark for at least several seconds even after the water-to-land transition. These results demonstrate that the innate visual attraction is gated by a transient, stress-like internal state that gradually increases during exposure to adverse stimuli and decreases over time.

SYMPOSIUM 13 · Comparing miniature cognitions
ORAL · Thu 20 Aug · 16:00 · K9 · Session 59 · Abstract ID 148591

Pain-relief seeking in bumble bees

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The possibility that insects experience pain beyond nociception is increasingly debated. In vertebrates, one approach to investigate pain experience is to assess whether animals actively seek analgesia. We tested whether bumble bees Bombus terrestris undergoing noxious stimulation (constant nociceptive pressure to the hind leg produced by two magnets) show analgesic-seeking behaviour. In a first experiment, we measured sucrose consumption over nine days in experimental (magnet-treated) and control bees. The same protocol was applied to four additional groups (two experimental and two control) in which sucrose was supplemented with the analgesic Gabapentin at two concentrations (0.12 and 1.2 mg/mL). Magnet-treated bees consumed significantly less sucrose than controls, suggesting a reduced motivation to feed induced by the noxious stimulus, as observed in vertebrates. When sucrose contained Gabapentin, consumption did not differ between magnet-treated and control bees. Moreover, magnet-treated bees consumed more sucrose plus Gabapentin than plain sucrose, consistent with self-administration to alleviate the injury. In a second experiment, magnet-treated bees were given a binary choice between plain sucrose and sucrose plus Gabapentin (0.12 mg/mL), each paired with a different colour (blue or purple). Magnet-treated bees were more likely to approach the colour associated with the analgesic solution, and, over six hours, they consumed more analgesic-containing sucrose than plain sucrose. Overall, these results support the hypothesis that bumble bees actively seek analgesia under noxious stimulation. This behaviour, expressed as increased self-administration of an analgesic and preference for an analgesic-associated cue, is consistent with vertebrate paradigms used to infer pain relief.

Role of cognition in determining contest success in Temnothorax rugatulus contests

Emiliano Calvo Alcaniz

The outcome of an animal contest determines the ability of each individual to access vital resources. While animals have a diverse set of behaviors–such as communication strategies, levels of aggression, and the ability to learn–the prevailing hypothesis is that body size is the single greatest determinant of success. However, the role of an individual's behavior, and the cognitive ability that underlies it, in determining contest outcomes has largely been overlooked in contest research. How then does repeated experience in a contest affect the outcome of future contests? To answer this question, I am conducting contests between individuals with differing levels of fighting experience to determine the importance of cognitive and learning abilities in determining contest success. Results of this study may indicate whether increased cognitive ability is beneficial during intraspecific conflicts.

SYMPOSIUM 13 · Comparing miniature cognitions
POSTER · Abstract ID 147365

Age and Attitude: How Longevity Influences Cognitive Biases in Honeybee Workers

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This study investigates how life expectancy shapes cognitive biases in honeybee workers (Apis mellifera) and their emotional states that influence decision-making. Emerging work shows that emotions affect behavior and thought across species, including invertebrates. We carried out three experiments to shorten bee lifespans and examine effects on judgment biases via a standard judgment-bias task. In the first study, we reduced lifespan by CO2 anesthesia or thoracic puncture. The second study exposed workers to Nosema sp. spores to induce infection and assess its impact on survival and judgment. The final study examined “rebel workers,” naturally longer-lived individuals. We trained bees to associate particular odors with rewards and punishments, then tested responses to ambiguous cues. The results revealed that life-shortening treatments produced more optimistic biases, evidenced by a greater probability of extending the proboscis to ambiguous odors. In contrast, rebel workers with extended lifespans showed more pessimistic biases, suggesting a cautious foraging strategy. Collectively, our findings indicate that honeybee decision-making closely tracks longevity, with shorter-lived bees adopting riskier strategies than their longer-lived counterparts.

Collective Associative Learning in the Rock Ant, Temnothorax rugatulus

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Collective performance in eusocial insect colonies relies on efficient sharing of information between colony members, with individuals exploiting signals produced by their nestmates. Despite this tight coupling between individual behavior and colony-level information transfer, learning abilities in eusocial insects have most often been studied in isolated individuals. How individual learning processes interact with information sharing at the colony level remains largely unexplored. To examine how the presence of colony members impacts learning performance, we conducted an associative learning assay on the rock ant Temnothorax rugatulus, a species with small colonies that transmit information by performing tandem runs. Both isolated individuals and whole colonies were exposed to a two-corridor task in which food was paired with colored Lego blocks, followed by a reversal of contingencies after a set number of trials. Colony-trained ants learned the association significantly faster than isolated ants and also reversed their associations more quickly, exhibiting greater flexibility. Incorporating social information during learning may not only enhance task performance but also increase flexibility when environmental contingencies change, potentially helping explain the ecological success of social insects across diverse and fluctuating resource landscapes. Potential colony-level mechanisms underlying the collective learning advantage observed in our experiment will be discussed.

Longevity and Cognitive Bias in Honey Bees under Prolonged Illumination

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Artificial light at night (ALAN) has become an increasingly pervasive component of anthropogenic environments and is recognized as a significant stressor disrupting natural light–dark cycles. While the effects of ALAN on the physiology and behavior of vertebrates have been widely documented, knowledge regarding its long-term consequences for invertebrates—particularly in terms of cognitive functions and lifespan—remains limited. The aim of this study was to assess the effects of light exposure on lifespan, learning ability, and cognitive biases in worker honey bees (Apis mellifera).

Forager workers originating from four unrelated colonies were exposed to five light regimes, ranging from constant illumination (L:D 100:0), through intermediate conditions (L:D 75:25, 50:50, 25:75), to complete darkness (L:D 0:100). A subset of workers was used to assess lifespan under caged conditions, while the remaining individuals were tested for learning speed and susceptibility to cognitive biases.

The results indicate that long-term exposure to light (L:D 100:0 and 75:25) significantly affects both survival and cognitive components of honey bee behavior. Workers maintained under increased illumination exhibited reduced lifespan, slower learning performance, and a tendency toward negative cognitive biases compared to individuals kept in darkness (L:D 0:100) or under more natural light–dark cycles (L:D 25:75 and 50:50). These findings suggest that ALAN may act as a chronic stressor, impairing individual functioning and potentially affecting entire colonies.

Keywords: artificial light at night; learning; circadian rhythms; environmental stress; cognitive bias; lifespan

Variation in social organization and supergene control along a latitudinal gradient

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Widespread species often experience vastly different environmental conditions across their range. In species with polymorphic traits under strong genetic control, we can investigate how environmental variation influences the distribution of traits and whether the strength of genetic control is consistent across environmental gradients. Here, we investigate the distribution of phenotypic and genetic variation in the ant Formica podzolica across 30° of latitude. This species shares a supergene that is associated with colony queen number and colony sex ratio with other congeners, but we detect a surprising six common supergene variants. Colonies with a single queen are more abundant in the north compared to those with multiple queens, although the queen number polymorphism is present throughout the range. In parallel, the frequency of supergene haplotypes also varies with latitude. Of the 170 colonies examined, 10.6% contained supergene haplotypes that did not match the queen number phenotype. The highest concentration of these ‘mismatched’ colonies occurred in one site, raising the possibility that the environmental conditions there override supergene function. While the supergene system in F. podzolica is complex, this species holds promise for understanding how an ancient supergene system evolves in a single species experiencing highly variable environmental conditions.

Multi-level selection drives supergene-mediated social and dispersal polymorphism in the ant Myrmecina graminicola

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Several supergenes determining social organization (monogyny versus polygyny) have been documented in several ant species, yet the selective forces allowing the long-term maintenance of their polymorphism remain poorly understood. Here, we investigate the role of transmission ratio distortion (TRD) and spatially varying selection in the ant Myrmecina graminicola.

This species exhibits a social and wing polymorphism determined by a supergene. The monogyne winged queens are homozygote at the ancestral haplotype (Mo), whereas polygyne apterous queens are heterozygote at the derived haplotype (Pa, dominant over other haplotypes). In addition, monogyne apterous queens occur and carry a duplication in the ancestral haplotype (Ma, dominant over Mo).

Genotyping adult workers and males at the supergene in polygynous colonies revealed departure from Mendelian segregation. Pa males were overrepresented (83%) as well as heterozygous workers (MoPa or MaPa) (65%). Moreover, PaPa workers decreased in frequency from larvae to adult stage, suggesting some deleterious recessive effects of Pa. Although the mechanisms underlying TRD remain unknown, the combination of transmission advantage and reduced fitness supports a role for both selfish genetic processes and supergene degeneration.

At the population level, spatially heterogeneous selection further shapes supergene frequencies. Based on foraging workers, Pa was more frequent in groves (28%) and urban parks (40%) than in forests (4%), suggesting that fragmented and/or recent habitats favor apterous polygyne queens. This pattern persisted in a region (Lyon), where wing polymorphism is nearly absent, suggesting that environmental pressures act on social polymorphism even in the absence of dispersal polymorphism.

Introgression of color pattern alleles generates extreme phenotypic diversity mediating visual individual recognition in a paper wasp

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Among the traits with the most extreme intra-specific variation are those used for

social recognition. Identity signals need to be highly variable among individuals within a population to allow for effective discrimination and identification. Despite the centrality of recognition to social behavior, the developmental and evolutionary origins of traits mediating recognition remains poorly understood. Here we present the results of GWASP, a genome wide association study of Polistes fuscatus paper wasp color patterns that mediate visual facial recognition. Analysis of over 800 whole genome sequences and color patterns revealed two genetically distinct populations of this species that differed in color pattern diversity. We find evidence of both shared and distinct alleles between populations mediating different stripes and color patterns that contribute to wasp visual appearance. Analysis of gene trees for Polistes fuscatus and population samples of related species revealed clear evidence of introgression between the two subspecies at color pattern loci. Additionally, we find strong evidence of balancing selection on color pattern loci in P. fuscatus. Introgression of rare alleles between the two populations has seemingly been a key mechanism facilitating the recent emergence of and maintenance of extreme polymorphism and impressive visual cognition abilities in this species. These data add to a growing literature highlighting the important role of introgression in generating novel adaptive traits and in this instance extreme phenotypic diversity within and between populations.

SYMPOSIUM 14 · Complex phenotypes in social insects: the interplay of genes and environment
ORAL · Mon 17 Aug · 11:15 · K10 · Session 6 · Abstract ID 149430

Remote control" of complex social behavior from outside of the brain: Lessons from functional genomics in Polistes

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Peripheral tissues outside of the brain, such as the gut and fat stores, are increasingly recognized as having the capacity to regulate behavioral traits. Peripherally-expressed genes are known to affect simple behaviors such as feeding, but what about complex behavior such as social interactions? Using Polistes fuscatus wasps, we investigated whether a cognitive behavior, the establishment of social dominance, is peripherally regulated. The best predictor for social dominance in these insects was high expression of a gene not found in the brain-- the egg yolk protein vitellogenin, or vg. Knocking down vg expression in the head fat body using RNA-interference resulted in reduced aggression during dominance contests between workers. vg knockdown also altered the expression of dozens of genes in head and brain tissue, including genes related to insulin/insulin-like signaling (IIS). A single cell gene expression atlas from P. fuscatus, in combination with whole brain RNA-seq, further suggested vg expression has the potential to affect expression of numerous genes in the head fat body, glial cells, and Kenyon cells of the mushroom bodies. These finding implicate vg as a potent peripheral regulator of social behavior through downstream signaling pathways between the fat body and brain. This work highlights peripheral tissues as important controllers not only of simple behaviors such as food intake, but also cognitively complex social behaviors.

SYMPOSIUM 14 · Complex phenotypes in social insects: the interplay of genes and environment
ORAL · Mon 17 Aug · 11:30 · K10 · Session 6 · Abstract ID 148297

The genomic architecture of ant social organization: insights from the Formica supergenes

Michel Chapuisat

University of Lausanne

Supergenes are clusters of linked genes that control complex phenotypes. In the Alpine silver ant, Formica selysi, one large supergene determines whether colonies have a single queen or multiple queens, through subtle effects on morphology and behavior, while another supergene influences colony sex-ratio. These non-recombining genomic regions preserve co-adapted allelic combinations, but they also have a dark side: the accumulation of deleterious mutations, transposable elements and selfish genetic elements that distort Mendelian inheritance. In this talk, I will draw on recent molecular, morphological and behavioral data from Alpine silver ants to explore how selfish genetic elements influence supergene dynamics and how supergenes determine social organization and life-history. These results indicate that multiple selective pressures, sometimes antagonistic across levels of biological organization, affect the evolution and maintenance of the genomic architecture underlying ant social organization.

SYMPOSIUM 14 · Complex phenotypes in social insects: the interplay of genes and environment
ORAL · Mon 17 Aug · 11:45 · K10 · Session 6 · Abstract ID 145831

Development and individual experience combine to shape defensive behavior phenotypes during worker-to-soldier differentiation in termites

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Defensive behavior is crucial for survival, especially in group-living animals that can attract predators and parasites. Individuals can improve their defensive behavior across the lifespan, allowing them to respond more efficiently to threatening situations. This behavioral flexibility might be accompanied by structural and functional neuroplasticity, including serotonin activity, 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 phenotypes and neuroplasticity, especially with respect to serotonergic activity. We combine worker-to-presoldier differentiation induced by a juvenile hormone analogue, aggressive encounter assays 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. It suggests that individual experience is important in shaping defensive response. Behaviors such as drumming and evading increased over the aggressive assays, 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 specific groups of serotonin-like immunoreactive neurons in the brain and suboesophageal zone (SEZ), an important nervous 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 indicate that development and individual experience combine to shape defensive behavior phenotypes in termites, an assumption hitherto unexplored for these insects.

SYMPOSIUM 14 · Complex phenotypes in social insects: the interplay of genes and environment
ORAL · Mon 17 Aug · 12:00 · K10 · Session 6 · Abstract ID 149189

Title: The effects of juvenile hormone treatment on caste development in Cardiocondyla obscurior ants

Devashree Joglekar; Eva Schultner
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Superorganismal insects are characterized by division of labor, which is facilitated by irreversible development into reproductive and non-reproductive castes, i.e., queens and workers. Juvenile hormone plays a major role in regulating caste-specific growth and development in ants, but the underlying mechanisms are not well understood. In Cardiocondyla obscurior ants, workers lack reproductive organs and caste is determined by late embryogenesis. We investigated the role of juvenile hormone in the regulation of development and morphology of female castes by feeding larvae and mated, egg-laying queens with the juvenile hormone analog methoprene. When females in the earliest larval stage were fed with methoprene, a majority developed queen-like morphology, whereas their reproductive anatomy (i.e., the presence of reproductive organs) was not affected. In contrast, when worker-destined mid and late instar larvae were fed with methoprene, caste-specific morphology remained unchanged, even though body size increased. Preliminary results indicate that when only egg-laying queens are fed with methoprene, the proportion of offspring with queen-like morphology increases, confirming maternally-mediated effects on caste development. Together, these results help us understand how juvenile hormone regulates caste-specific growth and development in ants.

The proximate bases of colony sex ratio in Formica selysi

Matteo Negroni[1]; Aneza Koreli[2]; Riddhi Deshmukh[1]; Michel Chapuisat[1]

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In many ant species, colonies differ in the proportion of male and female offspring they produce, yet the mechanisms underlying such split sex ratios remain incompletely understood. In Formica selysi, variation in sex allocation in monogynous colonies appears linked to a non-recombining genomic region with two haplotypes, A and D: colonies headed by A/D queens tend to produce more females, whereas A/A queens generally produce more males. To investigate how this pattern arises, we analysed haplotype frequencies in eggs and adult sexuals and compared morphological traits across genotypes. Although A/D females lay haploid eggs carrying either allele, the D allele was almost absent among adult males. This suggests that D carrying haploid brood experience developmental difficulties or that selective brood care by workers favours the survival of A carrying males. We also found morphological differences between sexuals depending on their colony's genotypic composition, including variation in wing shape and male head size. The respective contributions of queen genotype, worker genotype, and environmental conditions remain to be established. Overall, our findings suggest that several genetic, developmental, and social mechanisms interact to shape colony sex allocation and sexual phenotypes in F. selysi.

Regulatory plasticity underlying caste and sex determination in social insects

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In eusocial insects, reproductive division of labour is tightly linked to caste identity and reproductive potential. This connection has been extensively studied in Hymenoptera but remains poorly understood in termites. While Hymenoptera are generally haplodiploid, with males emerging exclusively for reproductive purposes, termites are hemimetabolous insects with an XY sex determination system in which both sexes occur across all castes. These fundamental differences make the comparison between these two groups particularly informative.

Lower termites exhibit pronounced developmental flexibility, as individuals can change caste during development. Under specific conditions, both males and females of these species may moult into sterile soldiers or into three types of reproductives: primary winged reproductives, secondary neotenic reproductives and tertiary neotenic apterous reproductives. A similar condition can be observed in the ant species Hypoponera opacior, which, unlike most ant species, presents both winged and ergatoid reproductives. The emergence of this similarity in such evolutionarily distant lineages makes the comparison especially compelling.

Using transcriptomic analyses and comparative genomics, the molecular differences between different castes of H. opacior have been tested. Our results suggest fine regulatory plasticity that underlies a clear distinction between ergatoid and winged reproductives' gene expression. Despite their nearly identical external morphology, ergatoid queens show gene expression profiles significantly different from those of sterile workers.

This study represents the first step of a broader comparative research project involving lower termites. By distinguishing species-specific regulatory mechanisms from potentially conserved expression patterns, such comparisons will help elucidate how eusocial reproductive polyphenism evolved across deeply divergent insect lineages.

Repeated evolution of supergenes on an ancient social chromosome

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Sex determination in many eukaryotic lineages evolved repeatedly from plasticity and environmental control to genetic control by sex chromosomes. Sex chromosomes are just one type of a supergene: a large genomic region with suppressed recombination that determines a complex polymorphic trait. “Social chromosomes” harbor supergenes that determine colony structure in polymorphic ant species, which form either monogyne (single queen) or polygyne colonies (with multiple queens). Two analogous supergenes evolved independently in two diverged ant lineages – Solenopsis and Formica. We discovered a third such system in Cataglyphis niger, by reduced-representation genomic sequencing (RAD-seq) of 20 individuals from each of 30 nests. Our analyses identify a large chromosomal region of suppressed recombination between two haplotypes, at least 6Mbp long, which is associated with colony social structure. Surprisingly, the Cataglyphis social chromosome is homologous to the Solenopsis chromosome, even though these lineages diverged more than 90 million years ago. We suggest that this conserved chromosome harbors an ancestral genetic toolkit that was reused for the repeated evolution of sociobiological traits across diverse ant species. A subset of genes with conserved synteny across ants and bees is enriched with olfactory functions, suggesting a central role for chemical signaling in the contribution of this chromosome to social evolution. The repeated evolution of supergenes in Solenopsis and Cataglyphis on an ancient social chromosome present excellent opportunities for the study of evolution and maintenance of the genes and genomic architectures underlying adaptive complex polymorphisms.

Parasites exploit plasticity to reprogram social wasps into extended phenotypes

Rafael Carvalho da Silva[1]; Juan Martín Ferro[2]; Natasha Vacca[3]; Elsa Hahn[3]; Sina Ghaemmaghami[3]; Karl Glastad[3]; **Floria Mora-Kepfer Uy[3]**

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Prolonged coevolution between hosts and parasites can generate novel and complex host phenotypes. Intriguingly, phenotypic plasticity intended to provide advantages to hosts can ultimately be reprogrammed for rapid phenotypic change that benefits the parasite. We leveraged the parasitic insect Xenos peckii (Strepsiptera) that infects the social wasp Polistes fuscatus to elucidate how traits can be decoupled and generate an extended phenotype. Both parasite sexes inhibit reproduction and manipulate the social behavior of worker hosts but not of male hosts. In addition, only adult female X. peckii remain as obligate endoparasites and extend the lifespan of worker hosts, but not of male hosts. Therefore, we hypothesized that the parasite controls caste-related plasticity that mediates traits critical for parasite survival and fitness. Using transcriptomic approaches, we first used a developmental time series of female hosts that revealed how developing parasites manipulated specific neural and caste-related host genes. Second, the brains of infected adult workers showed similar signatures to uninfected gyne brains, highlighting gene pathways shown to regulate longevity, reproduction, diapause, and neuromodulation. Proteomic comparisons confirmed that caste-related plasticity is critical to modify the behavior, physiology, and metabolism of workers. However, parasites cannot effectively manipulate some key pathways in male hosts, which supports our main hypothesis. Together, our results reveal novel insights about how caste plasticity facilitates reprogramming female wasps into an extended phenotype that decouples behavior, reproduction, and lifespan.

Population Genomics of the social parasite Vespula squamosa and host V. maculifrons

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Social parasites hijack the colonies of other species to jumpstart their own life cycle. Social parasitism has evolved repeatedly in wasps, ants, and bees. For example, the social wasp Vespula squamosa is a facultative social parasite of its relative V. maculifrons. These two species overlap for much of their range, but also exist separately on the edges of their respective ranges. Thus, these species provide a great opportunity to test hypotheses on the genome evolution of social parasites and their hosts. This study investigates the effects of social parasitism on genome evolution by studying the population genomics of V. squamosa and V. maculifrons across their native ranges. The first goal of this study is to assess the selective pressures operating on genes in the social parasite and its host. The second goal is to evaluate effective population size and gene flow, and determine how these factors impact selection. To this end, we have collected and are sequencing 25 V. maculifrons samples and 19 V. squamosa samples from the eastern United States across a range of 1813km from the southernmost to northernmost collection site. Preliminary analysis of mitochondrial gene sequences confirmed species identifications and showed some population structuring of samples within each species. Overall, this study provides information on how social parasitism shapes the evolution of both parasites and hosts.

Convergent Gene Expression and Epigenetic Regulation of Raiding Behavior in Slavemaking Ants

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Social parasitism has evolved repeatedly in social insects. In ants, slavemaking species raid host nests to steal worker brood, providing a system to study the genomic basis of complex parasitic behavior. We investigated the genomic and transcriptional correlates of raiding behavior, parasitic lifestyle, and host defense in the genera Temnothorax and Leptothorax, where slavemaking has evolved convergently multiple times. We focused on four independent origins of slave making—Temnothorax americanus, T. pilagens, T. ravouxi, and Harpagoxenus sublaevis—and their respective host species.

Using standardized raiding assays, we sampled active and inactive parasite workers and defending and non-defending host workers for RNA sequencing of antennae and brains. To test the role of epigenetic regulation, we inhibited histone acetylation and deacetylation via feeding prior to raiding trials. In T. americanus, brain transcriptomes of raiding and non-raiding workers differed only weakly, with a single vitellogenin-like lipoprotein gene upregulated in raiders. In contrast, host species showed pronounced transcriptional differences between defenders and non-defenders, including genes involved in juvenile hormone binding.

To assess transcriptional convergence among slave makers, we reanalyzed published whole-body transcriptomes. We identified 31 single-copy orthologs differentially expressed across three slave-making species, enriched for vitellogenin-like functions, and signaling processes, whereas no comparable convergent signal was detected among host species. Finally, manipulating histone acetylation altered raiding behavior, brood retrieval timing and tandem runs and increasing aggression and mortality among enslaved workers. Together, these results reveal partial convergent regulation of signaling pathways in slave-making ants and identify epigenetic mechanisms as modulators of complex social behavior.

Secondary acquisition of selfish genetic drive by an ancient social supergene in Formica

Riddhi Deshmukh; Hélène Boulain; Anthime Bretaudeau; Sarya Fark; Daniel Caballero Fernández; Michel Chapuisat

University of Lausanne

Polygyny, the presence of multiple reproducing queens in a colony, has evolved repeatedly in ants and often exists as a polymorphism with monogynous “morphs” that carry a single reproducing queen. In several ant lineages, polygyny is controlled by a supergene-like architecture involving large genomic regions of suppressed recombination. Social polymorphism in the Formica genus is associated with one of the oldest known supergenes (~30 My old) whose haplotypes determine the social form of a colony. Individuals from monogynous colonies exclusively carry the M haplotype, and individuals from polygynous colonies usually carry at least one copy of a P haplotype. In Formica selysi, the P haplotype of the supergene selfishly distorts its transmission through maternal-effect killing, rendering inviable all offspring from an MP queen that do not inherit the P haplotype. We used worker reproduction to test for the presence of this selfish drive in seven Serviformica species. We only found selfish drive through maternal-effect killing in three closely-related species, where among haploid offspring laid by MP workers in queenless conditions, only P carrying offspring survive. We identified candidate genes for maternal-effect killing by performing a GWAS across species. Finally, we found signatures of introgression among P haplotypes in species showing selfish drive, suggesting that selfish drive may have crossed from F. selysi into the other two species. Overall, our work suggests that selfish drive through maternal-effect killing did not originate with the social supergene and has been secondarily acquired.

SYMPOSIUM 14 · Complex phenotypes in social insects: the interplay of genes and environment
ORAL · Mon 17 Aug · 16:15 · K10 · Session 12 · Abstract ID 146286

The enigmatic conserved region of Cardiocondyla genomes

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Ants of the genus Cardiocondyla exhibit a pronounced case of male polymorphism, with winged and wingless (ergatoid) males that differ strongly in morphology and behaviour. This male diphenism is tightly linked to alternative reproductive strategies, where the ergatoid males engage in lethal fighting and intranidal mating, while the winged males disperse and reproduce outside their natal nests. We recently generated high-quality chromosome-scale genome assemblies for ten Cardiocondyla species. Despite extreme degrees of genome rearrangements in the genus, we identified a single genomic region spanning ca. 6.8 Mb that has remained remarkably conserved in this genus but is broken up in other ants. The persistence of this region contrasts sharply with the surrounding genomic instability and suggests an important functional role specific to Cardiocondyla. We hypothesize that this conserved region is linked to the evolution of the male polymorphism. To test this, we will combine functional with genomic approaches across different species, aiming to resolve the genomic architecture of the Cardiocondyla male polymorphism.

Transcriptomics of reprogramming: parasites exploit plasticity in caste and brain development of social wasps

Natasha Vacca[1]; Valeria Padilla-Choy[1]; Juan Martín Ferro[2]; Floria Mora-Kepfer Uy[1]

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The evolution of castes in social insects is one of the most spectacular examples of phenotypic plasticity. However, this adaptive plasticity could instead be exploited by parasites to develop an extended phenotype. We characterized the timing and molecular changes induced by the twisted-wing insect Xenos peckii (Strepsiptera) to manipulate developing social wasps, Polistes fuscatus. To complete their life cycle, these parasites reprogram short-lived female workers into long-lived phenotypes similar to gynes, while hindering ovary development and cooperative behavior. First, we used a developmental-time series of naturally infected and uninfected wasps to uncover if parasites manipulate the intrinsic developmental plasticity that evolved to produce queens or workers. We confirmed that parasite larvae infect most host larval instars. We also found robust stage-specific differences between uninfected workers and gynes, specifically in genes involved in insulin and dopamine pathways, neural development, and immune responses. Second, we experimentally infected fourth instar larvae, the most common attacked instar, while removing the effect of differential nutrition and social interactions towards caste-bias. Compellingly, parasitic manipulation of caste and neural genes remained consistent. Finally, experimentally infecting long-lived gynes that are not targeted in nature showed minimal parasitic exploitation. Therefore, these developing parasites manipulate specific plastic traits associated with caste-bias that facilitates an ideal, long-lived host. Our findings reveal how stage-specific targeting during development initiates this reprogramming of hosts towards the final extended phenotype that benefits the parasite.

Phylogeny of Messor structor lineages and the origin of cross-species cloning

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M. ibericus exhibits a unique reproductive strategy called xenoparity, in which females must clone males of M. structor because they require their sperm to produce the worker caste. The evolutionary history of this system appears as sexual parasitism that evolved into a natural case of cross-species cloning, resulting in the maintenance of a male-only lineage of M. structor cloned through M. ibericus' ova. Paralleling a domestication process, this clonal lineage of males appears genetically and morphologically divergent from wild M. structor lineages. To better understand the evolutionary history and origin of male domestication, we performed a more comprehensive sampling of Messor structor populations across its geographical range and conducted phylogeographic and population genomics analyses. These analyses enabled us to reconstruct the evolutionary relationships among the diverse M. structor lineages, giving insights into the geographic and temporal origins of xenoparity.

Evolution of two supergene systems in the ant Temnothorax rugatulus

wenfeng bai[1]; Giulia Scarparo[1]; Manfred Huber[1]; Florian Menzel[1]; Hugo Darras[2]; Susanne Foitzik[1]

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Supergenes are genomic regions composed of tightly linked loci that control complex adaptive phenotypes. In the ant Temnothorax rugatulus, previous work has shown that two supergenes located on different chromosomes independently control colony queen number and queen miniaturization. These supergenes evolved independently of those described in other ants. Monogynous macrogynes consistently carry the L and M haplotypes, whereas polygynous microgynes carry the S and P haplotypes. Recent findings further show that males carrying the S haplotype always also carry the M haplotype, thus displaying a pattern opposite to that observed in queens. In contrast to queens, neither supergene affects male body size. The mechanisms underlying the nonrandom distribution of these genotypes across social structures and between sexes remain unclear. Supergenes can act as selfish genetic elements, and chemical cues may contribute to worker mediated selection of genotypes. Building on this, we investigate the properties of the two supergene genotypes in T. rugatulus across developmental stages and test for non-Mendelian inheritance at the supergene loci. Furthermore, we examine whether supergene genotype is associated with variation in cuticular hydrocarbon composition. We will provide insights into the mechanisms regulating supergene genotype frequencies and clarify the role of chemical signaling in the organization and maintenance of social structure.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
ORAL · Wed 19 Aug · 14:30 · K9 · Session 41 · Abstract ID 148743

Genetic, social, and environmental influences on aggression in Temnothorax ants and their fitness consequences

Susanne Foitzik
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Social insects assess intruders and decide whether to attack. Individuals and colonies differ in aggressiveness, shaped by age, experience, and genetic composition. We analysed ecological, social, and genetic influences on aggression in Temnothorax ants, including mechanisms of intruder recognition via chemical signals and odorant perception. In T. nylanderi, cestode-infected workers reduce the aggression of healthy nestmates toward non-nestmates. In T. longispinosus, colonies with greater among-worker variation in aggressiveness show higher productivity. More aggressive colonies defend more effectively against social parasites after prior exposure to raiding parasites, and populations with more social parasites show increased aggression toward non-nestmates. Northern colonies show higher aggression. A population-level GWAS identified SNPs in 55 genes associated with aggressive behaviour. Intruder recognition depends on cuticular hydrocarbons and variation in odorant perception. Half of odorant receptors are differentially expressed between nurses and foragers, with the latter showing higher aggression. Chemical profiles differ among populations, and within-colony variation is higher where social parasites are common, likely hindering parasite mimicry. GWAS indicate a strong genetic basis for chemical traits, with SNPs under selection in hydrocarbon synthesis and odorant receptor genes, indicating joint evolution of signal production and perception. Variation in social organisation further affects behaviour and chemistry. Northern populations show polygyny, and we identified a supergene controlling queen number and size in T. longispinosus, which we test for effects on aggressiveness and hydrocarbon profiles. Together, these results show how behavioural and genetic variation interact with social and environmental conditions to shape aggression and recognition in Temnothorax ants.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
ORAL · Wed 19 Aug · 15:15 · K9 · Session 41 · Abstract ID 149702

Microbial regulation of the social brain in corbiculate bees

Joanito Liberti
University of Geneva

The gut microbiota is increasingly recognized for its influence on brain function, with consequences for social behavior. Most studies have focused on clinical perspectives of modulating the microbiota-gut-brain (MGB) axis to treat neurodegenerative diseases and behavioral dysfunctions, using experimental models of human genetics and disease. However, it remains unclear to what extent the MGB axis modulates social interactions across the tree of life and whether the proximate mechanisms underlying microbiota-host interactions are conserved. Corbiculate bees provide a powerful model to address these questions, as they exhibit complex social behaviors at both the individual and collective levels.

By coupling automated behavioural tracking with omics approaches, we recently discovered that the gut microbiota increases the frequency of social interactions among honeybees and accelerates the onset of their foraging activity. These effects are associated with changes in brain gene expression and increased concentrations of specific neuroactive metabolites. Follow-up work in our recently established laboratory, using synthetic microbial communities, has identified the relative contributions of distinct gut microbiota members to these social phenotypes and is revealing general neurophysiological mechanisms involved in the regulation of social interactions in honeybees. We are now extending these studies to other corbiculate bees and conducting field experiments to assess the role of gut microbiomes in the ontogeny of superorganismal societies and their ecological impacts as major pollinators. Together, our results suggest that the gut microbiota is a key determinant of social organization in bees, with potential consequences for their pollination services.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
ORAL · Wed 19 Aug · 15:30 · K9 · Session 41 · Abstract ID 147318

Paired, individual, and collective-decision making by dispersing termites

Nobuaki Mizumoto
Auburn University

Dispersal flight and colony foundation represent a critical phase in the life cycle of social insects. During this period, termite dispersers (alates) express decision-making across multiple organizational scales, shifting among a swarm of individuals, a single termite, and a coordinated mating pair. In this talk, I introduce how termites flexibly change the unit of decision-making to navigate these transitions. After dispersal flights, male and female alates shed their wings and walk to search for mating partners. Upon encounter, a pair moves in tandem while searching for a nest site together. By comparing the movement of tandem-running pairs with that of single individuals, I show that paired termites exhibit asymmetric roles between leaders and followers, resulting in functional differentiation within the pair. Leaders determine movement direction in a top-down manner, while followers constrain and stabilize movement through coordination. This interaction produces straighter trajectories than those of solitary termites, allowing a pair to explore the environment more widely than alone. Beyond pair-level coordination, I also discuss how groups of alates collectively regulate the timing of synchronized swarming flights, as observed in a group of workers. By integrating decision-making processes across individual, paired, and collective scales, this work highlights behavioral flexibility as a key mechanism underlying mating success and colony establishment in termites.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
ORAL · Wed 19 Aug · 16:00 · K9 · Session 41 · Abstract ID 149798

Testing choice overload in a pollinator: effects of option number and reward contrast

Claire Hemingway; Jessie Tanner
University of Tennessee, Knoxville

Decision makers often benefit from having multiple options, but increasing the number of alternatives can degrade performance when cognitive processing limits are reached, a phenomenon known as choice overload. In humans, choice overload is expressed as reduced decision accuracy and increased decision latency and is influenced by the similarity and quality of available options. Whether non-human animals experience comparable constraints during ecologically relevant decisions remains poorly understood. Here, we tested whether foraging bumblebees (Bombus impatiens) experience choice overload when encountering multiple flower types simultaneously, and whether the severity of this depends on the reward structure within the choice set. In laboratory experiments, individual foragers encountered one higher-reward ‘target’ flower type and either one, three, or five lower-reward ‘distractor’ types. We independently manipulated (i) reward contrast between target and distractors (close vs. distant sucrose concentrations) and (ii) overall choice-set quality. We measured target-selection accuracy and choice latency (inter-visit interval). Across experiments, the effect of option number on choice accuracy was primarily determined by the relative reward difference between the target and distractors. Bees maintained high accuracy as the number of options increased when reward differences were large, but accuracy declined with additional options when differences were small. Overall quality of the choice set did not influence choice accuracy. Results indicate bumblebee foragers are sensitive to assortment complexity, but choice overload is mitigated when reward differences are salient. In diverse floral communities, plants offering rewards that stand out relative to co-flowering species may therefore experience fewer reductions in visitation as diversity increases.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
ORAL · Wed 19 Aug · 16:15 · K9 · Session 41 · Abstract ID 149961

Superefficient teamwork in weaver ants

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Teamwork is often assumed to enhance group performance, particularly for physical tasks. However, in both human and non-human animal teams, the effort contributed by each member may, in fact, decrease as team size grows. This counterintuitive phenomenon, known as the Ringelmann effect is generally ascribed to poor coordination or differences in motivation. Weaver ants (Oecophylla smaragdina) display some of the most impressive feats of teamwork in the natural world, including self-assembly into pulling teams that fold leaves into nesting chambers. Here, we investigated whether weaver ant pulling teams suffer from the Ringelmann effect by measuring the force that weaver ant teams of varying sizes produce during nest construction. The average force contribution per individual almost doubled as team size increased, demonstrating that weaver ants not only avoid the Ringelmann effect but achieve the opposite—they are “superefficient” team workers. We propose that this superefficiency is facilitated by a division of labor within teams: “active pullers” work together to generate a pulling force that is stored in chains of “passive resisters,” which capitalize on the remarkable frictional strength of weaver ant attachment organs; weaver ant teams thereby act as a “force ratchet.” Our results highlight a novel mechanism of teamwork in a highly coordinated natural system and may inspire optimization algorithms for superefficient teams in distributed artificial systems, including swarm robotics.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
ORAL · Wed 19 Aug · 16:45 · K9 · Session 47 · Abstract ID 149842

Investigation of evolution rates of invidual vs. social locomotion behaviors across Temnothorax ants

Hailey Hutchison[1]; Grant Navid Doering[2]; Timothy Linksvayer[3]; Grace McKenzie-Smith[1]
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Ants are eusocial, phenotypically diverse insects, with a social structure that is characterized by multigenerational colonies that take collective care of brood items and other tasks within the nest. The emergent behaviors required for the colony to succeed are complex, arising from the interactions of many ants with varying information and life histories influencing their individual behaviors. Understanding these complex interactions is difficult, but high-resolution video data and new computational methods now allow us to carry out the type of high-precision measurements and time-series analyses that have been successful in other areas, such as the physics of active matter. Our focus is on the evolution of patterns of locomotion observed in solo (single ant) vs. social (groups of 5 ants) contexts. We use neural-network based postural estimation and unsupervised machine-learning behavioral classification to test our central hypothesis that social locomotor behaviors evolve more quickly than nonsocial locomotor behaviors. Using a broad survey of morphologically and phylogenetically diverse species of acorn ants in the genera Leptothorax and Temnothorax, we record 5 minute-long videos of ants in small arenas. Each video is then processed with a machine learning model within the multi-animal pose tracking software SLEAP that produces numerical pose tracking and identity data. We intend to employ a coarse behavior analysis based on postural data that will then guide behavioral comparisons and ultimately inform the use of phylogenetic comparative methods and subsequent fine-grained behavioral analyses.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
ORAL · Wed 19 Aug · 17:00 · K9 · Session 47 · Abstract ID 151979

Emergent Spatiotemporal Organization in Honeybee Colonies: Lessons from Large-Scale Behavioral Data

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Freie Universität Berlin

Honeybee colonies make collective decisions through distributed communication among thousands of individuals. Understanding how individual-level interactions give rise to colony-level behavior requires capturing these interactions at scale. Over the past decade, we have developed the BeesBook system, an automated tracking pipeline that records the lifetime trajectories and social interactions of individually marked bees in observation hives. By combining this high-resolution tracking with machine learning–based waggle dance decoding, we can reconstruct the colony's informational landscape with unprecedented detail. This data-driven approach represents a departure from classical hypothesis-driven workflows in biology, offering a powerful paradigm for uncovering the underlying rules governing complex animal societies. In this talk, I will present two examples of emergent spatiotemporal organization within the hive. First, I will discuss how a tiny drift in the waggle dance leads to a spatial sorting of dancers and followers, which in turn results in "echo chambers" that likely increase communication efficiency. Second, I will show how a simple mechanical interaction, we call "speed transfer," between individuals can lead to large-scale phase shifts in collective activity patterns, coupling the activity of foragers to that of younger in-hive workers. These results highlight how complex colony-level decisions and rhythms emerge from local, decentralized interactions, bridging the gap between individual behavior and superorganismal intelligence.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
ORAL · Wed 19 Aug · 17:30 · K9 · Session 47 · Abstract ID 149668

High-resolution tracking using machine-learning reveals the spatiotemporal dynamics of social immunity in Reticulitermes flavipes

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Özge KILIC, Peter DIno McMahon

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.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
POSTER · Abstract ID 145366

Flow and fabricate: morphogenesis of termite shelter-tube networks

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Subterranean termites must forage above ground while remaining hidden from predators and avoiding moisture loss. They meet this challenge by constructing intricate shelter-tube networks, collecting, shaping, and cementing soil grains even as thousands of nest-mates and food items stream through the same narrow passages. Despite their ecological importance, the collective rules that generate these structures remain poorly understood. Envisioning termite collectives as living granular matter that can both flow and fabricate, we present experiments and a minimal theoretical model to uncover the decentralized decision-making that drives shelter-tube morphogenesis.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
POSTER · Abstract ID 146525

TEMPORAL DYNAMICS OF SCOUT RELEASE-BEHAVIOUR OF TERMITOPHAGOUS PONERINE ANT, MEGAPONERA ANALIS

Rifilwe Victor Modiba[1]; Christian W. W. Pirk[2]; Abdullahi Yusuf[2]

[1] *Sol Plaatje University;* [2] *University of Pretoria*

Megaponera analis is an obligate termitophagous ant species endemic to sub-Saharan Africa. The species forages by sending out scouts to search for termites. Once termites are located, the scouts return to the nest and recruit nestmates. Scouts face unpredictable environmental conditions, including sudden flooding, temperature changes, gale winds and predation by natural enemies. We observed 519 scouting trips from 18 different colonies over three years to determine how long it takes for the colony to replace a scout that has likely died while on scouting duty or is lost due to environmental perturbations. Study areas were at Maremani, Musina, Masebe and D'nyala Nature Reserves in the Limpopo Province of South Africa. The closest distance between the reserves was 30 km, while the farthest was 295 km. We introduced definitions of scouting turnover, scouting trip, and scouting session. Since M. analis shows bimodal foraging behaviour, the morning observations were recorded as the first scouting session. In contrast, the subsequent session, which starts in the afternoon, was recorded as the second scouting session. The mean scouting turnover for all 519 trips was 9.36 ± 0.64 (SD) minutes. When turnover was divided into sessions, the first scouting session lasted a mean of 7.77 ± 12.17 (SD) minutes, while the second had 10.34 ± 18.32 (SD) minutes. The minimum turnover was zero minutes, and the maximum was 124 minutes.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
POSTER · Abstract ID 147422

Effects of surface roughness on scouting behavior and shelter tube construction in Coptotermes gestroi

Kukhyun Lim

Termites construct various architectural structures, including mounds, tunnels, and shelter tubes. These structures emerge through self-organization, whereby decentralized individuals respond to local environmental cues. Tactile cue is known to influence termite building behavior. However, previous studies on shelter tube construction had rarely considered the surface roughness of the substrate on which termites explored and built. In this study, we investigated whether differences in surface roughness affect scouting and shelter tube construction in Coptotermes gestroi (Wasmann). A laboratory-reared colony (>5 years old) was introduced into arenas with either smooth or rough surfaces. We quantified the time until the first five workers initiated scouting, the time until the first five workers reached the wood block, the time until a shelter tube reached the wood block, and the orientation of shelter tubes. Workers of C. gestroi initiated scouting and reached the wood block significantly earlier on rough surfaces than on smooth surfaces. Similarly, shelter tubes reached the wood block sooner on rough surfaces and exhibited straight orientation to the wood block on rough surfaces whereas radial tube formations were observed on smooth surfaces. Behavioral observations suggest that smooth surfaces interrupted exploration, as workers frequently fell during movement. Such locomotor constraints likely delayed resource discovery and promoted radial shelter tube construction. Because smooth substrates are rare in natural termite habitats, our results emphasize the importance of considering substrate properties in experimental studies of termite aboveground exploration and construction. We recommend that future studies explicitly report surface roughness when investigating termite aboveground behaviors.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
POSTER · Abstract ID 149357

Plant Protection Product Exposure Affects Honeybee (Apis mellifera) Behaviour, Gut and Brain

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Western honey bee (Apis mellifera) workers harbour a simple yet stable intestinal microbiota. Beyond digestion, the honey bee gut microbiota interacts with host gut and brain tissues through the microbiota-gut-brain axis, influencing signalling, learning and behaviour. Exposure to plant protection products (PPPs), even at environmentally relevant concentrations, is thought to disrupt this system, but the extent to which functional changes take place on all these levels remains understudied. Here, we show that although brain morphological changes were minimal, acute exposure to three commonly used PPPs (SIVANTO® prime, Cantus®, ClickPro®) induced widespread and persistent functional changes across the microbiota, gut and brain tissues. Specifically, brain energy metabolism pathways were increased in abundance, alongside pathways involved in transcription and translation. ClickPro® exhibited delayed metabolic effects in the gut, in line with a shift toward lipid-based energy utilisation. All PPPs persistently disrupted the microbiota composition, and altered short-chain fatty acid production, consistent with impaired microbe-microbe interactions. Moreover, we documented 16 different behavioural phenotypes, which were grouped into five larger categories (social, individual, brood care, colony maintenance, and foraging behaviour). Despite no noteworthy impact on mortality, varied in-hive behaviours were observed. The insecticide SIVANTO® prime significantly decreased colony maintenance behaviours, but increased the proportion of social grooming in the first days after exposure. The fungicide Cantus® increased resting behaviour, while Click Pro® decreased brood care behaviours, driven mainly by a decrease in the feeding of larvae. Together, these findings demonstrate that environmentally relevant PPP exposure induces coordinated functional disruption across multiple biological levels.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
POSTER · Abstract ID 149426

How Do Animal Groups Integrate Multiple Attributes in a Best-of-n Task?

Chun Kin Chow; Simon Garnier; Horacio Rotstein
New Jersey Institute of Technology (NJIT)

Collective decision-making in animal groups emerges from self-organized processes, where individuals integrate social and environmental cues through local interactions. A key challenge is selecting resources that best meet the group's needs, often requiring the evaluation of multiple attributes when choosing among multiple alternatives. However, most studies focus on simple binary decisions along a single attribute and the dynamics of collective decision-making remain largely unexplored for more complex scenarios. Here, I model cockroach groups processing single- and multi-attribute information in a best-of-n decision-making task. In this task, cockroach groups need to incorporate information about light levels and shelter size to identify the best shelter to aggregate under out of n alternatives. Using both mean-field and agent-based modeling, I show that the local interactions employed by cockroaches result in parallel processing at the group level, where the time taken for the group to find the best shelter remains relatively constant despite an increasing number of options. Through a dynamical systems theory-based analysis, I examine how the properties of these local interactions shape group decision-making, including the emergence of parallel processing, its sensitivity to initial conditions, and its limits. These findings provide insight into the mechanisms of collective decision-making in biological systems, with applications to artificial ones, such as swarms of robots and virtual agents.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
POSTER · Abstract ID 149482

Nesting in Anticipation: Spatial Ecology of Giant Honey Bees (Apis dorsata) in Chitwan, Nepal

Gerald Kastberger; Wolfgang Sulzer
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Seasonal migration and nesting of the giant honeybee Apis dorsata are linked to mass-flowering crops, yet how seasonally recurrent landscape structure shapes nest placement beyond site fidelity remains unclear. If agricultural landscapes were highly fragmented into fine-grained crop mosaics, colonies nesting at different sites would experience comparable access to floral resources, and nest-specific landscape signals would be indistinguishable from those at random locations.

We analyzed nest-centered landscape structure using three seasonal satellite-derived land-use maps (December 1999 - April 2000) at 15 × 15 m resolution covering ~1 200 km² of the central Chitwan plain, where nesting precedes crop flowering. Land-use composition was quantified radially around 55 nesting sites (≈300 nests) at 15 m increments up to 4 500 m and contrasted with spatially constrained random reference locations to isolate nest-specific patterns from background seasonal change.

From December to mid-March, two mass-flowering crops – mustard in December followed by buckwheat – showed the strongest and most spatially coherent associations with nesting sites, expressed as maxima in nest-specific land-use contrast within 1–3 km, matching the effective foraging range of Apis dorsata and exceeding spatially constrained random expectations ($P < 0.05$).

Nest-centered patterns likely reflect colony-level site fidelity shaped by past success rather than immediate responses to flowering crops. Colonies reoccupy traditional sites, commonly marked by wax remnants, where crop rotation has repeatedly provided forage. Because relocation and nest founding are costly, colonies tolerate some risk of local crop failure, producing a population-level bias toward landscape configurations that have proven reliable across seasons.

SYMPOSIUM 15 · Navigating the superorganism: molecular, behavioral, and computational perspectives on decision-making in social insects
POSTER · Abstract ID 149962

trackRai: An Open-Source R Package for Democratizing Machine Learning-Based Multi-Object Tracking and Developing Community Models for Social Insect Research

Simon Garnier; Nicholas Pape Simon
New Jersey Institute of Technology (NJIT)

Quantifying the complex behaviors of social insects requires robust multi-object tracking. State-of-the-art computer vision and machine learning algorithms offer increasingly accurate tracking performance, yet their steep learning curve remains a significant barrier for many biologists, especially those with limited computational experience. Here, we introduce trackRai, an open-source R package designed to make deep-learning-based tracking accessible to all researchers, even with little to no coding skills.

trackRai integrates the powerful YOLO11 architecture into a user-friendly workflow entirely managed through an intuitive “point-and-click” graphical interface built using the Shiny web application framework. This graphical interface guides users through every step of the pipeline—from automated training dataset preparation and model training to tracking execution and manual trajectory correction—without requiring direct interaction with the underlying code. By operating within the R ecosystem, trackRai also bridges the gap between sophisticated computer vision tools and a statistical environment most social insect researchers are already familiar with.

Beyond facilitating access to advanced tracking algorithms, we also propose an initiative to develop high-performance “community models.” Because trackRai standardizes data formatting, users can easily export and contribute their annotated datasets to a central repository. We invite the community to share these annotations openly, which can then be used by others with access to large computational resources to train and maintain robust, context-independent, and species-specific foundation models. Ultimately, the aim is to provide off-the-shelf and open tracking solutions for common social insect species, eliminating redundant effort and accelerating research across the social insect community.

SYMPOSIUM 16 · The role of innate and experience-driven chemical communication in regulating insect social behavior
ORAL · Thu 20 Aug · 14:30 · Halle 4 · Session 55 · Abstract ID 149614

Origin of the queen primer pheromone in the termite Embiratermes neotenicus

Jitka Štáfková[1]; Natan Horáček[1]; Ondřej Lukšan[1]; Jan Křivánek[1]; Romana Hadravová[1]; Karel Harant[1]; Lenka Ulrychová[1]; Ana Maria Costa-Leonardo[2]; **Robert Hanus[1]**

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Queen primer pheromones are fundamental components of communication in colonies of advanced eusocial insects. They signal the presence of fertile queens and ensure their reproductive monopoly. In termites, the chemistry of queen primer pheromones is currently known for only two species: the Japanese subterranean termite Reticulitermes speratus and the South American soil-feeding termite Embiratermes neotenicus. In the latter species, we recently ascribed the queen pheromone function to the sesquiterpene alcohol (3R,6E)-nerolidol, which is secreted by primary and neotenic queens and is also present on eggs. The discovery of the queen pheromone in E. neotenicus raised several questions that we address in our current research, including the biosynthetic origin of (3R,6E)-nerolidol and the identity of its production organ in queens.

In my talk, I will report on the identification in E. neotenicus of the terpene synthase EneoC, which converts farnesyl pyrophosphate into enantiomerically pure (3R,6E)-nerolidol. EneoC expression is strongly upregulated in queens compared to other castes and the same applies to EneoC protein abundances in the queen proteome. Silencing of EneoC expression significantly reduces the amount of (3R,6E)-nerolidol secreted by queens, providing functional evidence for the involvement of EneoC in queen pheromone biosynthesis. Using a combination of indirect immunofluorescence and immunogold labeling, we localized EneoC to epidermal secretory cells underlying the cuticle throughout the body, a finding corroborated by tissue-specific expression analyses and proteomics. In contrast, EneoC is absent from eggs, suggesting that the queen pheromone present on eggs is applied by queens rather than being synthesized by the eggs themselves.

SYMPOSIUM 16 · The role of innate and experience-driven chemical communication in regulating insect social behavior
ORAL · Thu 20 Aug · 15:00 · Halle 4 · Session 55 · Abstract ID 149618

Identification of the trail-following pheromone receptor in termites

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The chemical diversity of social insect pheromones has received considerable attention in both major groups of social insects, the eusocial Hymenoptera and termites. In contrast, the molecular mechanisms underlying pheromone detection have so far been investigated only in hymenopteran social insects, and no odorant receptors (ORs) have been functionally characterized in termites. Here, we present the first OR deorphanization in termites. Using data from the antennal transcriptome and genome of the termite Prorhinotermes simplex (Psammotermitidae), we selected four candidate OR sequences, expressed them in Empty Neuron Drosophila system, and functionally characterized them using single sensillum recording (SSR) and a panel of relevant termite semiochemicals. For one of the selected ORs (PsimOR14), we obtained strong and reliable responses for the main component of the P. simplex trail-following pheromone, the diterpene neocembrene. PsimOR14 showed a narrow tuning to neocembrene; only one additional compound out of 72 tested (geranylgeraniol) generated non-negligible responses. Subsequently, using SSR on P. simplex workers, we identified the olfactory sensillum specifically responding to neocembrene, thus likely expressing PsimOR14. We further demonstrated the caste-specificity of PsimOR14 expression, its role in caste-specific pheromone perception, and performed homology modelling and molecular dynamics calculations to address the functional properties of PsimOR14.

SYMPOSIUM 16 · The role of innate and experience-driven chemical communication in regulating insect social behavior
ORAL · Thu 20 Aug · 15:15 · Halle 4 · Session 55 · Abstract ID 145533

A social bee learns to associate a novel odor with social context

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Many pheromone responses are hardwired into insect neural circuits and underlie key behaviors such as mating, alarm signaling, and trail following. In social insects, workers are generally assumed to respond innately to queen pheromones, shaping their behavior and reproductive physiology. Yet growing evidence indicates that learning and experience can also modulate responses to social chemical cues.

To test whether responses to queen-associated odors can be learned, we exposed Bombus terrestris workers to a novel odor by perfuming the queen daily with unfamiliar floral scents, anisyl alcohol or methyl anthranilate. Perfumed queens established colonies, and we later assessed worker attraction and egg laying in the absence of the queen, either with or without brood. In a two-choice olfactometer, workers preferred the queen odor experienced during colony development. Exposure of queenless workers to the queen-associated novel odor influenced egg laying only in the presence of brood, unexpectedly increasing egg production. We repeated the study in B. impatiens to test whether workers learn a general nest odor or encode odor information specifically in association with the queen. We also examined the role of worker age in learning and whether additional social cues absent from the first experiment altered reproductive responses to learned odors.

Together, these results show that workers can learn novel odors within a social context and that these learned cues can modify worker social and reproductive behavior in a context-dependent manner.

The influence of juvenile hormone on chemical communication in a social bumble bee

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Social organization relies on individuals synchronizing their biochemical pathways and behaviors to produce and sense social signals in a timely manner. In social insects, including the annual eusocial bumble bee, Bombus terrestris, cuticular hydrocarbons (CHCs) are key mediators of social information, with CHC profiles varying between colonies, castes, and reproductive states. Nestmates detect these primarily via an array of antennal olfactory receptors (ORs). Little is known about the mechanisms regulating individual variation in signaling and sensing. We tested the hypothesis that juvenile hormone (JH), a key pleiotropic regulator of insect social behavior, physiology, and life history, coordinates the production and sensing of chemical social information. Previous studies suggest JH regulates CHCs in wasps and ants, and anecdotal evidence in flies and moths indicates an effect on chemical sensing as well. To investigate whether JH coordinates communication with physiology in B. terrestris, we examined antennal gene expression and CHC profiles in workers with JH levels experimentally manipulated with Precocene-I, and in bees with naturally varying JH levels. We found altered expression rates of genes associated with neural communication, as well as many ORs. Additionally, we found evidence that JH regulates specific alkenes in bumble bee CHC profiles. These results are consistent with the hypothesis that JH influences communication physiology along with other tissues involved in fertility and dominance regulation. However, differences in gene expression could not be observed among groups of bees with naturally differing JH titers, which may indicate that natural variation is not sufficient to observe these changes.

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ORAL · Thu 20 Aug · 15:45 · Halle 4 · Session 55 · Abstract ID 149974

Ethyl oleate regulates rapid JH changes during heat shock

Associate Professor Zachary Huang[1]; Thomas Rachman[2]

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Honey bee workers undergo age-related task transitions, with the shift from nursing to foraging modulated by the primer pheromone ethyl oleate (EO). The amount of this pheromone is high in foragers, and it presumably suppresses the programmed increase of juvenile hormone (JH) titers in younger honey bees when foragers are present. However, there is no direct evidence of whether this pheromone can modulate JH titers.

Here, we show that while heat stress elevated JH levels in isolated honey bee foragers, this effect was absent when bees were housed in groups. Moreover, when isolated honey bee foragers were under heat stress and EO was directly applied (5.5 mg per glass vial) a similar modulation in JH was observed as in grouped bees. These results identify a novel role for EO in mitigating physiological stress, and highlight pheromonal communication as a mechanism of social buffering that enhances colony resilience to environmental stress.

Our simple thermal stress assay provides a valuable tool for future investigations into endocrine regulation and colony resilience.

SYMPOSIUM 16 · The role of innate and experience-driven chemical communication in regulating insect social behavior
ORAL · Thu 20 Aug · 16:00 · Halle 4 · Session 55 · Abstract ID 149068

Self-organized ant colony size sensing through queen pheromone transmission and its possible constraints and adaptive significance

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Social insects can “sense” colony size even without visual information in a dark environment in many cases. For example, reproductive castes are generally produced when colony size (worker number) exceeds a certain level. How they achieve this is a challenging subject in social insect biology. We empirically tested a hypothesis on the proximate mechanism using the ponerine ant, Diacamma cf. inducum, in which queen pheromone is transmitted through direct physical contact between the queen and workers. Accordingly, the monogynous queen (gamergate) is known to increases the effort devoted to queen pheromone transmission behaviour (patrolling) as the colony grows, as if she perceives colony size. The negative feedback hypothesis assumes that, through repeated physical contact with workers, the queen monitors the physiological state (fertility) of workers and increases her patrolling effort when she encounters more fertile workers. Supporting this hypothesis, we found that the queen increased her patrolling effort in response to a higher ratio of fertile workers under the experimental condition of constant colony size. Furthermore, chemical analyses and bioassays suggested that cuticular hydrocarbons have queen pheromone activity and can mediate the observed queen–worker communication of fertility state. However, this communication system has a constraint. As the colony grows further, the queen's patrols become physically unable to sufficiently distribute pheromones throughout the entire colony. Consequently, the production of the reproductive caste, males through worker reproduction, emerges. Qualitatively, this switch appears to support the theoretically predicted adaptive pattern, but further research is needed to determine its real function.

SYMPOSIUM 16 · The role of innate and experience-driven chemical communication in regulating insect social behavior
ORAL · Thu 20 Aug · 16:15 · Halle 4 · Session 55 · Abstract ID 149879

Chemical communication of spatial information in the clonal raider ant

Tim Zetzsche; Ryan Alam; Sarah O'Connor; Tobias Köllner; Yuko Ulrich

Social insects are faced with the challenge of efficient resource management, such as brood care or foraging, within a colony. For this purpose, pheromones have evolved in a wide range of species. Ants in particular produce a wide array of pheromones with diverse biological functions, from trail marking to alerting nestmates. The clonal raider ant Ooceraea biroi is a relative of army ants and as such, is an emergent system to study the mechanistic bases of social behaviour.

Here, we use chemical analyses, chemical synthesis, and behavioural assays to identify two previously undescribed pheromones in adult workers. One of these, tentatively identified as a methyl salicylate derivative, elicits robust trail following behaviour under laboratory conditions. In contrast, the second, identified as (3Z,6E)-14-methyl-α-farnesene and accumulating in the Dufour’s gland, induces avoidance behaviour in T-maze assays. To further validate the function of these pheromones, we use CRISPR-based mutagenesis to knock out genes coding for biosynthetic enzymes.

Our results provide first insights into the underlying mechanisms of the clonal raider ant’s communication of spatial information.

Do volatiles allow early disease detection in ant colonies?

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Ants react to the presence of pathogens and sick individuals in the colony with sanitary behaviors and infection treatment. We previously found that these actions can be elicited by both, passive cues originating from the pathogen, such as the fungal membrane compound ergosterol – which acts as a grooming trigger – and by active disease signals released by infected hosts. For example, terminally-ill ant pupae alter their cuticular hydrocarbon profiles, in particular the abundance and isomeric composition of long-chained C33 alk(adi)enes. These disease markers are non-volatile and elicit targeted, contact-dependent responses by the ants.

It is still unresolved, however, whether volatile disease odors provide the colony with complementary, long-range information that allows ants to already detect infection risk via distance. Pathogens such as entomopathogenic fungi, as well as e.g. diseased honeybee brood, are known to emit characteristic volatile compounds, suggesting that volatile disease odors may play an additional role in regulating social immunity in ant colonies.

Here, we use garden ants and their natural fungal pathogen Metarhizium as a study system to characterize disease-associated volatiles by GC–MS of the colony airspace under infection. We further assess the behavioral relevance of these emitted odors by testing how they influence the social behavior of colony members in the absence of physical contact.

Previous own work:

Stock M, Milutinović B, Hoenigsberger M et al. Pathogen evasion of social immunity. Nat Ecol Evol 7, 450–460 (2023).

Dawson EH, Hoenigsberger M et al. Altruistic disease signalling in ant colonies. Nat Commun 16, 10511 (2025).

SYMPOSIUM 16 · The role of innate and experience-driven chemical communication in regulating insect social behavior
POSTER · Abstract ID 147614

Refining a sensitive window for social experience in B. impatiens

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Princeton University

Social isolation in early-life can impair typical brain development, physiology, and behavior in many social insects. The effects of this isolation can also vary in severity depending on whether or not the isolation occurs during a sensitive developmental window. In the common eastern bumble bee, Bombus impatiens, social isolation during the first ten days of adulthood has been shown to disrupt typical social interactions and brain development in workers. However, it has yet to be determined whether the effects of social isolation are limited to a specific time window or if they are cumulative throughout early life. To answer this question, we isolated newly emerged bumble bees and housed them in small, queenless groups for a range of timepoints in the first 10 days of life: 0-3 days, 3-6 days, 6-10 days, and 0-10 days. At the end of their treatment period, bees were paired with a partner in a social interaction assay and then scored for ovarian development. We discuss the effects of isolation across different developmental timepoints on social behavior and reproductive physiology in B. impatiens and relate our findings to the broader literature of social isolation in insects.

SYMPOSIUM 16 · The role of innate and experience-driven chemical communication in regulating insect social behavior
POSTER · Abstract ID 147985

Representation of worker mandibular gland pheromone-floral odor blend signals in the brain of Apis cerana japonica

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[1] Kobe University; [2] Fukuoka University

In Apis cerana japonica, worker mandibular gland pheromone (MP), the mixture of 3-HOAA and 10-HDA, is known as an aggregation pheromone. Classical conditioning has shown that honeybees learn linalool quickly when presented with MP, indicating its function to facilitate appetitive learning. The neural mechanisms underlying this phenomenon are still unknown because of a lack of anatomical and physiological knowledge of olfactory neurons in A. cerana.

To overcome this problem, we first anterogradely labeled olfactory receptor neurons (ORNs), and made the 3-D atlas of the glomeruli in the antennal lobe. We identified 164–172 glomeruli, 82 of which were found as analogs to those in A. mellifera, and divided them into six groups according to the tract of ORNs. Next, we intracellularly analyzed the responses of olfactory neurons to MP, linalool, and their blend. In total, twenty neurons exhibited excitatory responses to MP, and we classified them into three groups by comparing their responses to the blend with the component to which the neuron showed a stronger response (stronger component). Seven neurons responded to the blend more strongly than the stronger component (synergy). Another seven equally responded to the blend and the stronger component (hypoadditive). The other six showed a weaker response to the blend than to the stronger component (suppression). Neurons classified as hypoadditive or synergy tended to respond strongly to linalool, whereas those classified as suppression tended to respond strongly to MP. These response properties may take account for MP effect on facilitation of appetitive learning.

Kin and nestmate recognition mediate aggressive behavior in Asian weaver ants

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Group formation and cohesion are driven by the benefits of cooperative behavior. However, the joint roles of kin and nestmate recognition in establishing colonies and mediating cooperation are less explored. Here, we investigate how these recognition strategies maintain group cohesion and mediate aggressive behavior towards intruders in a population of Oecophylla smaragdina in the Solomon Islands. First, we compared aggression in the field between a resident and an introduced weaver ant, either from another colony or from the same colony as a control. We confirmed a dear-enemy pattern in inter-colony distance from a previous study in this population. After extracting cuticular hydrocarbons (CHC) and DNA from the resident and intruder ants, we used a genotype-by-sequencing approach that generated 3102 single-nucleotide polymorphisms (SNPs) to determine relatedness and a chemical ecology approach to determine CHC profiles for nestmate recognition. Further, we modeled logistic regressions to test the effect of distance, kin, and nestmate recognition on the behavioral response of resident ants. Finally, we ran a generalized linear model to test the main and joint effects of these recognition drivers. Our best fit model strongly predicted aggression based on genetic relatedness and inter-colony distance, which indicates a stronger effect of kin recognition compared to nestmate recognition. We are now exploring if our focal SNPs are associated with hydrocarbon synthesis, olfaction and/or gustatory cues, and if they are less variable among kin. Together, our findings suggest that in addition to nestmate recognition, kin recognition may also mediate aggression in eusocial insects.

The importance of being heterogeneous: the surprisingly complex phase behaviour of insect cuticular hydrocarbons

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Cuticular hydrocarbons (CHCs) are vital not only for chemical communication within a social insect colony, but also protect the insect from water loss. Effective protection against water loss depends on the phase behaviour of the CHC layer. Therefore, these two functions may conflict with each other. For example, temperature changes may require chemical changes to maintain CHC phase behaviour and hence water loss protection, but the chemical changes may affect the information content encoded in the CHC layer. However, we still know little about CHC phase behaviour, how it changes with temperature, and how insects can adjust it to cope with changing temperatures.

Here, we addressed these questions, studying viscosity of CHCs from two European ant species using microrheology. The CHC layers consisted of a gel phase and a liquid phase. The liquid phase itself was heterogenuous, characterized by a bimodal distribution of local viscosities. The higher-viscosity mode had a viscosity similar to honey (600-1000 mPa.s), while the lower-viscosity mode resembled olive oil (100-150 mPa.s). This bimodal distribution of local CHC viscosities suggests that each mode may fulfill a distinct function, such that conflicts between functions are reduced. Furthermore, ants kept under warm conditions showed a significantly more viscous CHC layer, tentatively suggesting that CHC composition is adjusted to maintain a homeostatic viscosity and minimize water loss. These insights contribute to our understanding of the physical mechanisms that facilitate the biological functions of the CHC layer and enable its multifunctionality.

The evolution of cuticular hydrocarbon perception in eusocial insects

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Eusocial insects critically depend on recognizing colony members and communicating with the reproductives of the colony. In many insect societies, this is accomplished through olfactory perception of cuticular hydrocarbons (CHCs), which mediate nestmate recognition and queen pheromone communication. To examine how CHC profiles evolve and are perceived, we studied their evolution and the ability to recognize and distinguish them at the behavioral, sensillum, and olfactory receptor levels in the ant genus Camponotus and the termite species Zootermopsis nevadensis.

Analysis of queen pheromone and worker CHC profiles in 26 Camponotus species revealed substantial interspecific variation, with no full profile conservation. However, terminally branched monomethyl-alkanes and methylolefins showed signatures of conservation in queen profiles. Workers consistently preferred queen over worker profiles, suggesting a conserved queen pheromone function of CHCs across Camponotus ants.

The critical role of CHCs in ant chemical ecology is associated with conservation of olfactory receptor function. The sensitivity to hentriacontane (C31) of a previously characterized olfactory receptor in the ant Harpegnathos saltator is conserved in C. floridanus at both the functional level and in key amino acid residues of the ligand-binding pocket. Despite this conservation and the ability to differentiate C31 from structurally similar hydrocarbons, no specific social function for C31 could be identified, suggesting the importance of maintaining broad detection capabilities of ubiquitous CHCs.

In contrast to ants, the termite Z. nevadensis does not respond to CHCs in bioassays or sensillum recordings, except for reproductive-associated CHCs, indicating different selection pressures on olfactory systems in ants and termites.

The influence of diet on cuticular profiles and recognition in wild ant colonies

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University of Central Florida

Among social insects, cuticular compounds function as colony-specific recognition cues and signals. Despite their relatively brief lives, many ant workers experience radical seasonal shifts in diet, temperature, and humidity. Corresponding changes in cuticular compounds could affect nestmate discrimination, begging the questions: Do long-lived workers update their nestmate recognition templates as cuticular profiles change, and how do differences in diet affect cuticular profile consistency? Here we track cuticular profiles and stable isotopes for colonies of three ant species with contrasting diets across an annual cycle, assess whether seasonal changes in aggression reflect cuticular changes, and measure the rate of template revision by measuring responses to previous colony odors. Preliminary results from field colonies found a consistent seasonal shift in cuticular profiles for Pogonomyrmex badius, reflecting a population-level shift from an insect-heavy to seed-heavy diet across the year. P. badius also exhibited seasonal variation in aggression. For Dorymyrmex bureni, an insect-focused scavenger, colony profiles changed subtlety over time, but not in a consistent way. Colonies of Trachymremex septentrionalis, a fungus gardener, showed a consistent seasonal profile shift despite their uniform diet of domesticated fungus. In the lab, cuticular profiles did not vary when fungus gardens were fed two distinct substrates, though profiles from both treatments changed over time in ways that largely mirrored field colonies. These findings demonstrate the influence of environmental factors on cuticular profiles and consider whether social insect workers must adjust nestmate recognition templates during their lives, which can exceed 300 days in the field.

Chemical, Behavioral, and Genetic Evidence for a Cryptic Species Complex in African carpenter ants

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Cryptic speciation poses a significant challenge to taxonomy, particularly in morphologically conserved lineages whose substantial evolutionary divergence is not immediately apparent. In eusocial insects like ants—where species boundaries are often maintained through chemical rather than morphological differentiation— integrative methodologies are critical for resolving taxonomic complexity. Here, we present compelling evidence for the recent divergence of African carpenter ant populations initially identified as Camponotus maculatus into two distinct cryptic species. We achieved this through an integrative systematics approach combining chemical, behavioral, and genetic analyses. Most strikingly, we identified two sharply contrasting chemotypes characterized by distinct cuticular hydrocarbon (CHC) profiles that separated the investigated ant populations. Aggression assays reveal that worker ants exclusively exhibit hostility towards individuals with opposing chemotypes, independent of colony affiliation. Genetic barcoding further corroborates these findings, indicating distinctive phylogenetic clusters concordant with the two chemotypes. Our results highlight the primary role of chemical differentiation in species divergence within eusocial insects. CHC profiles likely diverged primarily under ecological selection pressures, maintaining species boundaries despite morphological similarities. Furthermore, these findings underscore the importance of integrating multiple taxonomic modalities to resolve cryptic species complexes and provide valuable insights into the evolutionary mechanisms potentially driving early-stage speciation in ants.

A hydrocarbon pheromone mediates ant group cohesion

Matteo Rossi; Tiphaine Bailly; Jocelyn Millar; Thomas Schmitt; Erik Frank; Daniel J. C. Kronauer

Social insect colonies are among the most cohesive groups in the animal kingdom, yet the signals and sensory mechanisms underlying this cohesion remain poorly understood. Here, we show that cuticular hydrocarbons (CHCs), low-volatility compounds present on the insect body surface, play a central role in social cohesion in the clonal raider ant, Ooceraea biroi. The ants deposit CHCs onto the nest substrate, and these chemical residues are sufficient to induce aggregation and to promote group cohesion. Nest-associated CHCs elicit aggregation across distinct O. biroi genotypes, indicating that they function as a species-wide signal. In contrast, hydrocarbon mixtures from other ant species or synthetic hydrocarbons absent from the O. biroi cuticle do not elicit aggregation. We further show that behavioral responses to nest-associated CHCs vary with age and physiological state and correlate with the ants' propensity to leave the nest. This suggests that this variation contributes to age-based division of labor and other behavioral dynamics in the colony. Finally, we identify a specific component of the CHC profile, 11,15-dimethylheptacosane, that promotes aggregation: young workers are strongly attracted to this highly abundant CHC present both on the cuticle and the nest substrate. Together, these findings identify a pheromone-based mechanism underlying group formation, social cohesion, and division of labor in the clonal raider ant.

SYMPOSIUM 17 · Chemical communication in social insects – mechanisms, evolution, and applications
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Social isolation is associated with distinct cuticular chemistry in bumble bees

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Cuticular hydrocarbons (CHCs) support desiccation resistance and chemical communication in insects. Across social insects, CHCs often play a role in nestmate recognition, colony identity, fertility signaling, and other social cues. In honey bees and ants, social experience can influence CHC profiles, but we know less about how experience impacts species with flexible social organization. Here, we examine the effects of early-life social experience on cuticular chemistry in the common eastern bumble bee, Bombus impatiens. In B. impatiens, CHCs are associated with both reproductive state and social signaling, but their effects are strongly context-dependent, particularly with respect to worker reproduction. We compared head and abdomen cuticular extracts of size-, colony-, and age-matched 7-day-old workers reared from eclosion in isolation or in small, 4-worker social groups. We identified 51 unique compounds and striking differences between cuticular extracts of socially-reared and isolated workers in both tissues. Isolated bees also exhibited delayed ovarian development, reduced egg laying, and less honeypot and egg cell construction compared to their socially-reared counterparts. Together, these results demonstrate that early-life social environment plays a key role in shaping cuticular chemistry, reproductive physiology, and behavior, and highlights the importance of social context in shaping chemical phenotypes in social insects.

BumbleDate: Identification of key pheromones and neural mechanisms involved in bumblebee reproduction

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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.

Evolution of an olfactory subsystem in Hymenoptera: a potential springboard for eusociality

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The Hymenoptera present the highest number of eusocial species in insects and up to 9 independent origins of eusociality. By contrast, the eusocial lifestyle is virtually absent in other taxa, suggesting the existence of facilitating factors leading to advanced social organisation within Hymenoptera. As eusocial evolution is explained by the concept of inclusive fitness and the theory of kin selection, an ability to distinguish kin from non-kin could be instrumental for the advent of higher levels of sociality, by preventing costly altruistic acts towards unrelated individuals. Recent studies suggest that eusocial ants possess an olfactory subsystem that is specialised in the detection of cuticular hydrocarbons, providing a potential mechanism to detect social identity. It involves a particular type of sensilla on the antenna, the basiconic sensilla. They house olfactory sensory neurons (OSN) that are thought to express a group of odorant receptor genes with a distinctive 9-exon structure. These OSNs project to a segregated region of the primary olfactory centre in the brain, the antennal lobe. Strikingly, a similar suite of features has been observed in Vespid wasps which independently evolved a eusocial lifestyle, suggesting a potential link between this olfactory subsystem and advanced forms of social organization. By combining broad taxonomic sampling of Hymenoptera species with detailed neuroanatomical, functional and molecular characterisation of their olfactory structures, we aim to address the potential role of the basiconic-sensilla subsystem in social evolution.

Functional Conservation of a Long-Chain Hydrocarbon Olfactory Receptor Across Divergent Ant Species

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Ants rely on cuticular hydrocarbons (CHCs) for communication, yet it remains unclear how olfactory receptor (OR) function is maintained across species despite large, rapidly evolving receptor repertoires. OR repertoires expand through gene duplication, but functional conservation can persist through conserved binding-pocket residues, allowing specific odor responses to be retained even as new receptors arise. Whether individual ORs maintain selective tuning across divergent ant lineages, particularly for compounds without a defined ecological role, remains unknown. Some CHCs, such as methyl-branched hydrocarbons, can function as signals. At the same time, straight-chain n-alkanes like hentriacontane (C31) are present across ant cuticular profiles but generally lack a known social role. Previous work in Harpegnathos saltator identified an OR narrowly tuned to C31, providing an opportunity to test whether selective receptor function is conserved in the phylogenetically divergent Camponotus floridanus. Focusing on the 9-exon OR clade that includes the C31 OR from H. saltator, we identified candidate ORs in C. floridanus with conserved ligand-binding residues using phylogenetic and protein structure analyses. Functional characterization in transgenic Drosophila melanogaster flies and electrophysiological recordings established conserved selective responses to C31 and closely related hydrocarbons. Structural modeling revealed that the residues and geometry of the binding pocket are highly conserved across orthologous receptors. These findings show that selective sensitivity to a ubiquitous n-alkane is preserved across divergent ant lineages through conserved binding pocket residues and structure, establishing a molecular mechanism for maintaining sensory specificity over evolutionary time and demonstrating the importance of conserved odor detection in social insects.

Neuroethology of taste in the honey bee Apis mellifera: from behaviour to the neural circuits

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The honey bee Apis mellifera is a traditional model for the study of olfactory perception, information processing, and learning abilities. Surprisingly, this species' sense of taste remains largely understudied compared to the other sensory modalities. Nonetheless, honey bees'gustatory abilities are crucial for the survival of the species, and influence food choices and enable the avoidance of toxic substances. My project seeks to fill the gaps in the study of honey bee gustation by exploring the mechanisms underlying taste information processing through two complementary approaches: behaviour and neuroanatomy. First, through the adaptation of the Multi-Capillary Feeder assay (MultiCaFe), we inferred the bees'gustatory preferences to different tastants belonging to three gustatory qualities (salts, bitters, and amino acids) at multiple concentrations. Second, we developed a new set-up to perform appetitive associative conditioning experiments, in which bees associate gustatory stimuli with a sucrose reward. This allowed us to demonstrate that bees use taste quality to discriminate between stimuli, even if they have the same hedonic value. Finally, we performed a neuroanatomical study to describe the gustatory pathways in the honey bee brain by means of fluorescent tracer injections, both in the taste appendages (proboscis, antennae, and tarsi) and in the central brain. We showed that the spatial organization of gustatory appendages is centrally reflected in the distribution of gustatory afferents. The overlap of projections is notable among inputs from the same appendage origin (e.g., between mouthparts) and remains limited between those from different origins (e.g., antennae and mouthparts).

SYMPOSIUM 17 · Chemical communication in social insects – mechanisms, evolution, and applications
ORAL · Tue 18 Aug · 15:00 · K6 · Session 20 · Abstract ID 149016

You smell sick – The chemical and sensory bases of social immunity in the clonal raider ant

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Social insects live in densely populated colonies, which increases the risk of disease outbreaks. As a result, they have developed collective strategies for disease defense known as ‘social immunity.’ Social immunity includes behaviors, such as allogrooming, that rely on the ability to identify infected nestmates; however, the chemical and sensory bases of this detection remain poorly understood.

We explore the mechanistic bases of social immunity in the queenless clonal raider ant Ooceraea biroi, a blind species that likely detects sick nestmates primarily by olfactory cues. To this aim, the behavioral response of workers towards nestmates infected (either orally or via injection) with entomopathogenic bacteria, such as Pseudomonas entomophila, was characterized, and the odour profiles of infected ants were analyzed using standard chemical analyses (Gas Chromatography – Mass Spectrometry). We find differences in the chemical profiles of infected ants compared to controls, including changes in the abundance of cuticular hydrocarbons such as octacosane (n-C28), which can now be used in functional bioassays to test whether they elicit behavioural responses. We then investigate how the odor information of the candidate compounds is encoded in the brain through in vivo calcium imaging of the antennal lobe.

By combining chemical, neuronal, and behavioral analysis, we anticipate shedding light on the mechanistic bases of social immunity in insect societies.

Exposure to non-nestmate odours changes the odorant receptor profile in Acromyrmex echinatior ants

Mélanie Bey; Naomi Alex; Lisa Maczkowicz; Volker Nehring

Insects depend on a broad olfactory perception ability that involves many sensory receptors. Social insects, in particular, use olfactory cues to maintain colony cohesion. They recognize nestmates through colony-specific olfactory labels that individuals store as neural templates in their memory. The template is often considered to be located in higher brain centres and potentially a product of learning. However, some authors suggest it might be in the neural periphery, i.e. the antennae or antennal lobes, formed by habituation or receptor adaptation. Here we investigate a potential mechanism for the construction and functioning of the colony template in the peripheral nervous system: the antenna's odorant receptor (OR) profile and its dynamics. We exposed Acromyrmex echinatior leaf-cutting ants to non-nestmate odours and quantified changes in aggression and antennal OR gene expression. Consistent with other studies, prolonged exposure to non-nestmate odours reduced worker aggression towards the non-nestmate label, indicating habituation to the non-nestmate odour. Exposure also altered the expression of the OR genes. Notably, the OR profiles were colony-specific, mirroring the colony-specific recognition labels. When we exposed two different colonies to the same non-nestmate odour, the colony-specificity of the odorant receptor gene expression vanished. These results indicate that the peripheral olfactory machinery underlying nestmate recognition is highly plastic and is modulated by the current colony-specific chemical environment. Such flexibility at the level of odorant receptor expression may contribute to the maintenance of accurate social recognition in a dynamic olfactory landscape.

Cracking the chemical code of ant-aphid mutualism

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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.

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Characterization of variation in honeybee brood hygienic signaling in response to Varroa parasitism

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The success of social insect colonies relies on the coordinated activities of their members. This coordination, in turn, depends on social communication, and some of the most elaborate forms of animal communication occur in social insects. Chemical communication is used prominently in various contexts, including social immunity. Hygienic behavior, which involves the recognition, uncapping, and removal of diseased brood in honeybees, is an important social immune defense, particularly against the key threat posed by the ectoparasitic mite Varroa destructor. Most studies of hygienic behavior have focused on the nurse bees as the signal receivers. The brood as the signal producers and the signal itself have received less attention. To promote a complementary understanding of hygienic signaling from parasitized brood to nurse bees, we studied genotypically diverse sources of honeybees to identify variation in the brood response to Varroa destructor parasitism. We will relate variation in cuticular hydrocarbons to transcriptome profiles of the brood to reveal potential mechanisms of Varroa-specific signaling and markers to select honeybee stocks that are better at hygienic signaling. We will discuss our results in the context of bee breeding and social communication.

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Guest and farmer ants: Establishment, maintenance, and the threat of breakdown

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Formation of social cohesion between two distantly related species is rare, and to be successful, communication is essential. Megalomyrmex symmetochus guest ants are central to the emerging symbiotic species network model that encompasses ants, bacteria, and fungi. With obligate dependency, guest ants are challenged with finding and integrating with a Sericomyrmex amabilis host colony. We show that young M. symmetochus queens eavesdrop on host trail pheromones to find the host nest, and once inside, use their venom as a communicative signal to pacify their host. The guest ants live peacefully within their host's nest, exploiting resources but also offer protection against lethal invaders (i.e., predatory ants and microbes). When a lethal raiding ant enters their nest and threatens stability of the species network, the guest ants act as mercenary soldiers while the farmers hide; but when harmful fungi attack the garden, the two species become a united front. Our work reveals that Megalomyrmex symmetochus ants use alkaloidal venom in many ways: (1) as a communicative signal, (2) as a weapon against invaders, and (3) as a pest management substance. We believe that despite host exploitation, the guest ants act as a protective symbiont.

Exploring wound care by Pseudomyrmex ants on their host Vachellia trees

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Mutualistic ant-plant relationships are widely studied phenomena where plants provide shelter and food while ants offer protection from herbivores, competitors, and pathogens. When herbivore attacks occur, plants release volatiles that signal ants to defend them. While intraspecific wound care has been shown in ants, the role of ants in tending plant wounds is unclear. We hypothesize that ants not only defend plants but also tend to their injuries, even modulating their behavior depending on whether these wounds are contaminated. To test this, we injured Vachellia trees and observed the behavior of mutualistic Pseudomyrmex spinicola ants. We injured both the bark and leaves and exposed the wound to either a sterile or dirty solution. Our results show that P. spinicola ants accumulated at artificially induced bark and leaf wounds. Ants quickly aggregated at bark wounds, engaging in biting, allogrooming, and debris removal. At leaf wounds, ants spent more time manipulating contaminated wounds than sterile ones, suggesting that they can distinguish between clean and dirty wounds. These findings indicate that ants actively interact with plant wounds, especially when contaminated, revealing a potential role in wound care. Interspecific wound care in mutualistic ant-plant relationships could establish new insights into social immunity, host-plant fitness and our understanding of mutualistic relationships.

SYMPOSIUM 17 · Chemical communication in social insects – mechanisms, evolution, and applications
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Hidden Chemists: How Stenammini Ants Synthetize Nicotinic Alkaloids?

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Ants produce a wide range of chemical compounds with functions including nestmate recognition, trail following, and defence. 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 venom 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. 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. 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.

Evolutionary origin of terpenoid biosyntheis in termites

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Termites produce the most diverse array of terpenoids among metazoans, comprising over 200 structures involved in chemical communication and defense. However, their biosynthesis has not yet been elucidated. I will report on our identification of a gene family which arose through the duplication of geranylgeranyl pyrophosphate synthase in the common ancestor of Neoisoptera, the modern terpene-producing termite lineage. This family subsequently expanded into multiple paralogs and has been retained in neoisopteran genomes over 100 million years of diversification. We functionally characterized several proteins from this family as terpene synthases generating biologically relevant sesqui- and diterpenes. These include the queen pheromone (3R,6E)-nerolidol in Embiratermes neotenicus and the precursor of polycyclic defensive diterpenes (E,E,E)-neocembrene in Nasutitermes takasagoensis. We explored transposable element-mediated genomic mechanisms and selection pressures acting in the evolution of this gene family. Currently, we are extending these findings along two complementary directions. First, we investigate the structural basis for the emergence of terpene synthase function in termite isoprenyl diphosphate synthase-like proteins. Second, we broaden the comparative framework by identifying and characterizing related terpene synthase activities in additional social insects, including an ant species and the honeybee.

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Development of the queen pheromone composition: comparison of virgin and egg laying queens of the Western and an Asian honey bee species

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Honey bees exhibit a highly sophisticated communication system heavily relying on chemical cues and signals. Among other pheromones, the queen pheromone is of major importance for regulating the social organization of the colony and is primarily produced by the queen's mandibular glands. While most research on pheromone communication has focused on the Western honey bee (Apis mellifera), relatively little attention has been paid to other species within the genus Apis.

Although the composition of the queen pheromone is known to be plastic and to vary depending on the queen's mating status and age, the extent to which these factors influence the composition remains unclear. Studying the development of pheromones in honey bee queens reveals how and when they acquire their chemical identity, shedding light on the link between physiology and pheromone production.

We compared the mandibular gland secretions of queens from two cavity-nesting species, Apis mellifera and Apis cerana, to investigate changes in the pheromone composition throughout the queen´s lifespan. The queens were categorized according to their age and mating status: virgin queens under 24 hours old; virgin queens aged 1–5 days; virgin queens aged 5–10 days; and mated, egg-laying queens of unknown age. The mandibular secretions were analyzed using gas chromatography–mass spectrometry.

Our findings provide new insights into the evolution of queen signaling across species, shedding light on how this signal develops throughout the queen's life cycle. The results highlight both shared patterns and species-specific trajectories in pheromone development between Apis mellifera and Apis cerana.

Food-derived odors modulate chemical communication in the termite Reticulitermes flavipes

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Division of labor in social insects is characterized by a sophisticated communication system based on semiochemicals. In many social insects, workers cooperate to find new food sources and share information about food identity and quality. However, semiochemicals that communicate food identity and recruit receivers to a particular food source have not been previously documented. In this study, we discovered that foraging workers of the subterranean termite Reticulitermes flavipes use a chemical blend comprising aggregation pheromone and food-derived odors to communicate food source information to their nestmates and attract nestmates who previously ate the same food type. Gas chromatography-mass spectrometry analyses (GC-MS) and bioassays demonstrated that workers were attracted to aggregation pheromone secreted by their nestmates. However, when pheromone was combined with food-derived volatiles, which varied according to the type of food eaten, workers were more strongly attracted and preferred the blend secreted from nestmates on the same food that they had previously experienced. Furthermore, RNA-seq of antennae of the workers on different foods revealed that change from one food to a different food triggers remarkable upregulated or downregulated expression of chemoreceptor genes, suggesting that the foraging workers specialize in the chemical composition of the food they are currently feeding on by tuning their own olfaction and gustation through changes in chemoreceptor expression profiles. Our study opens new avenues for understanding the chemical communication system and foraging behaviors of social insects that can be modulated by additional odor cues to transmit more complex information than simple intraspecific chemical communication.

Label-free detection of ant pheromone trails using quantitative phase imaging

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Trail pheromones are chemical signals deposited by ants to mark routes between food sources and their nest. By following and reinforcing these scent trails, colony members collectively build efficient foraging networks without any central coordination, an emblematic example of self-organization in biological systems. While the chemical composition of many trail pheromones has been identified through gas chromatography, their direct visualization on the substrate has not yet been achieved. Pheromone deposition has therefore only been inferred indirectly, through ant traffic, abdomen-ground contacts, or more recently, speed decreases during marking. Early attempts at visualization, such as soot displacement on glass, have not been adapted to modern optical techniques, leaving quantitative characterization of pheromone trails a major unresolved challenge in the study of ant foraging dynamics. In this talk, we present the first direct observations and quantifications of pheromone trails laid by Lasius niger. Using quantitative phase imaging based on fast, high-sensitivity quadriwave lateral shearing interferometry integrated into a standard microscope, we are able to detect and measure pheromone deposits. Our results reveal a rapid evaporation of the solvent phase, followed by the formation of a long-lasting residue that remains detectable for several minutes. This breakthrough provides unprecedented access to the spatial and temporal dynamics of chemical communication in social insects, without labelling or invasive manipulation. Beyond deepening our understanding of collective behaviours and their relationship to individual decision-making, these measurements also provide key parameters for improving bio-inspired optimization frameworks such as Ant Colony Optimization algorithms.

Genomic drivers of parasitic behaviors in bees: evidence from gene family dynamics and selection patterns

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Parasitic behaviors have evolved multiple times independently in bees (Anthophila), yet their genomic and evolutionary underpinnings remain poorly understood due to limited taxonomic sampling. Considering that gene family composition, numerical dynamics, and selection patterns may shape behavioral evolution, here we present the first broad comparative evolutionary genomic analysis of parasitism across bees. We analyzed 43 hymenopteran genomes, including 40 bees (12 parasitic representing cleptoparasitism, social parasitism, and cleptobiosis) and three wasp outgroups. Curated, non-redundant proteomes (BUSCO completeness >90%) were used for gene count and orthology inference with OrthoFinder. These results supported phylogenetic reconstruction with the BUSCO-phylogenomics pipeline and IQ-TREE2, and were used in CAFE5 to infer orthogroup expansions and contractions. Finally, identified chemosensory soluble proteins (CSPs) were analyzed for selection patterns using HyPhy. Parasitic bees exhibited increased genomic dynamism, predominantly driven by gene family contractions. Distinct parasitic strategies showed specific genomic signatures: cleptoparasites displayed widespread contractions in odorant receptors (ORs), musculobuccal development, and housekeeping genes, alongside expansions in cuticle-related genes; social parasites shared contractions in chemosensory and juvenile hormone–related genes; and the cleptobiotic bee showed extensive ORs gains and losses and reductions in energy metabolism genes. ORs repertoires were highly variable, whereas gustatory receptors and CSPs were more conserved. Despite stable copy numbers, CSPs showed episodic positive selection in some parasites, particularly CSP3, CSP4, and CSP6, indicating functional diversification without numerical change. Overall, these results link parasitism evolution in bees to both convergent and strategy-specific genomic changes, driven by gene family turnover and chemosensory evolution.

Insights into the molecular underpinnings leading to the diploid drone discrimination in the western honey bee Apis mellifera

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Understanding complex phenotypes such as behavior and the underlying molecular basis belong to major questions in biology. Among social insects, the cannibalism of diploid drone larvae in the honey bee Apis mellifera by worker bees represents one remarkable behavior for which the molecular underpinnings are not known yet. The complementary sex determiner (csd) gene acts as the primary signal of sex determination in honey bees and diploid drones arise by homozygosity compared to diploid females (csd-heterozygous) and haploid drones (csd-hemizygous). Quantitative differences of larval cuticular substances, such as long-chain cuticular hydrocarbons (CHCs), have been proposed to be recognized by worker bees leading to the discrimination of diploid male and female early larvae. We follow the hypothesis that the regulatory signaling of the sex determination pathway affects the synthesis of cuticular substances in honey bee larvae.

We used early larval stages (12h, 24h, 36h, 48h after hatching) from an inbred cross reared in-vitro for transcriptome sequencing to investigate gene expression differences between diploid females, diploid males and haploid males. We identified several DEGs that strongly support our hypothesis, including genes that belong to elongases of long chain fatty acids, odorant binding proteins, terpenoid backbone synthesis and cuticular proteins. Analysis of cuticular extracts of these larval stages via gas chromatography mass spectrometry showed remarkable differences between the distinct sexes and time windows in the CHC profiles. Consequently, by integrating molecular and biochemical analysis we identified candidates that may act as connecting factor between sex determination and CHC biosynthesis pathways.

The Queen Central Module Gene Cytb5-r-a Regulates Queen Signaling In Cryptotermes secundus

Wei Zhou; Jana Werle; Judith Korb

The maintenance of reproductive division of labor in social insects requires reliable signaling of individual's physiological state. In the termite Cryptotermes secundus, queens are characterized by an elevated expression of a co-expressed gene network, the Queen Central Module (QCM). The QCM integrates genes associated with juvenile hormone (JH) biosynthesis and signaling, insulin/insulin-like growth factor signaling (IIS), cuticular hydrocarbon (CHC) biosynthesis, and fecundity. The QCM hub gene, Csec-Cytb5-r-a, is downregulated following JH-suppression, leading us to hypothesize that it functions as an indicator gene linking individual physiological states to chemical signaling. We used RNA interference (RNAi) to partially knockdown Csec-Cytb5-r-a in queens and evaluated the subsequent effects on behavior, CHC profiles and gene expression. GCMS analysis revealed that Csec-Cytb5-r-a partially knockdown disrupted the queen's chemical signal, specifically reducing some queen-specific long-chain and methyl-branched hydrocarbons. Correspondingly, despite the queen's physical presence, workers directed significantly more butting behavior toward RNAi-treated queens, which is a response typical of queenless colonies in C. secundus. To identify the molecular basis of this shift, we performed RNA-seq on queen head tissues. Transcriptomic profiling identified significant downregulation of Elovl4, a gene coding a key enzyme for the biosynthesis of long-chain CHCs. This molecular shift corroborates our observed chemical results, suggesting Elovl4 as the mechanistic link between Csec-Cytb5-r-a silencing and the loss of the queen-specific chemical signal. The expression of JH/IIS pathway and fecundity-related genes remained unaffected. Our results suggest that Csec-Cytb5-r-a is a important regulator of queen signaling.

Recruitment behavior by the Longhorn “crazy” ant Paratrechina longicornis

Ehud Fonio

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Chemical communication via pheromones and specifically recruitment during trail formation is one of the hallmarks of social insects. Nevertheless, despite extensive research during the last 50 years, basic quantitative phenomenological data about the properties of this behavior is surprisingly scarce. The longhorn ‘Crazy’ ant (Paratrechina longicornis) is a worldwide invasive species, known for its amazing cooperative transport capabilities. Pheromone markings deposited by these ants play a critical role in various contexts, including resource distribution between sister nests, nest relocation, recruitment to food sources, navigation during cooperative transport and collective obstacle clearing. Here we analyze the temporal and spatial properties of sequences of pheromone marking during recruitment behavior by these ants.

Investigation of host recognition systems in the temporary socially parasitic spiny ant: Polyrhachis lamellidens

Hironori Iwai; Masaru K. Hojo; Akiko Koto

Accurate recognition and discrimination between self and non-self individuals is essential for maintaining a society. In social insects such as ants, social behaviors including nestmate recognition are based mainly on chemical signals (e.g., cuticular hydrocarbons) detected by the antennae. By contrast, in so-called temporary social parasites, the newly mated queens are known to invade colonies of other ant species by overcoming this nestmate recognition system. However, how the newly mated queens of temporary social parasites recognize their hosts and establish social parasitism remains poorly understood. In this study, we focused on the antennae of the temporary social parasite Polyrhachis lamellidens and its host Camponotus japonicus, and examined the expression patterns of odorant receptors (ORs) involved in the detection of semiochemicals in especially the newly mated queens and workers of both species, with the aim of identifying reception mechanisms underlying host recognition specific to social parasites. We found that in C. japonicus there were no clear differences in OR expression patterns between the newly mated queens and workers, whereas in P. lamellidens approximately half of the ORs were expressed at significantly higher levels in queens. These results suggest that, in the newly mated queens of P. lamellidens, ORs may contribute to host searching and recognition.

Defense strategy of prey hornets against attack by giant hornets in Japan

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Mass attacks by giant hornets (Vespa mandarinia) make them serious predators of other hornets in Japan (i.g. V. crabro, V. simillima, V. dybowskii, V. analis and V. ducalis). Since mass attacks start with a giant hornet (VM) scout attracting nest-mates using foraging-site marking pheromone, early detection and elimination of the VM scout by the prey colony are critical for survival. While some prey hornet species have specific defensive "anti-VM" responses to VM workers and species odor, precise prey behavioral patterns and the active chemical components and locations remained unclear. This study identified two species-specific defenses among five Japanese hornet species: (1) wing-flapping while running with extended abdomen (V. crabro, V. simillima and V. dybowskii), or (2) persistent flight around the VM predator (V. analis and V. ducalis). These behavioral patterns appear to correlate with typical prey species colony size rather than phylogenetic relationships. Bioassays using V. crabro also revealed that diethyl-ether extracts from the head/thorax, Van der Vecht gland, and sting unit of VM workers all induced anti-VM responses similar to whole-body extracts. One foraging-site marking pheromone component, 1-methylbutyl 3-methylbutanoate, commonly detected from the Van der Vecht gland and venom in VM, did not trigger the anti-VM response. Therefore, the active components appear to be distributed throughout the VM body, rather than in a restricted organ. Overall, our results suggest that prey hornets use VM "body odor" as a kairomone to quickly detect their natural enemy, allowing initiation of species-specific, optimal defense behaviors.

Drawn to the dead: Fungus farmer Cyphomyrmex costatus (Formicidae: Myrmicinae) surrounds their garden with arthropod corpses

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Defense tactics, vital for surviving predation and parasitism, are achieved in varying ways across animals. While some species can be fierce using aggression and weaponry, others freeze or play dead, blending in with their environment. Cyphomyrmex costatus is a tiny fungus-growing ant that has a vestigial sting and plays dead when attacked. It is obligately dependent on its mutualistic fungus garden for food. Interestingly, workers collect arthropod remains (i.e., necromass). Although previously documented, the ecological drivers underlying this unusual behavior remains poorly understood. Once thought to be substrate to feed the garden, it is now clear that the necromass is never incorporated. We explore this strange behavior by: 1) describing the diversity of arthropods parts and their placement, 2) comparing chemical profiles of the ants, garden, and necromass, and 3) determining ant preference with choice assays. Necromass, consisting primarily of ant remains, surrounds the nest perimeter and likely reflects the nearby arthropod community. Behavioral assays indicate that neither cuticular hydrocarbon presence nor colony-origin influence preference. Chemical profiles were distinct, and the necromass contained oleic acid, the insect death compound. We hypothesize that necromass-collecting behavior evolved as part of a crypsis defense strategy, avoiding predatory threats while camouflaged among refuse. In future research, we would like to explore the origins of the cuticular hydrocarbons shared among the fungus, ants, and necromass as well as the predatory threats to C. costatus colonies.

Field bioassays reveal evidence of a gyne-produced sex attractant pheromone in social yellowjacket wasp

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There has been conflicting evidence of gyne-produced sex attractant pheromones in some vespid wasps. In Southern California, we monitored >150 nests of Vespula pensylvanica until nest senescence, including 10 perennial colonies. While all colonies produce males in late fall/early winter, we regularly observed a second pulse of males in early spring in the vicinity of perennial colonies. We observed males patrolling vegetation near areas with perennial nests and occasionally observed mating in the wild. These areas were prime habitat to test gyne attractiveness to wild (and unrelated) males in field conditions. Here we describe the development of field bioassays and evidence for a sex attractant pheromone produced by gynes of the western yellowjacket, Vespula pensylvanica.

Substrate-borne vibrations as a recruitment signal in ant tandem running

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Tandem running is a sophisticated recruitment behaviour employed by several ant genera, where an informed leader guides a follower to a target location. This communication strategy is known to rely on visual, chemical and tactile cues that mediate information transfer between the leader, who knows the destination and initiates the run, and the follower. In this study, we demonstrate that tandem running in the ant Diacamma indicum also includes a vibrational component, revealed using Laser Doppler Vibrometry (LDV). We located a stridulatory organ on the gaster and documented distinct substrate-borne vibrational signals in the 400–600 Hz range associated with tandem runs. These signals were emitted intermittently and had a relatively limited active space. Experimental masking of the stridulatory organ disrupted signal production. Because such signals can embed directional information, they are likely to enhance communication between tandem partners while navigating heterogeneous environments, thereby improving cohesion within the tandem pair. More effective tandem running, in turn, should help reduce colony fragmentation and promote rapid relocation. Our results highlight a previously underappreciated signaling channel in tandem running and open up opportunities to investigate the plasticity of these signals across contexts and to further appreciate the complexity of communication in social insects.

SYMPOSIUM 18 · Vibroacoustic signalling in (eu)social insects
ORAL · Wed 19 Aug · 17:00 · K7 · Session 45 · Abstract ID 149041

The shaking signal shapes the daily rhythm of work inside and outside the hive

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Honey bee colonies must match work to changing food. The shaking signal has often been described, but its daily timing and effect on behavior have remained unclear. We ran a simple series of tests with Apis mellifera observation hives where we controlled when food was available, mapped where and when shaking occurred, marked individual bees to record nest departures, and used a small device that imitated natural shaking. Three clear results emerged. First, shaking continued during short periods without food, rose sharply when food returned, and was concentrated in the middle comb of the hive where bees that are ready to leave often gather. Second, bees that were shaken in the morning were more likely to leave the nest, while bees that were shaken in the afternoon were less likely to leave and instead stayed to work inside. Third, the device produced the same responses as natural shaking, showing that the vibration itself caused the change in behavior. These findings establish that the shaking signal acts as a daily switch that mobilizes foraging early and shifts effort indoors later. By clarifying when and how this signal moves workers, our study offers a practical way to predict and guide colony effort across the day, with direct value for pollination and for managing colonies under variable conditions.

SYMPOSIUM 18 · Vibroacoustic signalling in (eu)social insects
ORAL · Wed 19 Aug · 17:15 · K7 · Session 45 · Abstract ID 141535

Audience effects shape the honey bee waggle dance

Ken Tan
中国科学院西双版纳热带植物园

Audience effects reveal the social intelligence and social awareness in animals. We provide the first evidence of advanced audience effects in a social insect. Variations in audience size and the proportion of non-foraging young bees significantly influenced the motivation of bees to dance and altered the referential information encoded in dances. A smaller audience or a higher proportion of young bees led to a reduced frequency of dancing and less precision in communicating the direction and distance to food sources. Additionally, even when they had the same average number of dance followers, dancers traded off accurately signaling distance and direction for audience-seeking when they experienced difficulty in gathering an audience. These findings show that honey bees dynamically adjust their dance behaviors in response to the social context, which indicates a sophisticated level of communication tailored to the specific needs of the colony. Honey bee waggle dancing, therefore, exhibits advanced cognitive control and fulfills several criteria for first-order intentionality in animal communication: goal-directed behavior, audience effects, and signal modification based on the receivers.

SYMPOSIUM 19 · Mechanisms and evolution of insect sensory systems: implications in the Anthropocene
ORAL · Wed 19 Aug · 10:15 · K8 · Session 34 · Abstract ID 145042

Adaptive evolution of odorant receptors is associated with elaborations of social organization in ants

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Cooperation in social insect colonies depends on complex chemical communication, requiring a large array of chemosensory receptors. Ant odorant receptors (ORs) were dramatically expanded compared to other insects, most notably in the “9-exon” subfamily, which was implicated in responding to cuticular hydrocarbons, a major class of signalling compounds. The Global Ant Genomics Alliance has compiled a large, high-quality dataset of ant genomes, enabling detailed study of OR evolution in unprecedented detail. Analysing 55,068 ORs across 163 ant species, we tested for association between sociobiological traits and adaptive evolution of ORs. Inference of OR expansions and adaptive sequence evolution allowed focused analysis of specific ant lineages. We identified strong enrichment of positive selection on 9-exon ORs in the ancestor of the formicoid clade, the largest clade of extant ants that evolved larger colonies and greater reproductive division of labour. This result indicates a key role of adaptive diversification of chemical communication in the early evolution of complex social organization. We also observed enrichment of positive selection on 9-exon ORs associated with the recent evolution of continuous worker polymorphism in multiple lineages. Surprisingly, the evolution of other sociobiological traits was associated with reduced positive selection on ORs. These results suggest that worker polymorphism involves more extensive adaptation of chemical communication compared to other aspects of ant sociobiology. By analysing the most comprehensive ant OR dataset to date, we provide new insights into the specific context in which ORs played a major role in the elaboration of social traits in ants.

SYMPOSIUM 19 · Mechanisms and evolution of insect sensory systems: implications in the Anthropocene
ORAL · Wed 19 Aug · 10:45 · K8 · Session 34 · Abstract ID 146279

The genomic underpinning of variation in vision across a global sample of ant workers

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The ants have evolved a stunning global diversity with more than 15,000 extant species belonging to over 330 genera. Their foraging strategies are highly diverse with some species relying entirely on chemical cues while others depend primarily on visual perception. Some species can discriminate between colors and exhibit remarkable orientation skills and visual acuity while other ants are blind. This functional diversity is correlated with substantial variation in eye morphology across the worker castes, ranging from prominent compound eyes to eyes having been reduced or entirely lost. Here, we provide new insights in the evolution of these visual systems using a comparative genomic dataset generated by the Global Ant Genomics Alliance (GAGA). Analysis of 163 ant genomes shows that the five genes encoding opsins – G-protein-coupled receptors in photoreceptor cells – are conserved across the ants, with episodic gene losses in some species potentially affecting the ability for color vision. The opsin genes also show different selection constraints and decreased expression in species with reduced eyes. We further show that reductions in eye size are related to foraging habits and diet. Finally, we identify signatures of selection on genes and pathways involved in Drosophila eye development, providing insights into the molecular mechanisms associated with the ants visual systems.

SYMPOSIUM 19 · Mechanisms and evolution of insect sensory systems: implications in the Anthropocene
ORAL · Wed 19 Aug · 11:00 · K8 · Session 34 · Abstract ID 149929

Molecular correlates of gustation and diet in ants

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Ant diets range from exceptionally narrow specialization to complex mutualisms, an extreme diet diversity associated with their extraordinary species diversity and social complexity. Despite the importance of taste in diet evolution, foraging ecology, speciation, and its sociobiological correlates, ant gustation is understudied. We annotated gustatory receptors (GRs), a large taste receptor family, from the 163 ant genomes sequenced and compiled by the Global Ant Genome Alliance (GAGA). After documenting diet information for each species in the dataset, constructing gene trees, and categorizing GRs into known subfamilies, we conducted phylogenetic generalized least squared (PGLS) analyses to investigate relationships between receptor numbers and a variety of dietary, social, and ecological traits. Results show correlations between metrics of diet diversity and expansions in the two largest GR subfamilies, F and GR8/9. Fungus-growing species also have gains and losses of specific GR subfamilies unique to this clade, whereas social parasites have fewer GRs across many subfamilies. We are also using AlphaFold2 and molecular docking analyses to predict the ligands of receptors in subfamilies whose functions are unknown to provide additional correlations with patterns identified in the PGLS analysis. Our research indicates coevolutionary patterns of diet and taste in ants and provides insight into the molecular basis of their ecological and evolutionary success. The agricultural and urban impact of ants is affected by diet and the invasiveness of ants indicates plasticity in food choice. Research on taste evolution consequently has implications for global change myrmecology.

SYMPOSIUM 19 · Mechanisms and evolution of insect sensory systems: implications in the Anthropocene
ORAL · Wed 19 Aug · 11:30 · K8 · Session 34 · Abstract ID 146414

Eyes in the City: Species-specific shifts in visual traits in bees and wasps

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The impact of land use changes (e.g. urbanisation) on the functional traits of bees and wasps is increasingly recognised, with the potential to jeopardise the pollination and pest control ecosystem services they provide. While many studies have focused on the effect of anthropisation on body size, fewer have considered morphological traits related to the visual system. Nevertheless, it is expected that habitat fragmentation favours sharper visual acuity (e.g. larger eyes, larger ocelli and more ommatidia), while also considering the effect of the Urban Heat Island (UHI) effect on reducing body size in ectotherms. We present here the most detailed studies to date on the variation of visual traits of wild bees and aculeate wasps across urbanisation gradients. Over the past four years, we have collected females (and occasionally males), in six Italian cities, for a total of 13 bee species (Apidae, Halictidae, Megachilidae), and 2 wasp species (Vespidae). Some species exhibited comparable trends. For example, females of Osmia cornuta (Megachilidae) and Seladonia gemmea (Halictidae) show a higher ommatidia density in more urbanised areas, suggesting sharper visual acuity, and males of Anthopora plumipes (Apidae) has larger ocelli, suggesting an improved orientation ability, in such habitats. In contrast, the wasps Polistes dominula and Vespula germanica showed no significant changes across urbanisation gradients. The species-specific results are not surprising, given the variety of habitats found in cities and the morphological and biological diversity of the studied species. However, they may point towards common responses when similar insects are exposed to similar conditions.

SYMPOSIUM 19 · Mechanisms and evolution of insect sensory systems: implications in the Anthropocene
ORAL · Wed 19 Aug · 11:45 · K8 · Session 34 · Abstract ID 149773

Searching in the shadows: the effects of UV-deficient environments on bumblebee foraging behavior

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Flowers have evolved elaborate, intricate visual displays to attract pollinators. Floral generalists like honeybees and bumblebees visit thousands of flowers each day, relying on these visual signals for efficient foraging. Ultraviolet (UV) light plays a critical role in guiding bees' foraging behavior, with many bee-pollinated plants exhibiting colors in the short-wavelength ranges of UV and blue. A common floral display consists of a central area that absorbs UV, with outer petals that reflect UV, creating a 'bullseye' pattern that helps flowers stand out against their background and guide pollinators to the pollen and nectar rewards within the flower. However, in Controlled Environment Agriculture (CEA, e.g., greenhouses, indoor grow facilities), UV light is greatly reduced or eliminated. Here, we investigated how these artificial light conditions interact with UV floral signals to affect foraging behavior in common eastern bumblebees (Bombus impatiens), a pollinator commonly used in CEA. We hypothesized that UV-deficient environments affect the efficacy of floral signals by reducing floral contrast and saliency. To test this, we presented foraging bees with arrays of both 'bullseye' patterned and plain flowers displayed against simple or complex backgrounds under three lighting conditions (full UV, limited UV, no UV). We measured approach latency to the first flower, search time between flower visits, and total number of flowers visited. Our results will inform agricultural practices, especially as CEA plays an important role in mitigating the effects of climate change on crop production.

SYMPOSIUM 19 · Mechanisms and evolution of insect sensory systems: implications in the Anthropocene
POSTER · Abstract ID 147630

Complex Effects of Multimodal Inputs in the Antennal Lobe of the Honeybee Apis mellifera

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Multimodal sensation is the process by which an organism integrates information from multiple sensory modalities to maximize the information about a stimulus and generate the optimal response. This information can be integrated at many different neurological levels, from a single sensillum to large regions of the brain, often occurring in multiple stages throughout the processing pipeline. Thus, sensory integration is a complex process whose neurological underpinnings we are only beginning to understand. We studied this integrative process in the honeybee olfactory system, which utilizes both olfactory and mechanosensory inputs from an odor plume to aid in odor identification and the subsequent behavioral response. To do this, we exposed bees to various combinations of air speed and odor concentration while simultaneously recording extracellular spike activity from within the antennal lobe (AL), which receives direct antennal input and serves as the first layer of processing within the bee brain. Responses were analyzed based on several factors including the spiking rate, length, and latency. We additionally developed machine learning algorithms to categorize the response’s shape, including the number of peaks, their locations, and any inhibitory responses. Integration occurred throughout the AL, showing some evidence within the local interneurons, but far more at the level of the projection neurons. This difference suggests a change in representations of sensory components depending on processing level. Future projects will further explore this change, and how it carries over to other levels of processing such as the mushroom bodies or lateral horn.

SYMPOSIUM 19 · Mechanisms and evolution of insect sensory systems: implications in the Anthropocene
POSTER · Abstract ID 149865

Phenotypic plasticity in visual traits is driven by caste and body size in a social wasp

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Understanding how phenotypic plasticity in sensory traits arises—and how such variation is shaped by body size and behavioural demands—remains a key challenge in evolutionary and developmental biology. To begin to address this, we examined body size and visual traits in queens and workers of the eusocial wasp Protopolybia sedula. Our analyses showed that queens typically possess larger bodies and eyes but fewer functional optical units (ommatidia) than workers. We also found caste-specific allometric patterns in visual investment: in queens, eye area is hypoallometric and ommatidial diameter hyperallometric relative to body size, whereas in workers, both traits scaled isometrically. These results reveal
distinct allometric rules governing sensory organ investment between castes and generate substantial variation within castes, with smaller and larger individuals exhibiting different eye
designs. Variation in visual traits both between and within castes may enable individuals to operate effectively under different light conditions and perform specialized tasks—potentially conferring an evolutionary advantage in social life.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 10:15 · K9 · Session 17 · Abstract ID 149829

Mapping the clonal raider ant brain at synaptic resolution

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Ants have been studied extensively due to their advanced social structure and communication strategies, though the neurobiological basis of these behaviors is not well-understood. The clonal raider ant Ooceraea biroi is particularly amenable to investigating the neural circuits underlying social behaviors, as it is uniquely experimentally tractable and genetically accessible.

To characterize the structural connectivity of the ant brain, we imaged a whole brain at synaptic-level resolution using transmission electron microscopy (TEM). This whole-brain EM volume allows us to reconstruct neurons, identify synapses, and ultimately create a complete wiring diagram, or connectome, of the ant brain. To accelerate circuit reconstruction, we applied machine learning based approaches to segment neurons and predict synapses, followed by ongoing manual proofreading to ensure accuracy.

To facilitate integration with existing resources, we registered the EM volume to a reference light-microscopy brain atlas of the clonal raider ant, enabling correspondence between cells identified across imaging modalities. Given the central role of olfaction and pheromone-mediated communication in ant social behavior, and the dramatic expansion of odorant receptor genes and olfactory glomeruli in ants, our initial reconstruction efforts focus on elucidating the wiring logic of the olfactory system.

More broadly, this segmented whole-brain EM dataset, and the eventual complete connectome, provide a foundational resource for studying the neural circuits underlying behavior in the clonal raider ant. This resource will support ongoing efforts to learn how neural circuit organization supports collective behavior, division of labor, and pheromone-guided decision-making in social insects.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 10:30 · K9 · Session 17 · Abstract ID 148735

The frontal gland in termites: Structure, Function, and Evolution

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Termites are the ecosystem engineers of tropical terrestrial habitats, with a global biomass comparable to that of ants or humans. The frontal gland is perhaps the most studied termite organ and a defining feature of the Neoisoptera, the most successful termite group in terms of species richness and abundance. While its presence in soldiers as a large, saccular defensive organ is notoriously known, the gland is also present in alate imagoes and workers of certain taxa, albeit in various forms. We examined the frontal gland's structure using 3D synchrotron scans of workers, soldiers and alate imagoes from 20 termite species, representing all major Neoisoptera lineages. This dataset enabled us to identify structural characteristics and secretion release mechanisms in particular groups. We also compared frontal gland use across different taxa and determined its importance in the context of species-specific defensive strategies.

The evolution of novel mouthpart interlocking mechanisms in ants (Hymenoptera: Formicidae)

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Ant lifestyles centre around the unique combination of eusociality, flightless workers, and often predatory habits. No morphological innovations in ants are known to relate to predation. Here, we explore an understudied ant novelty: the ability to close off their mouth. Ants lock their labrum in front of the maxillolabial complex through part of the maxilla pressing against labral hooks. Grooves on the maxillolabial complex additionally allow tighter labral fit in some groups. Variations in both mechanisms lead to different levels of mouthpart closure, with an evolutionary trend to switch from looser to tighter conditions across ants. We find predation to predict tight closure, but models of character evolution indicate that evolutionary dependence between these traits is not the only possible explanation for this pattern. Although tight interlocking is lost in some ants, we find no clear evidence for trade-offs with other functions, such as sensing with the palps. We discuss the origin of interlocking in ants and suggest that it might relate to a combination of predation, prognathous mouthparts, and multipurpose mandibles. We discuss the role of mouthpart closure in ant evolution but also highlight limitations of our comparative approach and emphasize the need for focused biomechanical investigations and enhanced natural history data to refine future inferences of adaptation.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 11:00 · K9 · Session 17 · Abstract ID 145917

Insights on the morphology of the ant digestive system from micro-CT scanning and evolutionary considerations on some of its key features

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Ants, as dominant insects in terrestrial ecosystems, arguably owe their ecological success to a combination of eusociality and the exploitation of diverse food sources. Ant resource preferences range from predation to herbivory. The basis for food uptake, as well as several social functions, is the ant feeding and digestive system, including glands of the mouthparts and foregut. While the anatomy of many of these features has long been studied, the variability of structures such as the cephalic sucking pump and even some glands has only recently begun to receive focused attention. New techniques, such as micro-CT–based 3D reconstructions, provide novel opportunities to document differences in these structures across ant species, castes, and developmental stages. This approach not only improves our understanding of these structures' evolution, but also of their functions in colony life. I will discuss published and unpublished results on the morphology of key structures of the digestive system, with a primary focus on the cephalic sucking pump. Clear evolutionary signal is evident in the sclerotized stabilizers and musculature of this structure, and functionally relevant differences appear to correlate with dietary preferences. Furthermore, structural differences among castes highlight their distinct roles within the colony, such as a more open structure in larvae allowing passage of larger food particles, and modified muscle proportions in males that likely reflect their reliance on worker-mediated feeding. I propose that adaptations of the feeding system play a crucial role in facilitating the social behavior and dietary diversity that underpin ants’ evolutionary success.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 11:15 · K9 · Session 17 · Abstract ID 149645

Biometrics and Quantitative Diet of the Western African Driver Ants Dorylus (Anomma) wilverthi & Dorylus (Anomma) sjostedti

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[1] Georg-August University Goettingen; [2] BIOPOLIS / CIBIO-InBIO, Centre of Investigation for Biodiversity and Genetic Resources

In Afrotropical ecosystems, driver ants of the genus Dorylus are dominant predators, conducting vast predatory raids across the forest floor, and are proposed as keystone species. Although these raids are fundamental to driver ant ecology, quantitative data on diet and prey transport across the worker demographic spectrum remain limited. We describe prey transport and diet composition of Dorylus wilverthi and D. sjostedti from primary and secondary rainforest in mainland Equatorial Guinea, using 2,933 prey samples from 25 raids across 16 colonies (4,610 measured workers). Both species exhibit continuous worker polymorphism but differ in demographic structure. Contrary to earlier studies, D. wilverthi shows three distinct worker size modes, including a large-worker mode absent from D. sjostedti (two modes). Worker allometries did not differ between species. Prey mass increased with worker mass ($\beta = 1.37$), whereas relative load per worker declined with worker mass ($\beta = -0.63$), indicating a size-dependent division of labour consistent with classical strength-scaling laws. Ants engaged in cooperative transport carried heavier absolute loads than solitary carriers. Cooperative transport was therefore primarily associated with larger prey items and did not function mainly to reduce individual loading, instead extending the upper limit of transportable prey. Driver ant diet was highly generalist with 25 prey orders identified; D. wilverthi and D. sjostedti exhibited near-complete order-level diet overlap (Pianka = 0.956). Our multifaceted approach provides a detailed description of prey transport ecology in driver ants, linking worker morphology and prey characteristics to reveal shared biomechanical constraints across two ecologically similar Dorylus species.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 11:30 · K9 · Session 17 · Abstract ID 148536

Understanding ant stinger evolution through morphology and function

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Morphological traits can reflect how organisms solve functional problems under dynamic ecological conditions. In social insects, venom delivery systems are especially informative because their form and mechanics are strongly influenced by their use. Ants are particularly notable in this respect, as their stingers range from robust piercing structures to reduced or non-piercing systems. Here, I examine the evolution of ant stingers by relating internal anatomy, mechanical performance, and macroevolutionary change. Detailed analyses of stinger valve morphology show that ants possess a distinctive internal organization of the valvilli, enabling coordinated movements that are rarely emphasized in other aculeates and suggesting a broader range of operational modes than usually assumed. Biomechanical analyses based on finite element modelling further indicate that substantial variations in stinger shape can occur without strong constraints imposed by puncture-related stresses. Here, performance appears to depend as much on behavioral use and ecological context as on mechanical optimization alone, and this functional flexibility can help explain broader evolutionary patterns. Comparative analyses across ants indicate that piercing stingers represent the ancestral condition, with repeated transitions towards reduced or non-piercing forms associated with shifts in diet and foraging strategy. These transitions are asymmetric, with loss occurring more readily than regain, and are accompanied by changes in evolutionary rates and morphological disparity. Overall, these results show how morphological data across scales relate fine anatomical modifications to functional changes and ecological diversification in social insects.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 14:30 · K9 · Session 23 · Abstract ID 147876

Architecture as morphology: A comparative analysis of ant nests as extended phenotypes

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In social insects, nests both provide shelter and structure the interactions among workers that underlie the colony's collective behavior. The architecture of subterranean ant nests emerges from interactions between soil conditions and ant digging behavior. Because ants determine the structure of the space they inhabit, natural selection can exert pressure on digging behavior to produce nest structures that benefit survival and reproductive success of ant colonies. There are many potential drivers of the evolution of nest traits, from shelter from biotic and abiotic environmental factors to the ways in which nest structure impacts social interactions that shape colony behavior. In my comparative analysis of ant nest architecture, I synthesize measurements of subterranean nest structures from the primary literature to quantify the extended phenome of ground-dwelling ants and pair measures of nest morphology with information about ants' natural history, behavior, and ecology to investigate the evolutionary drivers of nest architecture across the ant species. In this talk, I will survey my published and ongoing work that shows species differences in nest traits that are linked to colony size, foraging strategy and soil features. I will preview the next steps of my work that investigate the evolutionary relationships between abiotic factors (climate and soil properties), colony behavior (including recruitment to foraging), and nest architecture.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 14:45 · K9 · Session 23 · Abstract ID 149462

Nest architecture influences the colony-level defensive response of Honey bees

Peter Marting; Michael Smith
Auburn University

Nest architecture is not only a product of animal behavior, but a mechanism that influences it. Nests protect insect societies against intruders that plunder developing young or stockpiled resources. The nest entrance is a key architectural feature that contributes to colony defense since it is the access point for intruders as well as a chokepoint for aggressive workers fending off an attack. Using Western honey bees (Apis mellifera), we tested the hypothesis that nest entrance length influences colony defense behavior. We fitted standard bee hives (n=56) with either long or short entrance corridors, gave colonies 3 days to acclimate, and performed colony aggression assays quantifying bee attacks following a brick drop to the hive. We then repeated the experiment so that each colony received both entrance length treatments. Colonies had a 26% higher aggression scores when fitted with shorter entrances, showing that more bees attacked in the beginning of the aggression trials. Video analysis showed that with short entrances, more guards were positioned at the entrance opening while with longer entrances, they were distributed more throughout the corridor. During a defense episode, the charge front of attacking bees was able to exit the short entrance but was stalled in longer entrances. This shows that nest architecture can influence colony defensive behavior, a relationship that has received little empirical examination despite its profound implications for colony function and survival.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 15:00 · K9 · Session 23 · Abstract ID 147826

Combining AntWeb and Deep Learning to Reconstruct the Evolution of Ant Coloration

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Color variation in ant cuticles is likely to influence how species interact with environment, affecting processes such as thermal balance, visual concealment, and resistance to pathogens. Despite these important functional roles, the breadth and structure of color diversity within ants remain poorly documented, and no large-scale synthesis is currently available for this exceptionally diverse insect family.

To fill this knowledge gap, we built a unified computer vision workflow that integrates traditional image-processing techniques with AI-driven pattern recognition to generate high resolution color profiles across the ant body. Using more than 30,000 standardized specimen photographs from AntWeb—one of the most extensive digital repositories for ant biodiversity—we extracted color information for over 10,000 species. This automated approach provides a reproducible alternative to conventional descriptions, which typically rely on subjective human assessments or simplified quantitative metrics restricted to a single body region or a single axis of variation (most often brightness).

Our framework captures multidimensional color properties across entire specimens and eliminates the need for subjective classification. We compare its performance with existing methodologies and use it to revisit global patterns of color diversity within the Formicidae. For the first time, we deliver a large scale quantitative overview of ant pigmentation and investigate how it correlates with phylogenetic structure and environmental gradients that may have influenced the evolution of color. Finally, we highlight how this approach can contribute to macroecological studies and be extended to other groups of insects.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 15:15 · K9 · Session 23 · Abstract ID 146460

Macroecological drivers of red and black colour variation in ants

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Colour is a key biological trait involved in ecological functions such as camouflage, physiological protection and thermal regulation. Yet, the environmental drivers of colour variation remain poorly understood at large spatial scales. Recent syntheses emphasise that Gloger's rule reflects a complex interplay of temperature and humidity acting on different components of colouration, notably dark and red pigmentation, rather than a single uniform process. Moreover, this complexity has been explored mainly in birds and remains untested in insects. Ants provide an ideal model to address this gap and test multiple macroecological rules of colouration, as their colour variation is dominated by dark and red pigmentation in a globally distributed and ecologically dominant lineage.

Here, we examine global patterns of ant colour variation at the assemblage level using 34,331 images representing 10,400 species. We decompose species-mean colouration into two orthogonal axes, pale–dark and redness. Across 575 assemblages worldwide, these axes respond to distinct environmental gradients.

UV-B radiation and dry conditions strongly structured the pale–dark axis, with assemblages becoming darker under high UV exposure and low precipitation during the driest season, consistent with protective and water-retention functions of melanisation. Canopy height increased both darkness and redness, suggesting an influence of background matching. In contrast, temperature primarily shaped variation along the redness axis, with warmer regions hosting redder assemblages, as predicted by the redness component of Gloger's rule.

Together, these results highlight the complexity of macroecological colour rules, particularly Gloger's, and demonstrate the importance of analysing different colour gradients independently.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 15:30 · K9 · Session 23 · Abstract ID 149737

Ecomorphological evolution in Neivamyrmex army ants

Laís Barros; Scott Powell
George Washington University

Apex predators have wide-reaching ecological impacts and often function as keystone species. Despite this importance, the ecological pressures that shape the diversification of apex predator lineages remain underexplored. The 126 described species in the army ant genus Neivamyrmex span desert to tropical forest habitats, predation in foraging strata from strictly subterranean to arboreal, and a nearly three-fold difference in body size. They therefore represent a species-rich, ecologically widespread, impactful, and morphologically diverse lineage for integrative studies of the adaptive evolution of apex predators. Yet their evolutionary history and adaptive diversification with respect to major ecological niche axes are essentially unknown. Our work integrates comparative morphological analyses of extensive material from collections and rare colony series. We reveal a striking degree of caste polyphenism for a group that has historically been seen as the “monomorphic” army ants. This includes repeated origins of a larger caste with disproportionately large heads, extended mandibles, and long legs. Existing ecological data suggest this caste may function as a “porter” caste that specializes in transporting large and awkward prey. Our comparative analyses further revealed relationships between foraging stratum and evolutionary transitions in overall body plan, integrating changes in traits like body size, relative leg length, and eye size. This work provides a novel system for examining general themes in the morphological diversification of social lineages and apex predators in particular. It further highlights the value of integrating new morphological data from old and rare collections into modern comparative analyses of phenotypic evolution.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 15:45 · K9 · Session 23 · Abstract ID 149822

Caste-related constraints and ecological divergence drive modular evolution in turtle ants.

Aline Oliveira; Scott Powell
George Washington University

Morphological diversification often reflects the interaction between functional constraints and ecological opportunity, yet different body regions may respond to these forces in distinct ways. Turtle ants (Cephalotes) are a phenotypically diverse lineage, and the species-rich angustus and fiebrigi groups provide a powerful system for examining morphological evolution during rapid diversification. Although historically treated as morphologically distinct clades, molecular phylogenies recover fiebrigi within angustus forming a monophyletic radiation encompassing contrasting morphologies and key ecological characteristics. Here, we examine how these groups occupy morphospace and whether different body regions follow distinct evolutionary trajectories consistent with their contrasting ecologies. We used geometric morphometrics to quantify shape variation across multiple traits, focusing on head and mesosoma defensive morphology, which are involved in nest defense and foraging protection, respectively. Using 90% of described species within these groups, we find that head morphology is strongly structured by caste, with clear separation between workers and soldiers but substantial overlap between groups. This pattern suggests conserved allometric trajectories, potentially resulting from caste-related functional or developmental constraints. In contrast, mesosoma morphology shows clearer differentiation among groups, consistent with ecological divergence, particularly among species occupying South American “dry diagonal” habitats. Ongoing work will complete taxon sampling across this diverse clade and integrate new data on the variable expression of a unique form of social parasitism within this lineage. Together, this approach will clarify how functional constraint and ecological diversification interact across morphological modules and castes during the rapid diversification of social lineages.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 16:00 · K9 · Session 23 · Abstract ID 149769

Fossil ecomorphology enables hypothesis testing of niche evolution and displacement

Christine Sosiak
University of Alberta

Paleoecological estimation is fundamental to the reconstruction of evolutionary and environmental histories. In many taxa, including ants, morphology reflects ecology to the extent that quantitative estimations of ecology can be made from morphology alone. The fossil record of ants chronicles 100 million years of evolutionary history spanning broad ecological diversity and faunal turnover, and additionally preserves immense taxonomic diversity in three-dimensional fidelity. The synthesis of ecomorphological predictive models with the ant fossil record enables us to test ecological evolutionary hypotheses within a quantitative framework. Throughout the Cenozoic (66 million years ago to present), ants undergo a striking faunal turnover: clades that are taxonomically sparse and geographically restricted today were much more diverse and widespread in the early Cenozoic. Did competition from newly emerging lineages suppress these clades, or were other factors such as environmental or climatic shifts responsible? With quantitative ecomorphological models allowing us to estimate the ecology of long-dead taxa, we test the hypothesis of core ecological niche displacement as a driver of faunal turnover.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 16:45 · K9 · Session 29 · Abstract ID 149056

How contrasting forms of competition alter trait-meditated community assembly: insights from coexisting turtle ants

Scarlett Reis Epifanio; Scott Powell
George Washington University

Understanding how trait-mediated competition shapes species coexistence and overall community structure remains a central challenge in ecology. Nevertheless, how this process plays out in species-rich communities, and particularly whether different forms of competition alter the assembly process, remains unclear. A community trait-space approach offers a way to address this open question, but requires a full set of coexisting species and quantitative shape data for traits engaged in contrasting forms of competition, while also controlling for relatedness. Here, we apply this approach to an exhaustively sampled assemblage of 17 coexisting turtle ant (Cephalotes) species. Using 2D geometric morphometrics, we contrasted head, mesosoma, and gaster defensive traits engaged in contrasting “targeted” and “diffuse” competitive interactions across castes. Principal component analyses and phylogenetic comparative analyses of phenotypic disparity revealed contrasting direction and magnitude of morphological disparity across traits and castes. Head shape occupied a broader, more phenotypically complex morphospace than mesosoma shape and exhibited greater maximum disparity between castes, suggesting stronger functional differentiation and niche filling associated with head morphology. In contrast, mesosoma shape showed tighter clustering in trait-space and more modest caste separation, indicating more conserved morphological variation among coexisting species. These results support coexistence theory by showing that traits mediating intense, targeted competition exhibit greater distinction and caste differentiation, reducing niche overlaps and promoting stable coexistence in species-rich ant communities. Together, these results highlight how different trait axes contribute unequally to community structure and indicate the importance of considering multiple forms of competition in species-rich communities.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 17:00 · K9 · Session 29 · Abstract ID 145630

The impact of extinction on eusocial communities through deep time

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New Jersey Institute of Technology (NJIT)

Island biodiversity is significantly threatened by extinction processes and is challenging to study due to the complexity of the fossil record. Ants, with a well-preserved fossil history, offer valuable insights into extinction dynamics. The island of Hispaniola, located in the Caribbean, is known for its Miocene amber deposits dated to 16 million years ago. The ants of this island are ecologically and morphologically diverse, with more than 140 extant species and nearly 120 fossil species, making it a unique system for studying how extinction affects island communities. In this study, we describe patterns of faunal turnover evidenced by the fossil record of Hispaniola. To quantify structural changes over time, we constructed a morphospace that includes both fossil and modern ants. We then reconstructed the ecology of the fossils using a machine learning approach to assess the impact of niche occupation on community assemblages. We found significant differences in morphospace occupation, primarily related to the extinction of large-bodied ant species. We also found greater ecological diversity in the fossil record, indicating a significant reduction in ecological niche occupation on the island.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
ORAL · Tue 18 Aug · 17:15 · K9 · Session 29 · Abstract ID 149873

Morphological integration and ecological filtering across Neotropical and Nearctic ant assemblages

Rodolfo Probst[1]; Rogerio Rosa da Silva[2]; Aaron M. Ellison[3]; Heraldo Vasconcelos[4]; Fabricio Beggiato Baccaro[5]; Jerome Orivel[6]

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Morphological traits are central to understanding how ecological pressures and evolutionary history jointly shape organismal diversity, yet integrative frameworks linking fine-scale morphology to macroecological and macroevolutionary patterns remain underdeveloped. Ants provide an exceptional system for addressing this gap, combining extreme ecological diversification with repeated evolutionary transitions in body size, appendage proportions, and functional syndromes across continents and biomes.

In this talk, we will present an integrative research program aimed at quantifying how ant morphological variation reflects the interaction between environmental filtering, ecological specialization, and phylogenetic constraint across large spatial and biogeographic scales. Using standardized morphological measurements spanning head, mesosoma, and appendage traits, we examine multivariate trait space occupancy and morphological disparity across Neotropical and Nearctic ant assemblages, encompassing contrasting climatic regimes and evolutionary histories.

These data are being analyzed within a phylogenetic comparative framework to disentangle lineage-specific trait evolution from convergent morphological responses to shared ecological conditions. We focus on three core questions: (i) how morphological integration and trait covariation structure ant morphospace across regions; (ii) whether similar ecological contexts in different biogeographic realms give rise to comparable morphological solutions; and (iii) how historical contingency versus ecological filtering shapes patterns of morphological diversity at the community level.

Ongoing analyses combine trait hypervolumes, phylogenetic methods, and community-wide metrics to link morphology with both evolutionary history and present-day ecological assembly. By explicitly integrating morphology, ecology, and biogeography, this work aims to advance a predictive understanding of how morphological diversity emerges and is maintained across continents.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
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Morphological patterns across social origins in snapping shrimp

Claire Bailey[1]; Solomon Chak[2]; Kristin Hultgren[3]; Phil Barden[1]

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Shrimps in the genus Synalpheus exhibit a range of social behavior, spanning from pair-living to more gregarious and even eusocial lifestyles. Synalpheus also contains at least five independent origins of eusociality within the last eight million years. These features make Synalpheus an ideal system to rigorously identify morphological patterns associated with social evolution. For this work, we characterized morphology across social lineages to determine whether social syndrome shapes morphology. To do this, we generated an extensive morphological dataset using specimens from both the field and museum collections. Using phylogenetic comparative methods, we describe variation in allometry, weaponry, and sensory structures across social origins in snapping shrimp. Our findings will contribute to the field of social evolution while also highlighting the importance of morphology-driven research.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
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Key innovations in the rise of ant societies

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Ants are one of evolution’s most successful experiments in scaling social life. Yet their journey from simple societies to ecosystem-dominating superorganisms required overcoming fundamental challenges in development and resource allocation. Through integrative, phenomic-scale analyses spanning over 700 species, we identify two critical evolutionary transitions that reshaped ant macroevolution. First we show how shifts in larval feeding behavior granted colonies unprecedented control over developmental trajectories, enabling the decoupling of queen and worker phenotypes and facilitating extreme morphological specialization. Second, we reveal how the evolution of cheaper workers enabled the rise of massive societies. By reducing investment in costly cuticular structures, colonies navigated a fundamental tradeoff, favoring quantity over quality, ultimately accelerating diversification across the ant tree of life. Recent genomic advances now allow us to connect these phenotypic innovations to their underlying molecular mechanisms. Together, these findings illuminate how ants achieved ecological dominance: by evolving precise control over offspring development and the capacity to produce workers at unprecedented scales, thereby redefining the limits of social complexity.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
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The earliest fossil evidence for eusociality in ants and termites

Phil Barden

New Jersey Institute of Technology

How old is eusociality and how do we know? Fossil specimens and molecular clock estimates soundly establish ants and termites as the first living eusocial lineages; these oldest societies began at least 120 million years ago. While molecular-based age estimates provide a range for when last common ancestors might have lived, fossils provide direct insight into ancient behavior. Because they are frequently preserved in their entirety and in great detail, insect fossils are especially amenable to behavioral inference. This unique preservation, recent fossil discoveries, and well-established morphological signatures of social behavior permit a confident reconstruction of eusocial origins. This talk will synthesize the fossil evidence entombed in rock and resin that chronicles the early history of sociality in ants and termites.

SOLDIERS OF THE SUBTERRANEAN ARMY: A MORPHOMETRIC ANALYSIS OF WORKER CASTE POLYMORPHISM IN THE ARMY ANT LABIDUS COECUS

Jacob Sorrentino

Labidus coecus is perhaps the most abundant and widespread New World army ant species, with populations continuous from Oklahoma, USA through Buenos Aires, Argentina. Despite this, the highly hypogeic L. coecus remains relatively understudied when compared with other army ant genera, particularly the more epigeic Eciton species. In this study, I describe the allometry of the L. coecus worker caste based on dry mass and morphometric measurements, utilizing specimens collected across a wide geographic range in North and South America. Bivariate and multivariate analyses demonstrate that L. coecus possesses a highly-allometric but continuously polymorphic worker caste, notably lacking the distinct submajor and major castes present in many Eciton species. Differences in diet and the degree of epigeic activity may have produced this observed divergence in army ant caste structure.

Evolution and physiological constraints of ant leg amputation

Dominic Enzner; Zoé Douxchamp; Jakob Gopp; Erik Thomas Frank
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Ants frequently suffer injuries during foraging, exposing them to high infection and mortality risks. To deal with these threats, some ant species perform wound care behaviors. Megaponera analis for instance treat infected wounds using antimicrobial secretions from their metapleural glands. Others, such as some Camponotus species, which lack the metapleural gland, reduce the mortality by amputating infected legs instead.

We hypothesize that wound care strategies depend on species-specific morphological and physiological traits. Ants, which possess thick cuticles for protection but relatively weak bite force may be physically incapable of amputating legs and instead depend on antimicrobial treatment. In contrast, species with stronger mandibles and thinner cuticles may have evolved amputation as a mechanical alternative.

We investigate the evolutionary and morphological basis of ant leg amputation. Using micro-CT scanning, we create three-dimensional models of head musculature across several German ant species, with a focus on the mandible closing muscle (as a proxy for bite force) and quantify the cuticle thickness of the leg.

This is then linked to observed wound care in German ant species. For example, Formica rufibarbis and Tapinoma erraticum exhibit amputation, while Lasius fuliginosus does not.

By comparing species that perform amputations with those that do not, we aim to identify specific muscle configurations, mandible forms, or size thresholds that may enable or constrain leg amputations. Our findings will contribute to a better understanding of how morphology and physiology interact in complex social behaviors, offering insights into the evolutionary pressures shaping cooperative wound care in ant colonies.

Climatic correlates of body size variation in Ectatomma ants from the Brazilian Cerrado

Nataly Neves; Karen Neves; Heraldo Vasconcelos
Federal University of Uberlândia (Brazil)

Understanding how morphology responds to environmental gradients is a central question in ecology, as climate influences organismal performance and physiological processes. Here, we investigate how climate, particularly temperature and precipitation, is associated with body size variation of ants of the genus Ectatomma in the Brazilian Cerrado. Standardized sampling of arboreal and ground-dwelling ants was performed at 31 sites in the Cerrado biome using pitfall traps. A total of 600 workers from eight Ectatomma species (E. brunneum, E. edentatum, E. lugens, E. muticum, E. opaciventre, E. permagnum, E. planidens and E. tuberculatum) were measured for seven morphological traits related to metabolic characteristics, diet, and habitat perception. Climatic conditions were characterized using five bioclimatic variables related to temperature and precipitation extracted from WorldClim. Results showed that body size variation in Ectatomma was better explained by temperature variables than by precipitation. However, this pattern was detected only for some species, indicating species-specific responses rather than a general pattern across the genus. Individuals of E. edentatum, E. opaciventre, and E. permagnum tended to be smaller in warmer environments, consistent with predictions of Bergmann’s rule. In contrast, E. permagnum and E. opaciventre showed positive relationships between body size and temperature annual range, with larger individuals occurring in areas with greater thermal variability. No significant relationships were detected for the remaining species, possibly reflecting restricted distributions and limited exposure to climatic gradients. Overall, temperature influenced body size in some Ectatomma species, but responses were not consistent across the genus, reinforcing the importance of examining individual species.

Scraping away the cost: the antenna cleaner’s role in reducing the contamination risk of allogrooming

David Moreno Martínez; Sylvia Cremer
Institute of Science and Technology Austria (ISTA)

One of the early defence lines of ants against disease is their allogrooming response, where healthy ants clean their exposed nestmates in particular from externally-infecting pathogens like fungal spores that have attached to their body surface. In addition, contaminated individuals often clean themselves by selfgrooming. The efficacy of grooming is determined by the morphology of the structures used for hygiene, like mouthparts and the antenna cleaner. The latter has been shown to effectively remove particles in a broad range of sizes from the antennal surface, through the mechanical action of cuticular projections and specialisations in the tibia and tarsus of the forelegs, forming a comb-like structure. Moreover, the tarsal surface of the forelegs also supports cleaning the head and pronotum of the thorax.

Allogrooming bears the risk of pathogen transfer to the caregiver, and it was observed that caregivers often groom themselves after having groomed an infectious colony member. We asked how important selfgrooming following allogrooming is for the health of the helping individual in Lasius ants when exposed to the pathogenic fungus Metarhizium. To this end, we generated a functional knockout of the antenna cleaner by gluing together the tibial spur and basitarsal surface and evaluated how this affected the caregivers’ pathogen load and survival when in contact with a highly exposed nestmate. An impaired function of the antenna cleaner indeed increased the risk of allogrooming, as the groomer became contaminated with more spores than with an intact antenna cleaner, demonstrating the protective role of selfgrooming in hygienic caregiving.

SYMPOSIUM 20 · Integrative evolutionary and ecological morphology
POSTER · Abstract ID 152089

Solar reflectivity and thermal resilience in an ant community along an elevational gradient

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Solar heat challenges the survival of social insects and their capacity to reflect solar radiation combats this thermal stress. Thermoregulatory compensation varies across environmental gradients of temperature and precipitation, often corresponding to elevational changes. .We hypothesize that ant species found at higher elevations will exhibit reduced infrared reflectivity, and ants found at lower elevations, in hotter environments will be more reflective. We sampled the ant community across an elevational gradient in the Chiricahua Mountains of Southeastern Arizona to test the near infrared reflectivity of multiple species and recorded data from multiple weather stations to examine the correlation between solar radiation and reflectivity of the ants. We found an extraordinary capacity of ants in hot environments to reflect solar heat, and the adaptive nature of this trait varied across taxa.

SYMPOSIUM 21 · Transgenic approaches for studying the biology of social insects
ORAL · Wed 19 Aug · 10:15 · K9 · Session 35 · Abstract ID 146268

Implementing Molecular Tools for Circuit Neuroscience in the Clonal Raider Ant

Daniel J. C. Kronauer

The Rockefeller University, Howard Hughes Medical Institute

Ants have served as model systems in ethology for over a century due to their rich and well-characterized social behaviors. Despite this long-standing interest, progress toward understanding the neural circuits underlying ant behavior has been limited by the lack of genetic accessibility in most species. This barrier is now beginning to lift with the implementation of the first neurogenetic tools in the clonal raider ant, Ooceraea biroi. Owing to its asexual reproduction and absence of a queen caste, O. biroi uniquely enables the creation and propagation of stable transgenic lines.

In this talk, I will describe our recent efforts to establish key molecular and physiological approaches for circuit neuroscience in this species, including functional calcium imaging and optogenetics. In parallel, we are generating comprehensive neuroanatomical resources for the clonal raider ant, including a fully segmented electron microscopy volume of the entire brain at synaptic resolution. Together, these tools and datasets will provide an integrated framework for recording from and perturbing ant neural circuits with unprecedented experimental precision, opening new avenues for mechanistic studies of social behavior.

Genetic dissection of brain functions related to foraging ability in the honey bee through analysis of mKast knockout workers

Hiroki Kohno; Takeo Kubo
The University of Tokyo

The European honey bee (Apis mellifera) has long been studied as a model social insect, however, many aspects of molecular and neural bases regulating its behaviors in the brain remain unclear. One useful approach to investigate these mechanisms is to examine behavioral defects in individuals in which the function of genes selectively expressed in specific brain regions of interest has been disrupted. Here, we focused on mKast, which is mainly expressed in a specific subtype (middle-type) of Kenyon cells in the mushroom bodies (MBs) and optic lobes (OLs) of the honey bee brain. We successfully produced homozygous mutant workers by crossing individuals whose genomes were edited by CRISPR/Cas9 targeting mKast. The function of mKast-expressing neurons was inferred from the localization of the mKast protein in the MBs and OLs, as well as from comparative analysis of honey bee and Drosophila OL single-cell RNA-seq data. Using mKast mutant workers and behavioral assays, including a newly established paradigm, we found that mKast is involved in bimodal learning and memory based on olfactory and visual information, direction-specific motion sensing, and survival outside the colony. Our findings suggest that mKast modulates brain function which are presumed to underlie the foraging ability of honey bees, and provide novel insights into the functional differences among three KC subtypes. Furthermore, our study demonstrates the usefulness of leveraging insights from Drosophila together with neuroanatomical knowledge from honey bees, to elucidate the roles of genes of unknown functions, such as mKast, in the honey bee.

Bee on time: investigating circadian clock gene function via gene editing in honey bees (Apis mellifera)

Katharina Beer[1]; Jana Seiler[2]; Felix Schilcher[1]; Laura Degirmenci[1]; Charlotte Helfrich-Förster[1]; Martin Beye[2]; Ricarda Scheiner[1]

[1] University of Würzburg, Biocenter; [2] Heinrich-Heine-University

Honey bees efficiently supply the colony by concertedly allocating foragers to flowering patches at correct times of daily flower blooming. The honey bee demonstrates a remarkable time memory enabling her to recall several time points per day and forage precisely at these times at affiliated flowering patches.

The circadian clock genes period (per), cryptochrome insect type 2 (cry2), Clock (Clk), cycle (cyc), par domain protein 1 (pdp1) and vrille (vri), build a Transcription-Translation Feedback Loop (TTFL), which drives circadian rhythms in behavior and physiology. Furthermore, in the complex neuronal clock network, the neuropeptide Pigment Dispersing Factor (PDF) conveys time information between the clock cells and brain regions involved in the regulation of downstream behavioral processes such as locomotion, sleep or learning and memory. However, functional analyses on honey bee clock genes are still largely lacking.

Via CIRSPR-Cas9, we introduced loss-of-function mutations of the clock genes per and pdf in honey bee worker eggs, thereby interfering with clock function on the central TTFL level and the output level of the clock, respectively. Accordingly, bees with biallelic frame-shift mutations in the target genes lost their ability to express behavioral rhythms under constant laboratory conditions, compared to in vitro raised control bees. Protein/peptide production was radically disturbed in these mutants, resulting in loss of antibody binding in whole mount brain immuno histochemical experiments.

Future studies with these clock mutant honey bees may provide a deeper understanding of time memory in honey bees and the function of the clock in their foraging behavior.

SYMPOSIUM 21 · Transgenic approaches for studying the biology of social insects
ORAL · Wed 19 Aug · 11:00 · K9 · Session 35 · Abstract ID 151039

Olfactory receptor mutants to tackle pheromone processing in the honey bee brain

Jean-Christophe Sandoz[1]; Julia Mariette; Gaëlle Claisse; Camille Faber; Lohan Valadares; Julie Carcaud[1]

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To ensure reproduction, animals must efficiently detect and process intraspecific cues, such as sexual pheromones. In this study, we ask how the brain of the honey bee, Apis mellifera, processes the single sex pheromone described in this species, 9-oxo decanoic acid (9-ODA), which triggers male attraction to virgin queens during mating. Previous work has shown that 9-ODA is detected by olfactory receptor AmelOR11, the most overexpressed receptor in male antennae compared to workers. It also activates a specific, enlarged glomerulus in the antennal lobe, called macroglomerulus 2 (MG2). This neuronal pathway is the only one described for the processing of 9-ODA within the male honey bee brain. To test whether it is exclusively responsible for male attraction, and to better understand how this pheromone is processed in the male brain, we generated AmelOR11 knock-out males using CRISPR-Cas9 genome-editing. In mutant males, no response to 9-ODA were found in their antennae using electroantennography and in their antennal lobe using in vivo calcium imaging recordings. Moreover, MG2 was absent or greatly reduced in the antennal lobe of KO males. Using a four-way olfactometer, we found that AmelOR11-KO males do not respond to this compound. However, in appetitive conditioning experiments, mutant males were still able to associate 9-ODA with a sucrose reward, revealing a capacity to detect 9-ODA. Thus, while the neural pathway involving OR11 and MG2 may be responsible for sexual attraction, other receptors and circuits enable the detection of 9-ODA in other contexts.

SYMPOSIUM 22 · Beyond-omics: new perspectives on social insect big datasets
ORAL · Wed 19 Aug · 16:45 · Halle 4 · Session 43 · Abstract ID 149181

What bee genes, caveman statistics, and learning machines can teach us about 'differential expression'

Benjamin Taylor[1]; Brock Harpur[2]

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The concept of 'differential expression' is fundamental to studies across a huge range of fields in biology, so why do we have no true consensus about what constitutes a 'differentially-expressed gene'? Alternate differential expression analysis methods can produce starkly different results. Does this indicate that some of our methods are wrong, or is it a reflection of the fundamentally arbitrary nature of differential expression? And what can we learn about biological reality from methodological inconsistency?

In this talk I'll discuss these questions in the context of honey bee transcriptomic data that my group has generated to explore the regulomic basis of caste evolution. I propose that the our inability to achieve a consensus across approaches does not constitute a failure of our methods, but rather an opportunity to more closely examine what it is that we are measuring when we examine gene expression; in other words, that we can only get to the right answers by asking the right questions. I'll further discuss the implications of our results for our understanding of honey bee social evolution.

SYMPOSIUM 22 · Beyond-omics: new perspectives on social insect big datasets
ORAL · Wed 19 Aug · 17:15 · Halle 4 · Session 43 · Abstract ID 150361

Haplodiploidy accelerates mito-nuclear coevolution

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Recent empirical work has shown that mitochondria and mitochondria-related nuclear genes show systematically higher substitution rates in haplodiploids than in diplodiploids. This could be for several reasons, and what is perhaps the most elegant one goes as follows. Since the autosomes of a haplodiploid are completely exposed to selection in males, newly arisen recessive alleles are under stronger selection than in closely related diplodiploids. This can indirectly increase the strength of selection on any mitochondrial genes that are coevolving with the autosomal genes. We construct mathematical models to test this idea, both on the microevolutionary timescale of a specific allele appearing and fixing in a population, and on the longer timescale of several substitution events. These results will shed new light on the landscape of selection pressures affecting many social insects, and produce predictions for how various aspects of their life-histories affect their rates of evolution. I will also use this collection of results to argue that mathematical modelling is a particularly powerful way to make sense of, generate hypotheses for, and thus utilise, big datasets.

SYMPOSIUM 22 · Beyond-omics: new perspectives on social insect big datasets
ORAL · Wed 19 Aug · 17:30 · Halle 4 · Session 43 · Abstract ID 146229

Transposable Elements in Ant Macroevolution

Lukas Schrader[1]; Janina Rinke; Mohammed Errbii; Scott J. Teresi; Esther van den Bos; Zijun Xiong; Joel Vizueta; Jacobus Boomsma; Jürgen Gadau; Guojie Zhang

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Transposable elements (TEs) are key contributors to genome evolution, yet their macroevolutionary role in the adaptive radiation of the ants remains poorly understood. We analyzed 163 ant genomes spanning 12 of 16 extant subfamilies to characterize TE impacts over the past 100 million years. We identify convergent TE bursts in ancestors of the most speciose ant clades, preceding rapid diversification following the Cretaceous–Paleogene extinction event approximately 66 million years ago. We demonstrate that TEs associate with expansions of olfactory receptors and other key gene families, and reveal striking compartmentalization of ant genomes into faster-evolving TE-rich and more conserved TE-poor regions. Our findings demonstrate the broad-scale impact of TEs on ant genome evolution and their particular impact on the diversification of the chemical communication systems.

A transcriptomic catalog of two leafcutter ant pests, Atta sexdens and Atta laevigata

Milene Ferro[1]; Karine Felix Ribeiro[1]; Paula Maria Moreira Martins[1]; Cynara de Melo Rodovalho[2]; **Mauricio Bacci[1]**

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Leafcutter ants of the genus Atta are economically important herbivores whose pest status has motivated genetic and physiological studies. However, comparative information on coding sequence variation between closely related Atta species remains limited. Here, we present a descriptive comparison of orthologous coding sequences identified from de novo transcriptomes of Atta sexdens and A. laevigata. A total of 252 shared orthologs were recovered, of which 147 exhibited 80–99.9% nucleotide identity, and 105 were identical between species. Annotation analyses revealed that the two groups differ in the number and distribution of Gene Ontology terms, InterPro domains, and enzyme classifications, with the variable set containing a broader diversity of annotated catalytic and metabolic features. Conserved genes exhibited a narrower annotation profile, enriched for structural and general cellular functions. Several genes contain domains that, in other insects, are associated with processes targeted by existing insecticides or involved in detoxification, development, or cuticle formation. These associations are annotation-based and provide a catalog of 16 candidate gene targets for future experimental investigation into molecular insecticides and subsequent functional, ecological, and applied research. Our study refines a previous broad candidate list into a smaller, higher-confidence set of genes relevant to leafcutter ant biology and future pest-management research. These foundations are essential given the recent regulatory restrictions on widely used chemical insecticides for leafcutter control.

Combining genomic and transcriptomic approaches to unravel the evolution of a supergene underlying wing and social polymorphisms

Romuald Laso-Jadart; Elise Gay; Joshua Ducancel; Pascaline Chifflet-Belle; Stefano Mona; **Claudie Doums**

EPHE-PSL, ISYEB

Recombination suppression through large genomic inversions contributes to the evolution of complex phenotypes. By locking together combinations of genes, a supergene prevents the production of unfit intermediate phenotypes. However, recombination suppression is expected to limit purifying selection, leading to the accumulation of repetitive elements and deleterious mutations in the derived haplotype. To investigate the evolutionary dynamics of inversions, we combined genomic and transcriptomic approaches to study a social supergene (monogyny vs. polygyny) associated with a wing polymorphism (apterous vs. winged queens) in the ant Myrmecina graminicola.

We assembled the genomes of one male from each supergene haplotype, the ancestral Mo and the derived Pa, using long-read sequencing and Hi-C data. The alignment highlighted two large inversions (6.5; 13.6 Mb) and an increase in repetitive elements in Pa. Whole-genome resequencing of 118 individuals revealed an origin of both inversions approximately 1 MYA B.P., with Pa exhibiting slightly higher mutation load than Mo.

Transcriptomic comparisons between 10 monogyne and 10 polygyne queens identified 29 differentially expressed genes. Of these, 18 were located within the supergene and were overexpressed in polygynes, including five genes absent in monogynes. Sequencing depth analyses revealed signatures of gene duplications from other autosomes for these five genes, including a strong candidate gene involved in the inhibition of wing development, awing.

Together, these results support a recent origin of the social supergene and highlight an alternative route to phenotypic divergence, driven by the capture of functional elements through gene duplication into non-recombining regions rather than by differential gene expression.

Complex effects of climate on bumblebee fitness

Ruth Archer[1]; Paul Schmid-Hempel; Regula Schmid-Hempel; Lena Wilfert

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Climate change is a growing and global biodiversity threat. To assess how species will respond, there is a need to establish how variation in climatic conditions affects individual life-history traits (e.g. growth, survival and reproduction). These data will help us understand how a changing climate might affect individual fitness and what mechanisms could be responsible. Not surprisingly, climate can have complex effects on life history traits. Long-term data linking insect life-histories and climate parameters are therefore particularly valuable but none-the-less, rare. Here, we focus on a key European pollinator, the buff-tailed bumble bee Bombus terrestris, to test how climatic variation affects health, survival and reproduction in this model species. We relate climatic variation experienced by developing queens in the field, caught between 2000 and 2014, to fitness traits assayed in these queens under otherwise constant lab conditions. We show that wet years consistently reduced queen fitness, while warm temperatures had positive as well as negative impacts. Behind these annual effects, lies strong seasonality. In particular, climatic conditions experienced by young queens as they forage, mate and enter hibernation are vital in determining whether they reproduce the following spring. Results suggest that climate effects are partly due to resources: climatic drivers that reduce resource acquisition prior to hibernation, or disrupt diapause and thus accelerate resource loss over winter, are especially detrimental to spring queen fitness. This result suggests a strategy to mitigate the negative effects of climate change is ensuring high-quality forage late in summer before queens enter diapause.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Mon 17 Aug · 10:45 · K7 · Session 3 · Abstract ID 145911

Ant behaviour in the Anthropocene: A meta-analysis of human-induced environmental change effects on ant behaviour

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Determining how recent and ongoing global changes will impact species is a key challenge facing modern biology. In particular, an important issue is investigating the extent to which species are able to cope with human-induced rapid environmental change (HIREC). Physiological and morphological changes caused by HIREC have been extensively evaluated in recent years, but the impact on behaviour has received less attention. This is quite surprising, given that changes in behaviour are often the first adaptive response to environmental disturbances, and can therefore be quickly detected. In (eu)social species, like ants, this behavioural plasticity can occur both at the individual and colonial level. Furthermore, due to their remarkable geographical distribution and therefore different exposures to human changes, ants are an ideal model to quantify the effects of HIREC on behaviour. We thus performed a systematic literature review on the effect of HIREC on ant behaviour. We used strict guidelines and an artificial intelligence-aided meta-analysis protocol. Of the 1394 studies assessed from the original WoS search, 52 were included in the qualitative and 45 in the quantitative analysis. We highlighted a bias towards studies assessing temperature increase and focusing on foraging behaviour. Considering the different behaviours observed, we found no general pattern, but positive and negative effects associated with specific types of disturbance (e.g. a negative effect of habitat degradation and drought on mutualistic interactions). We discuss the significance of our results, emphasising the necessity to extend and diversify studies on ant behaviour in response to global changes.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Mon 17 Aug · 11:00 · K7 · Session 3 · Abstract ID 144796

Asphalt Ecology: Trait Syndromes Behind Urban Ant Success

Clint Penick

Auburn University

Alongside pigeons, rats, and cockroaches, ants are among the most common urban animals —yet only a small fraction of the world's 15,000 species thrives in cities. Many of these have spread globally with humans and evolved into urban specialists, but the traits underpinning their success remain poorly resolved. Drawing on 15 years of research in New York City, a model system for urban ant ecology, this talk synthesizes emerging patterns across behavioral, physiological, and life-history traits. Comparative work across NYC's parks, streetscapes, and sidewalks reveals how traits linked to supercoloniality, tolerance of urban heat, nesting flexibility, and shifts in diet and foraging behavior contribute to urban success. Together, these insights help clarify what defines an "urban ant," highlighting a blend of pre-adaptations and plastic responses that repeatedly characterize successful city-dwelling species. By integrating case studies from New York City with broader comparative perspectives, this work identifies common trait syndromes shared by thriving urban ants while also capturing the diversity of strategies that enable ants to flourish in human-dominated environments.

Effects of environmental features on social insects: from species and communities to ecological processes

Sabine Nooten

University of Wuerzburg, Germany

Social insects are an essential part of global biodiversity. They contribute to terrestrial food chains and perform key ecosystem services. They are also sensitive to changes in their environment. I am using social Hymenoptera (ants and bumblebees) as model organisms to tackle questions related to global patterns, species traits, and key ecological processes at different scales. On the global scale, my research shows that there is large variety in the sheer numbers and densities of insects across biomes, regions and habitats. On smaller scales, regional communities are associated with land use types and habitat features. In climatically challenging environments, only species with a specific suite of traits can persevere. Given the current loss of insect biodiversity in terms of species richness and abundance, it is vital to understand the relationships between insect species, their functional roles and their resilience to environmental change.

Termite abundance and species distribution along an altitudinal gradient in northern Morocco

Aya NAJJARI[1]; David Hernández-Teixidor[2]; Ahmed Taheri[3]

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Altitude is a key environmental gradient influencing insect communities, yet its effects on termites in Mediterranean ecosystems remain poorly documented. This study assesses how termite abundance, species distribution, and microhabitat preferences vary along an altitudinal gradient in northern Morocco. Field surveys were conducted at nine forest sites ranging from 125 to 1700 m a.s.l. in the western Rif Mountains, most of them located within the Intercontinental Biosphere Reserve of the Mediterranean. Termites were sampled using standardized active-search transects across four microhabitats: under rocks, dry dead wood, dead trunks, and buried dead wood. Abundance was estimated as encounter density, and species were identified morphologically. Statistical analyses were used to evaluate relationships between altitude, termite density, and microhabitat preferences. Three species were recorded: Reticulitermes grassei, Kalotermes flavicollis, and Amitermes sp. Overall termite density decreased significantly with increasing altitude. Reticulitermes grassei was present across the entire gradient and showed no significant relationship with elevation, indicating broad ecological tolerance. In contrast, K. flavicollis and Amitermes sp. were restricted to low and intermediate altitudes and exhibited strong negative relationships with elevation. Microhabitat preferences also shifted along the gradient, with buried dead wood dominating at low elevations and stone-associated or standing dead wood becoming more frequent at higher elevations.

Microclimates as thermal refugia: behavioral plasticity in wood ants under climate change

Cleo Bertelsmeier[1]; Olivia Bates[2]; Anne Freitag[3]; Aymeric Bonnamour[4]; Sébastien Ollier[5]

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Ongoing global climate change has already profound impacts on species' distributions and ecosystems and is predicted to become a leading driver of species extinctions in the future. So far, progress has been made in forecasting future large-scale scenarios of climatic conditions and in developing predictive models of species responses to these future climates. However, small-bodied organisms such as ants, experience climatic variations as fine-scale thermal mosaics and not at the large scales of several kilometers that are typical of these forecasts. In temperate woodlands, microclimates can differ by more than 30 °C within a single day, potentially offering refugia against macroclimatic extremes. To test this buffering capacity, we monitored 76 colonies of wood ants (Formica paralugubris) across a macroclimatic gradient and diverse microclimates over three years. We quantified nest temperatures at multiple depths, surrounding soil and air temperatures, solar radiation on nest domes, and surface activity patterns over time. This multi-scale approach revealed pronounced behavioral plasticity: colonies adjusted foraging and nest positioning to maintain favorable thermal conditions under different macroclimates. Our findings demonstrate that microclimatic heterogeneity enables effective thermoregulation, highlighting its role as a climatic microrefugium. Integrating such fine-scale complexity into predictive models is essential for understanding social insect persistence under global warming.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Mon 17 Aug · 12:00 · K7 · Session 3 · Abstract ID 147417

Socio-ecological Priming of Heat Stress Responses in a Facultatively Eusocial Bee

Ren Weinstock; Karen Kapheim
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Climate change is altering thermal environments worldwide, with important consequences for the stability of social insect systems. Social bees are often more heat tolerant than solitary species, potentially due to division of labor that buffers physiological stress. Yet, how temperature mediates social behavior and physiology across ecological contexts remains poorly understood. Facultatively eusocial species provide a powerful framework for addressing this question, as their social strategies are environmentally contingent. We investigated how heat stress responses vary across socio-ecological environments in three populations of the facultatively eusocial sweat bee Halictus rubicundus. While ecological drivers of social variation in this species are well described, the physiological and molecular mechanisms underpinning this plasticity are largely unknown.

We hypothesized that heat shock proteins (Hsps) are primed by the socio-ecological environment and serve as a mechanistic link between thermal stress and social behavior that will shape bee responses to climate change. Bees from each population were exposed to acute (4 h) and chronic (48 h) heat stress, after which we quantified changes in aggression and expression of heat shock proteins in the brain. We predicted that heat stress will increase aggression, with population-specific patterns of Hsp expression mediating divergent relationships between behavior across environments. By integrating behavioral and molecular responses, this work links thermal ecology to social evolution and plasticity, providing insight into how climate change may reshape social organization and resilience in bees.

Infrared thermal ecology and evolution of ants and their prospects of climate resilience

Terry McGlynn[1]; Megan Barkdull[2]; Kaitlin Baudier[3]; Clint Penick[4]; Allison Shultz[2]

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As the planet continues to heat up, organisms are experiencing greater thermal stresses. Ants are particularly at risk because foraging often places them in direct exposure to sunlight, which results in the absorption of thermal radiation in visible and near-infrared wavelengths. One mechanism available to ants is using the cuticle to reflect away solar radiation. Here we report on a series of experiments testing the capacity of ants to reduce heat gain by reflecting near-infrared radiation, quantitatively revealed by multispectral photography. We test within and among species whether there is evolutionary potential for ants to evolve greater infrared reflectivity on temporal and spatial scales that are responsive to climate change. By evaluating reflectivity of the full solar spectrum and particularly within the near-infrared across latitudinal and elevational gradients, comparing differences among castes, and across behavioral traits and contrasting life histories, we assess the significance of near-infrared reflectivity for the thermal budgets of ants and the prospects for biological conservation in light of climate change. We demonstrate there is extraordinary variability in near-infrared reflectivity in ants, attributable to microscale features of the cuticle, that are responsive on short-term evolutionary time scales and indicate that this is a highly adaptive trait for ants, that is literally invisible to our eyes but critical for their functional biology.

Distribution and thermal tolerance of two wood ant species and their hybrids in Southern Bavaria.

Adriana Crhonková; Florian Nebel[1]; Jonna Kulmuni[2]; Patrick Krapf[2]; Richard Merrill[1]

[1] LMU Munich; [2] University of Amsterdam

Thermal tolerance, the ability to withstand temperature changes, is a crucial trait in assessing species' vulnerability to climate change. European mound-building Formica wood ants, forest keystone species and ecosystem engineers, provide a suitable model for studying thermal limits and the potential role of hybridization in adaptation to a changing climate. While extensive hybridisation has been observed in Southern Finland, the extent of hybridisation in Southern Bavaria remains mostly unexplored. In this study, we aim to fill this geographical knowledge gap by assessing the species distribution along the hybrid zone and determining the hybrid ancestry using whole-genome sequencing. Further, we focus on thermal tolerance of two species, F. aquilonia and F. polyctena, and their hybrids. To compare their thermal limits, we test whether elevation and/or species identity predict their thermal tolerance using heat knockdown test (HKT) and chill coma recovery test (CCRT). I will present our results in comparison to findings from Southern Finland, highlighting the importance of geographical context in shaping the outcomes of hybridization.

Thermoregulatory mechanisms in termites and its effects on termites' distributions on some species of termites found in the savannah.

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Termites are known for their abilities to regulate the conditions within their nests through the mounds that they build or the location of the built mound which assist in keeping the internal temperature within the requirement of the colony. Temperature plays a crucial role in regulating the abundance, distribution, and diversity of termite species. Consequently, termites are highly sensitive to climate change and must adopt various adaptive strategies to avoid extinction. The mechanisms to regulate vary between species, with some species adapting passive behaviours such as nest site selection and nest structures that permit passive heating or cooling. Here we studied seven species of mound building termites from five genera in two different savannah and determined some of their passive thermal control strategies. Seven species of termites; Amitermes sp., Cubitermes oculatus, Macrotermes bellicosus, M. subhyalinus, Odontotermes sp., and two species of Trinervitermes were identified from the two savannah ecosystem. We found no significant difference in internal mound temperatures between the species. In both savannah types most of the termites built their nest under the shade. We discuss the adaptive implications of building mounds under the shades as seen in species of M. bellicosus, M. subhyalinus and Odontotermes sp. Or those building mounds with unique shapes as seen in C. oculatus with mushroom shaped mounds for their roles in thermal regulation within the nest and how this represents a response to environmental conditions.

Niche and spatial segregation define the distribution of sympatric red wood ant species

Elia Nalini[1]; Felix Puff[1]; Marco Mina[1]; Carlo Polidori[2]; Julia Seeber[3]; Elia Guariento[1]

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Interspecific competition is a key ecological and evolutionary mechanism shaping the spatial structure of communities. To minimise competition, species often differentiate their environmental niche and/or avoid co-occurrence (i.e., niche partitioning and spatial segregation). These mechanisms are particularly pronounced among closely related species, which typically share similar ecological requirements, and in social insects, which are usually site-bound and consist of numerous individuals. An example of evolutionarily recent species is the Formica rufa species - group (red wood ants), which includes highly competitive species. Using Ensemble of Small Models at regional scale, we tested how niche differentiation and spatial segregation influence the distribution of red wood ants. Our results indicate that both niche and spatial segregation shape species occurrence in a different manner depending on the species considered. Syntopy (local co-occurrence within 100m) was rare among the five sympatric red wood ant species. Three species (Formica rufa, F. polyctena, and F. pratensis) exhibited clear niche segregation, whereas others (F. lugubris and F. aquilonia) shared similar environmental preferences. Regional coexistence thus emerged both through reduced niche and spatial overlap and through contrasting life-history strategies—some species being more competitive, others more dispersive. By integrating niche and spatial segregation analyses, our study clarifies the main mechanisms influencing the Formica rufa group occurence and provides a solid baseline for anticipating how these socially complex and ecologically important insects may respond to future climatic changes.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Mon 17 Aug · 15:30 · K7 · Session 9 · Abstract ID 146772

Interactions between wood ants and bark beetles: Eco-evolutionary implications on forest ecosystems

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Mound-building wood ants and bark beetles are keystone species in temperate and boreal forests. Under certain conditions, they can have large-scale impacts on these ecosystems and are thus regarded as ecosystem engineers. Wood ants contribute to seed dispersal, plant decomposition, predation, or soil bioturbation, influencing nutrient cycling, food webs, and vegetation cover. Bark beetles are among the first colonisers of dying or recently dead plant material, and thus important for decomposition of plant biomass, but a small number of species has the capacity for eruptive outbreaks, leading to forest mortality on a landscape scale. Here, we will highlight interactions among these common insect groups and discuss the effects of environmental conditions and changes on their ecological and evolutionary success. We will discuss how wood ants and bark beetles shape forest ecosystems, how this affects their immediate habitats, and how they impact the population dynamics of each other, creating 'feedback loops'. Furthermore, we will discuss the effects of anthropogenic changes, including habitat fragmentation, increasing temperature, or drought on wood ants and bark beetles, their reciprocal interactions, and cascading effects on forest ecosystems. Alterations of ecosystem processes will also have downstream effects on biodiversity and ecosystem services, including societal and economic impacts.

Drought events reduce reproductive success of a long-tongued bumblebee species

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Climate change challenges pollinators through rising temperatures, altered precipitation regimes and an increased frequency of extreme weather events. Drought events are becoming more frequent and severe, with largely unknown effects on pollinator fitness and associated ecosystem services. In a large-scale field experiment, we compared bumblebee colony performance of a long-tongued non-commercially bred bumblebee species between a drought year and a year with average climatic conditions. Colonies established from wild queens were placed in 25 high-quality semi-natural grasslands and either received sugar-water supplementation or not to evaluate resource limitation effects. Colony lifespan was shorter in the drought year, and both colony weight and reproductive output (male and queen numbers) were strongly reduced. Sugar-water supplementation enhanced male production and colony weight only during drought, suggesting that nectar scarcity limits colony performance to some extent during dry periods. However, queen production was unaffected and fed colonies performed much worse during drought, implying that pollen is crucially drought-limited. We conclude that increasingly frequent droughts pose a major threat to bumblebee populations and the pollination services they provide, even in flower-rich protected areas. Adaptive conservation management could enhance tree shade in open grasslands and promote wetlands for extended water retention during drought events.

Impact of heat waves on colony foundation in ants

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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.

The sand termite Psammotermes allocerus shows extraordinary resilience in the extreme environment of the Namib Desert

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Termites play a crucial role in ecological processes, especially in extreme environments. The desert-adapted sand termite Psammotermes allocerus Silvestri, 1908 (Neoisoptera: Psammotermitidae stat. n.) exemplifies how complex social insect structures and ecological engineering enable survival and resilience in harsh conditions. In the hyper-arid Namib Desert this species accomplishes this, by creating and maintaining fairy circles. The termites remove plants through local herbivory on stems and roots, leading to the formation of a ring of tall long-lived grass tussocks around a bare inner area. This activity was observed using web cameras and personal observations. The bare patch remains free of vegetation due to these activities and the inhibitory effects of their symbionts. Soil moisture measurements beneath the bare patch and adjacent matrix vegetation were conducted to investigate the water storage. The removal of plants leads to a reduction in soil moisture loss in the bare patch. The polydomous nest structure and the tunnel system within and between neighboring fairy circles were excavated and documented to understand adaptations of the colony to scarce water availability and environmental changes. In the desert, this species secures the long-term storage of rain-water, facilitates the perennial persistence of its own colony, other subterranean insects, and surrounding plants and fauna. In areas with MAP above 150 mm, sufficient water is available without the necessity to create fairy circles. Our studies provide insights into how a termite adapted to aridity. This provides an example of how eusocial insects may cope with future climate trajectories.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Tue 18 Aug · 10:30 · K7 · Session 15 · Abstract ID 145508

Impact of Thermal Stress on Early Colony Behavior in the ant Lasius niger

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Global warming negatively affects organisms, from molecular processes to behavior. Social insects are particularly vulnerable because their body temperature depends on environmental conditions. We experimentally investigated the effects of thermal stress (1) on nest excavation by Lasius niger queens and (2) on foraging by incipient colonies. Founding queens were placed alone or in groups of three queens in 2D nests and exposed to mild, medium, or high soil surface temperatures, allowing us to evaluate how temperature influences both the speed and depth of nest construction. Incipient colonies were subjected to heat stresses of varying duration and intensity. For short stresses, colonies were reared at 25 °C:20 °C (day:night) and foragers were exposed for 10 min or 1 h at 25 °C (control), 30 °C, 35 °C or 40 °C. For chronic stress, colonies were reared for two weeks at 25 °C:20 °C (control) or 35 °C:30 °C. We measured the latency to start foraging and the number of foraging trips immediately after these stresses. In agreement with the Thermal Death Time (TDT) and Thermal Load Sensitivity (TLS) frameworks, we predicted that a mild or short heat stress would have minimal effects on excavation and foraging, whereas an intense or prolonged stress would increase nest excavation and decrease foraging (or delay it when possible). Our findings support these predictions and provide insights into how thermal stress shapes early colony dynamics, nest establishment, and behavioral plasticity in ectotherms under climate change scenarios.

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

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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.

Quantifying the impacts of cold snaps on bumblebee colonies

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Extreme climate events (ECEs) are increasing in frequency and intensity with human-induced climate change. Research has predominately focused on heatwaves, but other ECEs such as sudden cold snaps are also expected to intensify yet remain comparatively understudied. This is particularly important for pollinators, whose vulnerable life stages in early spring may coincide with such events. Bumblebees, for example, are initiating colony development during this period with a single queen supported by only a few worker bees, limiting their ability to buffer against extreme temperature changes due to a small work force. Yet despite this vulnerability, little is known about how cold snaps influence their early colony growth and foraging behaviours. Here, bumblebee (Bombus terrestris) colonies were exposed to either a simulated cold snap regime or a typical spring control, both derived from UK climate data with diurnal temperature cycles and then transferred to flight cages provisioned with mass-flowering Phacelia. We monitored how this shaped subsequent foraging behaviour and colony development using RFID-assisted tracking and behavioural observations. Cold snap exposure led to reduced individual foraging behaviour and impaired early colony development, with effects extending beyond the exposure period. Over time, colony responses shifted, with indications of recovery emerging later in the season. Together, these findings highlight spring cold snaps as an overlooked but ecologically important component of climate change, with implications for pollinator vulnerability and resilience under increasingly variable climates.

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ORAL · Tue 18 Aug · 11:15 · K7 · Session 15 · Abstract ID 145471

Behavioral responses of Argentine ants to changes in climatic factors

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To predict the likely impacts of climate change on social insects, it is imperative to develop a thorough understanding of how individuals and colonies respond to changes in climatic factors. Here, we examine quantitatively how temperature and relative humidity interactively influence the performance of key social traits of ants (e.g., interaction rate, movement speed). We further examine the extent to which colonies of the same species from different environments differ in their social behavior as a result of adaptation to local climatic conditions. We sampled Argentine ants (Linepithema humile) from several locations spanning a climatic gradient across California. We then exposed each colony to 10 combinations of temperature and relative humidity and recorded colony behavior. These experiments generated high-resolution trait performance datasets, which we analysed using novel temperature-humidity performance surface models. Our results provide key insights into how social traits respond to climatic factors, how such responses differ across environments, and how climate change may alter the geographical range of this highly invasive species.

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ORAL · Tue 18 Aug · 11:30 · K7 · Session 15 · Abstract ID 145983

Foraging activity, cuticular hydrocarbons and water stress management in the red harvester ant

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We examined how the collective behavior that regulates foraging activity to manage water loss is associated with the cuticular hydrocarbons (CHC) of the red harvester ant, Pogonomyrmex barbatus. Colonies must spend water to obtain water and food, because foragers lose water through evaporation while searching for food, but obtain water by metabolizing the fats in seeds. An outgoing forager decides to leave the nest on its next trip based on its olfactory interactions with returning foragers, a cue to food availability, and its recent experience of current humidity conditions.

Our project draws on a long-term study that has monitored since 1988 a population of colonies through their 20-30 year lifetimes, at a site in the southwestern United States in intensifying drought conditions. Colonies differ consistently in how they regulate foraging on dry days. In risk-averse (RA) colonies, foragers make fewer foraging trips on dry days, sacrificing food intake to save water. Risk-tolerant (RT) colonies do not reduce foraging on dry days.

A comparison of CHC profiles shows that RA colonies have a higher abundance of n-alkenes in their CHC profiles than RT colonies, making them more sensitive to water loss. In laboratory experiments, we exposed workers to a range of different temperature and humidity conditions, We will discuss how RA and RT colonies, which differ in the regulation of foraging behavior, also differ in their capacity to adjust CHC profiles, and the effects on survival and water loss rates.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Tue 18 Aug · 11:45 · K7 · Session 15 · Abstract ID 146344

Effects of high ground temperature on learning behaviour of Camponotus aethiops ants

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In our rapidly changing world, organisms are increasingly exposed to high temperatures. While elevated temperatures have been shown to impair learning in vertebrates, including humans, their effects on insect cognition are not well understood. Learning enables animals to respond adaptively to environmental stimuli, for example by forming predictive associations between environmental cues that guide decision-making and enhance survival. We investigated whether associative learning abilities are impaired when ants forage at high ground temperature in Camponotus aethiops, a Mediterranean species inhabiting xerotherm grasslands. Freely-walking individual ants underwent a differential conditioning task. At the edge of a circular arena, three odorants were presented, of which one (CS+) was rewarded with sugar and two (CS-) were not. The task comprised four training trials followed by a single unrewarded memory test. The substrate temperature was maintained at 25°C, 30°C, or 35°C throughout the task. Ants trained at 25°C and 30°C decreased their latency to find the reward across the training trials, while no such improvement was observed in ants at 35°C. During the memory test, ants from all three temperatures spent more time near the CS+ zone compared to the CS- zones. However, ants from the 35°C treatment spent overall less time near the odour zones. Naïve ants tested in an open-field without reward covered greater distances at 30°C than at 25°C or 35°C, indicating that locomotor differences are unlikely to explain the differences observed in learning behaviour. We conclude that a temperature of 35°C negatively impacts ant learning behaviour while not impairing it.

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ORAL · Tue 18 Aug · 12:00 · K7 · Session 15 · Abstract ID 148635

Monitoring behavioural markers of environmental stress: the case of Fukushima bees

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CNRS

In March 2011, a 15-meter tsunami struck the Fukushima Daiichi nuclear power plant, causing a nuclear accident. Massive releases of cesium, a radionuclide with a half-life of 30 years, permanently contaminated the soil, and several areas are still designated "exclusion zone." Our research, in collaboration with the University of Fukushima, explored the sublethal impacts of environmental radio-contamination on social insect pollinators and predators. Here I report a series of innovative field experiments demonstrating morphological, behavioral and cognitive impairments of managed honey bees (Apis mellifera) and wild giant hornets (Vespa mandarinia) exposed to various levels of low radio-contamination doses in the Fukushima area. Altogether, our results suggest that the legacy cesium contamination profoundly impact social insects, with potential deleterious effect on ecosystem services more generally through impaired key ecological interactions. Our work emphasizes the importance of developing field-tractable behavioral markers of sublethal stress, for environmental monitoring, conservation efforts and public health.

New and rapid techniques to uncover the macrophysiology of European ants

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A key issue for 21st century ecologists is to predict which species will move, adapt, or die in the face on ongoing global climate change. The field of macrophysiology is important here as it seeks to investigate the general relationships between organismal traits - such as thermal tolerance and performance - and the environment. Currently, however, we hampered by a lack of quality data with which to ask macrophysiological questions. Here, we attempt to remedy this for European ants by using a new technique based on infrared beam detections to quickly, easily, and relatively cheaply construct thermal performance curves for over 50 species spread from Spain to Sweden. Our analyses linking these thermal performance curves to current and future temperatures, as well as to an ant phylogeny, reveal three key findings. First, the variability in ant performance curve shape suggests a classic trade-off between thermal specialists and generalists across the continent. Second, the end points of the curves, but not their shape, are phylogenetically conserved. This indicates that ant species could adapt to warmer climates by shifting the temperatures under which they are most active. Third, climate forecasts up the year 2100 show that the release from low temperatures is likely to be a large factor in driving the potential reorganisation of European ant communities over the next 75 years. These results emphasise the need to use alternative data collection techniques to achieve macro-scale understanding, and of the importance of monitoring changes in both minimum and maximum temperatures.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Tue 18 Aug · 15:00 · K7 · Session 21 · Abstract ID 149028

Nutrition as a modulator of thermal tolerance in ants under climate change

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Anthropogenic climate change increases both mean temperatures and thermal extremes, challenging ectotherms such as ants. At the same time, global change is profoundly altering the availability and composition of nutritional resources. Yet, nutrition remains largely overlooked as a driver of thermal tolerance and, consequently, of species responses to climate change. Here, we investigate how dietary composition modulates critical thermal limits (CTmax and CTmin) in ants, integrating nutritional ecology with thermal physiology. Using controlled laboratory experiments, we exposed colonies of different ant species to contrasting diets differing in macronutrient composition and to different thermal regimes. We quantified thermal tolerance under these conditions and explored how dietary effects interact with temperature, trophic level, life stage, and duration of dietary exposure. Our results indicate that diet composition can substantially modulate both heat and cold tolerance in ants. Importantly, these effects are context dependent: the magnitude and direction of dietary effects vary with temperature, species trophic ecology, developmental stage, and exposure time. This suggests that nutrition does not act as a simple energetic buffer, but instead interacts with thermal stress through multiple physiological pathways. Candidate mechanisms include the synthesis of heat-shock proteins, lipid accumulation and membrane remodeling, and the activation of key metabolic enzymes. By showing that thermal limits are nutritionally plastic, our study identifies nutrition as a key driver of ant resilience to climate change, with implications for predicting species responses to warming, extreme events, and cascading effects from physiology to communities and ecosystem functioning.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Tue 18 Aug · 15:15 · K7 · Session 21 · Abstract ID 149057

The thermal biology of a giant: Heat tolerance and metabolic rate in Dinoponera quadriceps (Formicidae: Ponerinae)

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Global warming has caused significant impacts on animal survival and distribution. Temperature is a key physiological and behavioural modulator in ectotherms, including ants, which perform essential ecosystem functions. In this study, we investigated the heat tolerance of Dinoponera quadriceps, an important seed dispersal ant native to the Brazilian Atlantic Rainforest, where it has been observed foraging at air temperatures close to 40 °C. We evaluated the effect of thermal stress on survival and metabolic rates under heat exposure in four colonies, acclimated at 25 ± 1 °C in the laboratory. Individuals were subjected to high-temperature challenges (44–50 °C) to assess loss of righting response (LRR) and subsequent mortality. To evaluate heat tolerance, we estimated the critical thermal maximum at which the animal exhibited LRR after one minute (CTmax(1min)) and 1 hour (CTmax(1h)). In addition, we evaluated individuals' metabolism using closed-system respirometry to measure the volume of CO_2 produced at control (25 °C) and experimental temperatures (44-50 °C). The results revealed a strong negative effect of temperature on D. quadriceps survival. The CTmax(1min) and CTmax(1h) of the individuals were 63.2 °C and 36.8 °C, respectively. Respirometry analyses showed a strong positive correlation between temperature and CO_2 production, reaching an estimated peak at 57.6 °C, after which it presumably declined, likely due to physiological failure. This study is the first to characterise the physiological capacity of D. quadriceps to cope with thermal stress and provides insights into how social insects may respond to global warming.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Tue 18 Aug · 15:30 · K7 · Session 21 · Abstract ID 149790

"You're all individuals": quantifying inter- and intraspecific responses to climate to predict bumblebee thermal niches and their interactions with plants

Richard Gill
Imperial College London

Predicting insect responses to climate change requires a combined understanding of the direct impacts, such as a population's thermal limits, and the indirect impacts, such as how temperature mediates the trophic/mutualist interactions they depend on. An increasingly recognized approach to developing a predictive framework is to apply trait-based methods, such as using aspects of morphology to determine species responses. To date, however, species are often assigned mean trait values, overlooking how intraspecific trait variation is being shaped by climate and how it maps across ecological interactions. This represents a particular issue for the study of social insect responses, since evolved strategies such as polyethism are considered important in adapting to environmental challenges. In this presentation, I will present findings from an ongoing long-term field study (8+ years) of a montane Arctic community. Focusing on a bumblebee community, this project links how the morphology of every individual in the community maps to each respective host plant interaction (>6K observations) across a microclimate (temperature) gradient. I demonstrate the importance of considering intraspecific trait turnover in space and time, and how using a thermal trait-based framework using microclimate helps understand bumblebee and plant interaction likelihoods and network robustness under climatic change.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Tue 18 Aug · 15:45 · K7 · Session 21 · Abstract ID 141492

A. mellifera CHC profiles respond to the environmentally driven desiccation pressure

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Cuticular hydrocarbons (CHCs) form a waterproof coating on the surface of insects' cuticle, protecting them from desiccation by minimizing transpiration. Insects can acclimate to novel temperature and humidity conditions by changing their CHC composition, improving their tolerance to the environmentally exerted desiccation stress. Apis mellifera has diverged into several subspecies with geographically restricted distributions. These subspecies need to cope with the environmental conditions within their native distribution ranges and exhibit distinct CHC profiles. Here, we performed a reciprocal transplant experiment to investigate whether the plasticity of the CHC profiles of A. mellifera in response to distinct environmental conditions is adaptive. We assessed the CHC composition and the expression of specific desaturase- and elongase-encoding genes in A. m. carnica and A. m. iberiensis nurse and forager bees. We present evidence that the CHC profiles of honey bee workers vary in response to the environmental desiccation stress. This effect was stronger in forager bees than in nurse bees, probably due to the higher desiccation stress faced by the forager bees when flying outside of the hive. The absence of a correlation of the expression of the assessed CHC biosynthesis-related genes and the location-specific CHC compositions suggests that the difference in CHC composition between locations is also influenced by other biosynthesis-related genes or emerges as the result of the interaction of several biosynthesis-related genes.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Tue 18 Aug · 16:00 · K7 · Session 21 · Abstract ID 149758

If You Can Make it There, You'll Make it Anywhere: Social Insect Adaptation to Urbanization from the Perspective of Native and Invasive Species

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Extreme urbanization is characteristic of growing global populations. Urbanized environments like New York City can provide novel habitats where species must rapidly adapt to stressors including pollution, habitat fragmentation, and urban heat island effects. In the face of climate change, urban heat islands provide opportunities to study the influence of extreme weather on insect behavior, physiology, social structure, and the molecular mechanisms of adaptation to changing temperatures. Social insects are a key component of urban environments; several bee species such as Bombus impatiens and Apis mellifera are important pollinators in urban greenspaces, and notable invasive ant species, such as Tetramorium immigrans and Lasius emarginatus are documented to thrive in urban spaces. Studying social species in Manhattan provides an avenue to study adaptation to urban stress in a social context of both native and invasive species to understand how some species compete and establish in these environments. In this study, four social insect species were collected across lower Manhattan during three seasons and during extreme heatwaves. We utilized both qPCR and comparative transcriptomics to identify which genes may be important in adapting to both novel environments and extreme heat events. Additionally we analyzed protein sequences from a notable heat shock protein, Hsc70-4 from 30 Hymeopteran species to draw conclusions about the role of this gene in the ability for species to overcome extreme temperatures. Research in this system can provide information as to how insects can adapt to urbanized environments, to develop novel strategies in conservation and management.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Tue 18 Aug · 16:15 · K7 · Session 21 · Abstract ID 149861

Simulated heatwaves differentially impact bumblebee sucrose responsiveness and memory

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Bumblebees are essential pollinators. Climate change is influencing bumblebee populations, with some species expected to lose ~30% of their ecologically suitable habitat by 2061. In addition, extreme climate events (ECE), such as heatwaves (periods of three days or more in which daily mean temperatures exceed the 90th percentile), are also increasing in both their severity and frequency. The impact of heatwaves on bee learning and memory has been previously studied; however, how these events influence the cognition of individuals exposed to the ECE as larvae or pupae remains unexplored. Here, we evaluate the effects of a simulated heatwave on bumblebee (Bombus terrestris) learning and memory when individuals were exposed at different life phases. We exposed bumblebee colonies to a simulated heatwave based on real-world climate data (July 2022, UK) and trained ~600 bees to learn a colour association in a free-moving absolute conditioning experimental setup. We found that bee memory was not impaired by heatwave-like temperatures, but the proportion of bees responding to a sucrose stimulus during training was significantly lower (OR = 0.30, 95% CI [0.09, 0.98]) when adults were exposed to high temperatures. Individuals exposed to heatwave temperatures as larvae or pupae were unaffected. These results raise the possibility that adult bumblebees exposed to heatwave temperatures may be less likely to initiate foraging, and that the impact of heatwaves on bumblebee cognition is dependent on life phase.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Tue 18 Aug · 16:45 · K7 · Session 27 · Abstract ID 144575

Bumblebee parasites and their distributions in a changing world

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Social insects live in dense, low genetic diversity groups, ideal for infectious agents to spread. Annual eusocial bumblebees have become a model system to understand parasites in social insects. However, despite this, and despite the link between parasites such as Nosema bombi and bumblebee declines, there has been no systematic study of global bumblebee parasite distributions.

We conducted a systematic review of 1,346 papers and then collated data from 86 studies that detected the major bumblebee microparasites (Crithidia bombi, Nosema bombi, Apicystis bombi), yielding 1,274 unique occurrence locations spanning all continents except Australia and Antarctica. We used these data to ask: (i) what is the global distribution of these parasites, (ii) what factors associate with it, and (iii) how might their distributions shift under climate change?

Using Maxent models, all three parasites are predicted to be globally distributed, with Nosema bombi spanning almost the entire bumblebee range. Temperature-based bioclimatic variables were the strongest predictors of parasite presence, while land cover did not improve model performance. Under pessimistic climate scenarios, these parasites, including the high impact but currently narrowly distributed Apicystis bombi, are projected to shift latitudinally, with potential impacts on previously unexposed bumblebee populations.

Our results suggest that while land use may shape infection prevalence, it is climate that determines the global distribution of these parasites. Moreover, their predicted range shifts under climate change will present a major threat to naive hosts. This work represents a significant step forward, and a blueprint for the global study of social insect parasites.

A long-term field experiment to assess alternative treatments for a global honey bee pathogen - the Varroa mite

Egehan Onat Ozfen DVM[1]; Julia Jones[1]; Darren O'Connell[1]; Cristina Botías[2]; Fiona Hutton[3]

[1] University College Dublin (UCD); [2] Alcala University (Spain); [3] Teagasc

Honey bees (Apis mellifera) are vital pollinators, supporting biodiversity and more than 75% of global crops. However, honey bee colony losses are rising due to exposure to a combination of stressors, including pathogens, particularly the ectoparasite Varroa destructor. This mite is the most severe honey bee pathogen globally, and is consistently listed as the primary reason for colony losses. It feeds on both larvae and adult bees causing reduced brood development and worker immunity, and is also the vector for numerous harmful viruses. To avoid colony losses, beekeepers commonly treat their colonies with synthetic chemicals. While synthetic chemicals are effective in reducing mite infestation, they pose several risks for honey bees and human health such as the evolution of mite resistance and the persistence of chemicals in honey, pollen and beeswax. Given these drawbacks, there is an urgent need for alternative, environmentally sustainable strategies for combating the Varroa mite, such as using organic acids, mechanical strategies and developing honey bee strains that are resistant to the mite. Here we present a two-year field experiment with 75 honey bee colonies, and evaluate the performance of multiple alternative Varroa control strategies – including treatment-free colonies bred for Varroa resistance – against a synthetic chemical (amitraz). In this experiment we evaluate a comprehensive suite of metrics, including colony health and productivity, Varroa infestation levels, pathogen co-infections and environmental conditions. This work provides an unparalleled assessment of the potential for effective and sustainable Varroa control in honey bees.

Commercial rearing sensitises bumblebees to pesticides

Darren O'Connell[1]; Edward Straw[2]; Alison O'Reilly[3]; Niamh Kennedy[1]; Sarah Larragy[2]; Holden Taylor[4]; Jeanette Carlsson[1]; James Rooney[1]; Julia Jones[1]; Jane Stout[2]

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Commercial bumblebee colonies (Bombus terrestris) underpin bee-safety testing in Europe, yet long-term captive breeding and simplified indoor rearing create strong ecological and physiological divergence from wild populations. Whether these differences bias pesticide toxicity estimates has been little studied. We compare acute oral susceptibility of wild-caught and commercially reared worker bumblebees to three pesticides (thiamethoxam, cyantraniliprole, and the fungicide formulation Amistar). Exposure to the different pesticides caused substantial mortality in commercial bees, while the same doses produced no significant increase in mortality among wild bees.

To determine whether this divergence reflected genetic differentiation or environmental effects, we ran two common-garden experiments. Commercial colonies placed outdoors for 5–6 weeks produced workers that were markedly less susceptible to thiamethoxam, indicating rapid hardening under field conditions. Conversely, workers of wild genetic origin, reared entirely indoors from wild-caught queens, became sensitised and matched the high susceptibility of commercial lab-reared bees. These reciprocal shifts demonstrate that recent rearing environment—rather than lineage—is the primary driver of acute oral pesticide susceptibility in B. terrestris.

Our findings show that standard laboratory-reared commercial colonies can produce vastly different toxicity assessments relative to wild bumble bees, with major regulatory implications. Commercial bees could remain viable surrogates for ecotoxicology only if rearing protocols are redesigned to approximate realistic field conditions. Without such changes, current testing frameworks risk producing inaccurate toxicity estimates for wild pollinators.

Differential sensitivity of Australian stingless bees and honey bees to dimethoate: implications for pollinator risk assessment

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Stingless bees (Hymenoptera: Apidae) are eusocial insects that play a vital role in pollination across tropical and subtropical ecosystems and can be managed for crop pollination much like honey bees. However, their populations are increasingly threatened by agricultural intensification, habitat loss, and pesticide exposure. Understanding their sensitivity to commonly used insecticides is essential for protecting these important pollinators and sustaining pollination services in agroecosystems. Despite their ecological importance, stingless bees are rarely considered in pesticide risk assessments, which typically rely on the western honey bee (Apis mellifera) as a surrogate species. The extent to which honey bee data represent the responses of stingless bees remains uncertain, especially for the diverse species found in the Asia–Pacific region. In this study, we evaluated the acute oral and topical toxicity of dimethoate—a reference insecticide used in regulatory testing—on A. mellifera and three Australian stingless bee species: Tetragonula carbonaria, T. hockingsi, and T. mellipes. We determined species-specific median lethal endpoints: LD_{50} and LC_{50}, and calculated relative sensitivity ratios. All stingless bee species showed greater susceptibility to dimethoate than A. mellifera for both exposure routes. Safety factors (10×) based on honey bee data underestimated stingless bee risk, particularly for oral exposure. However, adjusting toxicity by body weight largely reduced interspecific differences. These findings demonstrate that pesticide sensitivity among bees is influenced by body size and exposure route. The study provides the first baseline toxicity data for Australian stingless bees, contributing to more inclusive and ecologically realistic pollinator risk assessments.

SYMPOSIUM 23 · Social insects' responses and challenges in a changing world
ORAL · Tue 18 Aug · 17:45 · K7 · Session 27 · Abstract ID 149327

No Signal: Sublethal pesticide exposure interferes with honeybee worker responses to queen mandibular pheromone.

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Global declines in pollinators threaten food security, ecosystem stability, and biodiversity, with pesticides – such as neonicotinoids – being implicated as key drivers of these declines. Honeybees (Apis mellifera), the world's most important managed pollinators, rely on a highly organised social system for colony function and survival. Central to this organisation is queen mandibular pheromone (QMP). A crucial semiochemical in the honeybee colony, QMP maintains colony harmony by repressing worker reproduction, attracting young workers for retinue behaviour, or "queen care", and slowing the behavioural transition from nurse to forager. Disruption of QMP-mediated communication has the potential to destabilise colony structure, yet the effects of pesticides on pheromone-driven social behaviour remain poorly understood. Here, we investigate whether exposure to two globally common agrichemicals, Imidacloprid and Sulfoxaflor, alters worker responses to QMP. Using a combination of behavioural assays and RNA-sequencing to assess both social behavioural and underlying molecular responses, we show that sublethal pesticide exposure can impair social communication in honeybees, with potential consequences for colony cohesion and productivity. Our results demonstrate that pesticides can disrupt social communication in honeybees at sublethal doses, highlighting social behaviour and chemical signalling as critical, yet often overlooked, components of pollinator risk assessment and colony-level health and productivity.

Delayed but successful: Resilience of ant colonies facing a biotic stressor to an abiotic stress

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Ants live in dense colonies with closely related nestmates. They engage in various biotic and abiotic interactions which increase their exposure to several infectious agents and cause potential health risk to the colony. .Even while facing the biotic stress imposed by infection, colonies would have to continue with essential tasks to ensure their survival.

To examine how the trade-off between investment into fighting infection and the need to save their colony from a physically damaged nest, we conducted a set of experiments. When Diacamma indicum colonies were infected with GFP-tagged E.coli, and challenged to relocate to a new nest they were significantly delayed as compared to controls. Infection caused significant delays in time taken for nestmates to respond to invitations for tandem running recruitment to the new nest and the transportation itself was significantly delayed. Both behavioural and network analysis revealed that the work distribution among the sham infected and infected were altered as compared to controls colonies. Interestingly, ants who conducted the relocation – tandem leaders had significantly lower bacterial loads as compared to their nestmates. Infection together with relocation stress caused significantly higher mortality as compared to controls.

These findings highlight both the vulnerability of ants to stress caused by the pathogens and the resilience of colonies, particularly tandem leaders, in maintaining collective response to major disasters.

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Too hot, too cold, or good enough: linking nest microclimate, thermal physiology, and decision making in a rock nesting ant

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Temperature strongly influences biological processes, particularly for small ectotherms whose body temperatures closely track the local microclimate. For cavity-nesting ants such as Temnothorax rugatulus, rock crevices filter external temperature variation, creating a more stable thermal profile inside the nest. Climate change may shift these microclimates toward the physiological limits of colony members. Predicting the ants' responses requires linking nest microclimate, thermal physiology, and collective nest choice. In this study, I combine field measurements of ambient and internal nest temperatures, laboratory estimates of upper and lower thermal limits, and outcomes of colony decisions between nests of different temperatures. For colonies tested during the summer season, the estimated upper and lower thermal limits are 45.5˚C and 8.3˚C, respectively. In contrast, summer crevice temperatures rarely exceed 33˚C, indicating a wide safety margin for heat. However, winter crevice temperatures can fall below 0˚C, which implies potential cold stress unless lower limits shift seasonally. In binary nest-site selection experiments, ants avoided nests at 17˚C and showed equal preference for nests at 25˚C and 33˚C. Thermal-gradient assays indicate an average preferred temperature of 24.8˚C by the ant colonies, so this equal preference for warmer nests during emigration suggests a decision rule that balances preferred temperatures against potential gains in brood development rate. By integrating microclimate measurements, physiology, and collective decisions, this study provides a mechanistic framework for understanding the resilience and limits of cavity-nesting ants in montane habitats under climate warming.

Microclimate shapes African ant competition and community structure

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While coarse-scale studies often link biodiversity patterns to climate, far less is known about the role of microclimate at the fine scales directly experienced by small organisms.

We tested the "microclimate maze" hypothesis in ant communities, which proposes that fine-scale heterogeneity in climatic conditions promotes coexistence by partitioning ant activity across space and time. We conducted ant surveys in the Cederberg mountains in South Africa across two seasons, 16 plots and four diel periods. Ants were collected from baits and we recorded local abiotic variables on coarse as well on microclimatic scale.

In total, about 50 ant species were visting our baits, we found that a complex interaction combination of macro - and microclimatic variables predict ant activity best. Microclimatic shifts corresponded to temporal turnover in ant activity, leading to temporal niche partitioning. We found that 5 of the 49 ant species share the baits much less often than expected at random. Of these five species, four had a high activity niche overlap with other species and therefore use behavioral means of exclusion, while one ant species (Ocymyrmex barbiger) is a heat specialist that has low niche overlap with other ants.

Our findings suggest that microclimate structures ant communities by both constraining their activity and by influencing ant competition. By identifying the drivers of biodiversity on a micro-scale, we emphasize both the unparalled adaptions of ant species to microclimatic extremes as well as uncertainty behind climate change assumptions that rely on macroclimatic parameters alone.

Some elements in honey harvested for over a decade (2013 – 2025) from Samaru, Kaduna State, Nigeria

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Elements are part of non-degradable components of honey being used in biomonitoring. Thus, assessing elemental composition of honey will give an insight into the implications of anthropogenic activities within a locality. The apiary of Samaru College of Agriculture was established in 2012 and honey was harvested from five to ten hives between February – June annually. Harvested combs are pressed, while honey obtained are usually bulked and bottled. Composite honey samples are taken from each year's harvest and stored in a bottle on an open shelf. Elements such as iron (Fe), zinc (Zn), lead (Pb), copper (Cu), manganese (Mn) and cobalt (Co) of the stored honey samples were assessed in 2025. Honey samples harvested between 2013 – 2025 showed that Iron ranged between 86.65 mg/litre (2017) – 158.90 mg/litre (2022) however a spiked value of 681.35 mg/litre was recorded in 2018. Manganese was least with 0.05 mg/litre (2015, 2021 and 2025) and highest with 1.60 mg/litre (2018). Zinc was least with 2.40 mg/litre in 2020 and highest with 13.15 mg/litre in 2019. Lead ranged from 23.75 mg/litre (2014) to 49.95 mg/litre (2019). There was a continuously annual increase in copper from 6.35 mg/litre (2013) to 39.95 mg/litre (2025). Cobalt also continuously increased annually with least of 8.50 mg/litre in 2013 which increased to 41.30 mg/litre in 2025. The continuous increase in copper and cobalt and their bioavailability should be of concern while the probable causes of the steady increase needs to be further investigated

The role of microclimate in determining activity and physiological response of harvester ants

Lina Bajić[1]; Marko Bračić[1]; Antonia Smolić[1]; Jonathan Shik[2]; Jelena Bujan[1]

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Global warming is reshaping thermal landscapes with particularly strong consequences for insects, due to their small body size and rapid heat exchange with the environment. Ground-foraging insects are sensitive to small-scale temperature variation because their body temperature directly depends on surface temperature. We hypothesised that thermal microclimates shape insect behaviour and physiology. To test this, we measured the activity, thermal tolerance, and physiological performance in the harvester ant Messor wasmanni.

We first tested how nest surface and foraging trail temperatures impact activity of 24 colonies across 14 days, on a cooler Northern and a warmer Southern Adriatic Island. We then measured the thermal tolerance of each colony, as well as the temperature sensitivity of worker metabolic rate from 10 of these colonies with constant volume respirometry. We show that elevated nest and trail temperatures reduced overall foraging activity. In contrast, heat tolerance increased with higher trail temperatures, but showed no significant relationship with nest temperatures, suggesting that trail temperatures govern harvester ant heat tolerance. Metabolic rate across a range of 7 temperatures showed a non-linear response, but it did not differ across colonies from the warmer and the cooler site.

Our results show the importance of trail temperatures in shaping activity and heat tolerance of harvester ants. However, ants' metabolic rate seems to be constrained across populations, suggesting that thermal microclimate does not impact this part of ant performance. Together, our results show the critical role of microclimate in shaping behavioural and certain physiological traits of ground-foraging insects.

Safe or at risk? Consequences of environmental stress on social insect behavior and fitness

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Insects play important roles in ecosystems as pollinators, decomposers, scavengers, and food for many organisms. The alarming global decline of insects, driven primarily by habitat destruction, exposure to anthropogenic pollutants, and climate change, seriously threatens ecosystem stability. Among these stressors, rising levels of anthropogenic pollution, particularly from agrochemicals, are especially concerning as human activities continue to intensify. Rising temperatures can amplify these effects by imposing additional physiological stress and altering species behavior. Eusocial insects, such as ants (Formicidae), termites (Blattodea), bees (Apidae), and wasps (Vespidae), are especially vulnerable to pollutants and temperature rise due to their multigenerational colonies and semi-sessile nature. To better understand potential differences in vulnerability, we are conducting a systematic review and meta-analysis comparing flying and non-flying eusocial insects, focusing on the effects of pollutants and temperature on survival, foraging behavior, and fitness. Preliminary results reveal a strong research bias, with 78% of studies focusing on bees and over half of those concentrating on the genus Apis. Research on ants and termites was much less common, each representing around 10% of all studies, while wasps accounted for only 1%. Most studies focused on survival, whereas fitness received the least attention, being examined in only 8% of studies. Overall, pollutants lowered survival, disrupted foraging activity, and reduced key fitness traits. These findings provide a critical foundation for future research into how multiple stressors influence the behavior and fitness of these overlooked yet essential social insects.

Buzzing beyond the Queen: Optimising drone rearing for future research

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Within eusocial insect species like the honeybee (Apis mellifera), research has primarily focused on queens and workers with only a relatively small focus on drones. Yet drone quality, especially sperm viability is critical for the success of a colony. Despite this, drone biology remains underexplored especially in response to environmental stressors. While field studies provide essential ecological context understanding the specific effects of individual and multiple stressors on sperm viability and drone physiology is best studied in a controlled environment such as the laboratory where variables can be controlled. However, to our knowledge, there is no established protocol for keeping adult drones in standard laboratory cages. Here, we show that newly eclosed drones cannot survive in the absence of workers in cages in the laboratory and that worker-to-drone ratios play a major role in the survivability of drones in a caged laboratory setting. We are now focusing on optimising drone production for these studies, as well as continuing optimisation of the laboratory setting by assessing other drone:worker ratios and troubleshooting why drone survival is lower than workers in the optimal ratio 25 drones to 75 workers and if changes in food consumption is a good indicator of impeding mortality . We also outline future directions for this system, including its use in testing environmental stressors (e.g., temperature extremes, pesticide exposure), and its potential for investigating how these stressors may affect sperm quality and colony success.

Spatial-trophic niche partitioning of ants along a tree species richness gradient in a young subtropical forest

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Ants are abundant, functionally diverse consumers whose distribution across microhabitats makes them sensitive indicators of effects of tree species richness (TSR). In our study we tested whether increasing TSR alters ant taxonomic and functional diversity, niche specialisation and community structure, as predicted by biodiversity–ecosystem functioning theory.

We sampled different spatial-trophic groups of ants (litter-dwelling, scavenger, arboreal, saproxylic) in 64 plots across a gradient of 1-24 tree species in a subtropical biodiversity experiment in South-East China. We predicted that higher tree diversity would increase ant diversity, promote resource specialisation and partitioning, and reduce niche overlaps. We quantified expected taxonomic and functional diversity for the whole ant assemblage and for each spatial-trophic niche. Community composition, niche dissimilarity and inter-niche overlap were characterised along the TSR gradient using multiple indices. We identified indicator species for each niche, and shifts in their functional traits, resource specialisation and niche fidelity across TSR levels.

Contrary to predictions, ant species richness did not generally increase with TSR but BEF relationships between trees and ants varied in their strength among spatial-trophic niches. Community composition was predominantly shaped by resource use, with relatively low compositional overlap among niches also at low TSR levels, and niche-specific indicator species occurred consistently along the whole TSR gradient.

These findings show that ant specialisation to microhabitats and trophic niches can decouple consumer responses from TSR effects, implying that, at least in early successional forest stages, tree species richness alone does not automatically translate into predictable changes in communities at higher trophic levels.

How native California harvester ants survive despite Argentine ant invasion

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The Argentine ant (Linepithema humile) is a highly successful invader in Mediterranean ecosystems worldwide with demonstrated negative impacts on many native ant species. For example, harvester ant declines associated with Argentine ant invasion have been well documented in cool coastal California. While such patterns have been studied primarily at the population level, the behavioral interactions shaping patterns of local decline are still poorly known. Here, we examined interactions between L. humile and the native harvester ant Pogonomyrmex californicus in a hot, dry inland fragment of California sage scrub habitat where the two species have co-occurred for at least a decade. We hypothesized that P. californicus might avoid L. humile by spatially and/or temporally limiting foraging activity. We routinely observed raids by Argentine ants at harvester ant nest entrances; frequently raided colonies sometimes either ceased activity altogether or excavated a new entrance several meters away. In a series of Y-maze choice experiments, we found that while P. californicus did not respond to the scent of L. humile foraging trails, they actively avoided chemicals extracted from refuse piles of L. humile colonies. Such avoidance behavior could help P. californicus survive Argentine ant invasion in areas where hot, dry conditions limit Argentine ant activity to cooler, moister microclimates. This initial work sets the stage for a larger study comparing behavioral interactions between Argentine ants and harvester ants across an environmental gradient, from the cool coastal regions where harvester ant populations are in decline to the dry inland regions where they still thrive.

Binary neonicotinoid exposure impairs colony founding in Bombus terrestris queens

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Queens of Bombus terrestris are among the earliest pollinators to emerge from hibernation in spring, initiating nests when floral resources are often scarce. During this critical nest-founding phase, mass-flowering crops such as winter oilseed rape/canola can provide important forage. However, pollen and nectar from these crops frequently contain residues of neonicotinoid insecticides, leading to exposure of bumblebees in agricultural landscapes.

Although the outdoor use of several neonicotinoids has been restricted or banned in regions such as the European Union, these compounds remain widely used elsewhere and are still the most extensively applied class of insecticides globally. Neonicotinoids can persist in soils and be taken up by plants, resulting in prolonged exposure. In addition, pollinators are commonly exposed to mixtures of pesticides, including parent compounds and their metabolites, while regulatory risk assessments mainly consider single substances.

Here, we investigated the effects of field-realistic neonicotinoid exposure on B. terrestris queens during nest founding, focusing on binary exposure. Queens were fed pollen and nectar contaminated with thiamethoxam (TMX), its primary metabolite clothianidin (CLO), or both. A total of 120 wild-caught queens were assigned to four treatments: control, TMX, CLO, and TMX + CLO. While all neonicotinoid treatments reduced colony size, only combined TMX + CLO exposure significantly increased queen mortality and reduced ovary weight and nest-founding success. These results demonstrate that pesticide mixtures can amplify negative effects and highlight the need to incorporate combined exposures into pollinator risk assessments.

Polluted pollinators: Expression analysis of Bombus impatiens shows physiological changes when exposed to environmental contaminants

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The Common Eastern Bumblebee, Bombus impatiens, is widely recognized as an essential native pollinator. As their native habitats become increasingly influenced by humans in both an agricultural and urban context it is important to assess their physiological response to man-made environmental stressors, particularly environmental contaminants, so strategies to increase their health may be implemented. Of particular importance are the sub-lethal effects of environmental contaminants which can impact the brain and endocrine systems, and in these studies, we look at the molecular characteristics and gene expression patterns of B. impatiens exposure to them. Juvenile hormone analogs are a commonly used mosquito larvicide that in addition to retaining juvenile characteristics, has also been documented to have varying behavioral and physiological effects on numerous adult insects. Juvenile hormone is regulated seasonally in B. impatiens so we conducted a comparative analysis of JH manipulated bees in late and early season workers to identify genes of interest that could be mediated by manipulating doses of a JH analog, methoprene. In a collaborative study we also identified how plant stressors such as chromium may influence gene expression patterns of foraging workers. Chromium has already been documented to have an influence on the neuroendocrine system, so our goal was to characterize genes that could be associated with stress from environmental contaminants. Research conducted on the functional role of genes could provide valuable insight into determining stress responses to contaminants. This may provide novel strategies for conservation and management.

Drone thermal mapping reveals fine-scale thermal heterogeneity in ant habitats

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Predictions of species' vulnerability to global warming often rely on temperature averages, although most habitats exhibit substantial thermal heterogeneity. Such heterogeneity is especially important for ectotherms such as insects, which can use it to maintain their optimal body temperature by foraging in cooler areas when it is too hot. Despite its importance for behavioural thermoregulation, this fine-scale thermal variation and its influence on foraging remain poorly quantified. We hypothesised that thermal heterogeneity around nests of harvester ant Messor wasmanni influences foraging activity of this ecosystem engineer.

To test this, we mapped ground surface temperatures around 40 ant nests using drone thermal imaging across six sites, with surveys repeated three times per day across multiple days. Preliminary results revealed pronounced spatial and temporal heterogeneity in temperatures around ant nests. Heterogeneity was highest at midday: average temperature variation around nests was 2 °C, with differences of up to 25 °C between surface areas just a few centimetres apart. Moreover, nests showed a distinct spatial structure of thermal heterogeneity across surveys, with some surrounded by a larger surface area of cooler patches than others.

These findings indicate substantial temperature differences around and between ant nests, at a magnitude and spatial scale relevant for behavioural thermoregulation during foraging. Ongoing work will assess this relationship between thermal heterogeneity and foraging activity using in-situ behavioural observations. Uniting microclimatic and behavioural data will help uncover insects' potential to cope with climate warming.

Sublethal oral exposure to sulfoxaflor alters brain transcriptomic profiles in the stingless bee Melipona quadrifasciata anthidioides

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Sulfoxaflor is a systemic insecticide targeting nicotinic acetylcholine receptors and is detectable in nectar and pollen, exposing bees through contact and ingestion during foraging. Evidence suggests that stingless bees are particularly vulnerable to pesticide exposure, yet risks to this group remain poorly understood. Foraging Melipona quadrifasciata anthidioides were orally exposed to a sublethal dose of sulfoxaflor (LC_{50}/75 = 0.73 ng/µL), and brain transcriptomes were analyzed after 24 h. Surviving bees were anesthetized by cooling, and brains from 36 individuals (12 per replicate) were dissected for RNA extraction and sequencing (paired-end 2 × 150 bp). Reads were quality-checked, de novo assembled, mapped, and analyzed for differential gene expression and functional annotation. The assembled transcriptome comprised 140,768 transcripts and 92,826 genes, with a GC content of 37.61%, an N50 of 3,319 bp, and 92.87% completeness (BUSCO). A total of 331 differentially expressed genes (FDR < 0.05) were identified, including 208 upregulated and 123 downregulated genes. Upregulated genes were mainly associated with xenobiotic metabolism and antioxidant defense (e.g., Cytochrome P450 9e2, ABCC4, Prx1, and MOCS3), energy and lipid metabolism (AK, NDUFA10, DGAT2, and Tret1), and cell adhesion and cytoskeletal organization (Dumpy, Filamin-A, Laminin, and Ena). In addition, genes related to neuronal signaling and plasticity (GlyRs, SIFamide receptor, OTX2, and Glass) were induced. Overall, these findings demonstrate that sublethal oral exposure to sulfoxaflor elicits coordinated transcriptional responses in the stingless bee brain, affecting detoxification, metabolic balance, and neural homeostasis.

A next-generation pesticide is detrimental to paper wasps

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Paper wasps provide important ecosystem services as natural enemies of agricultural pests, yet they are frequently exposed to pesticides applied in crop systems. Flupyradifurone (FPF), a novel butenolide insecticide promoted as a safer alternative to neonicotinoids, has been poorly evaluated for its effects on non-target social wasps. Here, we evaluated survival and sublethal behavioral and molecular effects of topical FPF exposure on adult females of the paper wasp Polistes versicolor. Wasps were exposed to either the label-recommended concentration or 20% of this dose, and compared with negative (water) and positive (Imidacloprid) controls. We quantified survival, locomotor activity, sexual attractiveness, and the expression of immune-, oxidative stress-, and detoxification-related genes. While FPF did not increase mortality relative to controls, it induced pronounced sublethal effects. Exposure at the label rate significantly reduced horizontal and vertical locomotion and impaired male sexual responses, as evidenced by decreased antennation frequency and mating attempts. At the molecular level, FPF triggered the upregulation of immune and oxidative stress markers (Defensin, Hymenoptaecin, and Duox), alongside a marked downregulation of the detoxification gene CYP9E2. These results indicate that FPF disrupts behavioral and physiological processes critical for individual performance and reproductive interactions, despite the absence of acute lethality. Our findings demonstrate that mortality-based risk assessments alone may substantially underestimate pesticide impacts on beneficial social wasps and highlight the need to incorporate sublethal behavioral and molecular endpoints into pesticide risk evaluation frameworks.

Differences in thermal physiology may explain the temporal distribution of foraging activity among different-sized workers in the seed-harvesting ant Messor barbarus

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One of the most stressful factors for insects is increasing temperature because of the risk of potentially fatal dehydration linked to their small size. We used respirometry to study the effect of both temperature and body mass on the general activity, percentage of water loss and metabolic rate in individual workers of the Mediterranean seed harvester ant Messor barbarus. This species is characterized by a high degree of polymorphism of its worker caste, which correlates with the division of labor observed within its colonies. We found that the relative activity of workers inside the respirometric chambers in the range of temperatures tested (15-35°) increased with decreasing body mass and increased non-linearly with increasing temperatures, in the same way for ants of different sizes. Moreover, as expected, we found that large ants exposed to increasing temperatures have a lower rate of water loss than small ants and that their mass-specific metabolic rate increases more slowly. However, counterintuitively, the measure of worker sensitivity to changes in temperature, as assessed by the instantaneous Q10 value, i.e., the rate of change across 10°C temperature intervals, shows that large ants are more sensitive than small ants to changes in temperature in terms of both water loss and metabolic rate. Such differential sensitivity allows to make testable predictions on the temporal distribution of foraging activity among workers of different sizes in polymorphic ant species, as well as how these species may alter their colony demographics in response to rising temperatures in the context of global change.

Climate change risk as a function of soil stratum: Are epigeic or hypogeic ants more negatively affected?

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In a world transformed by anthropogenic climate change, social insects face different challenges across the many unique microhabitats they occupy. Our understanding of how thermal tolerance limits are shaped by climate across different spatial scales is ever improving. Here, we develop a new methodology to marry these widely collected physiological performance data with high-resolution climate data in a biologically relevant way: by quantifying the percentile of accessible diel temperatures. Using this approach, and previously published data on thermal tolerance in 14 species of army ant (Formicidae: Dolichoderinae) collected throughout northern Costa Rica, we test for effects of microhabitat use on climate change risk.

Comparative effect of natural and commercial Cu2O on the mobility of ants

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The industry of nanomaterials is one of the most dynamic economical factors of the 21st century. Nanomaterials with photocatalytic activity of are on the verge of being used on industrial scales, therefore knowledge concerning their effect on our environment is crucial. The ecotoxicology of photocatalytic nanomaterials is a field with a severe lack of knowledge, even studies claiming to be of ecotoxicological interest mainly concern matters of environmental toxicology, lacking the study of effects on ecological phenomena.

It is a basic requirement for all these materials, that they should be inert, stable and environmentally friendly. The latter concept is, however narrowly considered in modern materials science as most of the publications are using standard ecotoxicological tests, which are covering only short impact effects, such as mortality, growth, etc. These tests however might not reveal the finer sublethal effects. Despite the availability of these tests, none of them are covering long, ecologically significant effect, therefore a potential knowledge void appeared.

In the present work nonconventional ecotoxicological tests were created for studying the effect of natural and industrial photocatalysts on the mobility of three ant species (Myrmica gallienii, Formica polyctena and Lasius niger).

These tests proved that effect of naturally occurring Cu2O on ant mobility is observable but statistically not significant, while commercially available Cu2O has a significant effect.

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"Assessing Temporal and Urban Effects on Polistes Nest Dynamics in the Midwestern United States"

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Paper wasps (genus: Polistes) provide important ecosystem services, including pollination and biological control. Ongoing climate change and urbanization have altered the phenology of many organisms, yet possible shifts in the nesting phenology of Polistes remain poorly characterized. Increased spring temperatures may advance nest initiation, while extended autumn warming may delay nest senescence. Similarly, urban environments may promote earlier nest establishment and extended nesting seasons relative to natural habitats. We tracked nesting behavior by deploying nest boxes in natural areas surrounding St. Louis, Missouri, and measuring data on nest establishment date, number of cells, number of foundresses, date of nest senescence, and nest success rates. Nest growth rates were quantified using changes in cell number over time. To assess temporal changes in Polistes nesting phenology, contemporary data was compared with historical nest box records from the same region collected 30 years ago. To evaluate the influence of urbanization on nesting dynamics, opportunistic observations of urban nests were compared to nest box data from natural areas. Together, these analyses characterize current Polistes nesting phenology and assess shifts in phenology or growth dynamics across decades and along an urban–natural gradient. Preliminary results show shifts in nesting phenology over time and along an urban-natural gradient.

Swimming skototaxis is stronger in open-nesting honey bee species

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Honey bees are capable of swimming on the water surface toward a dark region, a behavior known as skototaxis that facilitates escape from water. While this behavior has been observed in honey bees and solitary bees, little is known about how its strength varies among different honey bee species. In this study, we compared skototaxis during swimming among four honey bee species representing two nesting types: open-nesting (Apis dorsata and Apis florea) and cavity-nesting honey bees (Apis cerana and Apis mellifera). Individual bees were released into a water-filled arena containing a dark sector, and landing angles were measured. All species exhibited significant directional swimming toward the dark sector. However, open-nesting species showed a stronger preference toward the dark region. Chi-square tests revealed no significant differences between replicate colonies within species or between species sharing the same nesting type, but a highly significant difference between open- and cavity-nesting groups. These results demonstrate that skototaxis strength differs between the two nesting types of honey bees within Apis, consistent with phylogenetic structure and supporting an evolutionary context for variation in this escape behavior.

Climate and Community Structure Shape Worker Allometry in Pheidole

Steven Wang
University of Texas at Austin

Climate-driven shifts in precipitation are expected to alter selective pressures on insect species,

yet the traits most sensitive to these changes remain unidentified. We examine

climate-associated variation in the Big-headed Ants (genus Pheidole), a globally dominant ant

lineage defined by their strong worker caste polymorphism. Pheidole species frequently coexist

at fine spatial scales despite similar foraging and recruitment strategies, raising questions about

how caste structure and worker morphology are driven by ecological change and competition.

We focus on head size, shape, and cuticle investment in major and minor workers—traits tightly

linked to feeding behavior, task performance, and competitive interactions. Using standardized

morphometric measurements from thousands of workers collected across ~150 sites, we test

whether caste allometry and head morphology vary predictably with precipitation and local

species coexistence. Preliminary analyses show Pheidole community assemblages varying

directly with precipitation regimes and divergence in head size classes among co-occurring

species, consistent with climate-mediated selection on worker function.

Testing a scalable monitoring protocol for social wasps (Vespidae) in Italy

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Social wasps are key ecosystem services providers, yet they remain largely excluded from standardized monitoring schemes. This taxonomic gap limits our ability to detect population trends and integrate social wasps into conservation planning. Here, we assess whether the monitoring protocol employed by the Italian Institute for Environmental Protection and Research (ISPRA) for bees and butterflies can be reliably applied to social wasps. We compare this method, a modified Pollard transect, with two commonly used methods for social wasp monitoring: active search and passive sampling using baited traps. Fieldwork was conducted along two routes per site, at four sites in Italy, once every two weeks over six months. For each method, we quantified genus richness, diversity, and relative abundance. Preliminary analyses indicate no significant difference in the number of genera detected by ISPRA monitoring walks and active search, supporting the effectiveness of ISPRA monitoring walks for capturing social wasp diversity. Ongoing analyses suggest that both active methods outperform baited traps in terms of taxonomic coverage and consistency. Our results demonstrate that standardized walking transects represent a low-cost, scalable, and transferable approach for monitoring social wasps. Integrating this protocol into existing insect monitoring frameworks would facilitate cross-regional comparisons and support evidence-based conservation of social vespids. Moreover, because field identification within the ISPRA monitoring walk is required only at the genus level (and European social wasps fall into only three morphogroups) this protocol is well-suited for citizen science initiatives and could help addressing the current lack of large-scale data on social wasp populations.

SYMPOSIUM 24 · Social insect conservation
ORAL · Thu 20 Aug · 10:30 · K7 · Session 51 · Abstract ID 148991

Ants as bioindicators: Feasibility and ecological value in multi-taxon biodiversity monitoring of European forests

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EURAC Research

Biodiversity monitoring programs target taxa with indicative value for biodiversity, increasingly enlarging the taxonomic scope to be more representative. Traditionally, the selection of bioindicator groups has focused on taxa that are well-known, widespread, and comparatively easy to sample and identify. As a result, the actual suitability of such taxonomic groups to inform overall biodiversity and the relation between them is rarely investigated.

Ants are ubiquitous in terrestrial ecosystems, where they act as keystone species and ecosystem engineers, strongly influencing energy flows, biomass distribution, and ecosystem functioning. Their long-lived, site-bound colonies make them optimal bioindicators. However, ants are rarely included in biodiversity monitoring schemes, largely due sampling and identification challenges they pose compared with more accessible taxa such as plants, birds, or butterflies.

In this study, we assessed ant communities in forest sites included in the Biodiversity Monitoring South Tyrol program spanning over a 1870m elevation gradient and covering multiple forest types. We combined standard sampling approaches (pitfall traps, soil cores, litter samples, vegetation beating) conducted by non-specialists with targeted hand samplings by expert myrmecologists. We then compared ant community metrices with other monitored bioindicators such as other taxa and forest microhabitat diversity.

We found new insights and correlations between the ant communities and indices of other taxonomic groups, confirming that ants are a valuable addition in biodiversity monitoring programs. This work provides insight into the feasibility and ecological added value of including ants in multitaxon biodiversity monitoring schemes and contributes to evaluating their potential as complementary bioindicators in forests.

SYMPOSIUM 24 · Social insect conservation
ORAL · Thu 20 Aug · 10:45 · K7 · Session 51 · Abstract ID 149756

From Native Grasslands to Croplands: Impacts of Intensive Agriculture on Ant Assemblages in Madagascar

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Agricultural land expansion is a major driver of biodiversity loss, but its impact varies depending on the type and intensity of land use. While most tropical studies focus on forest-to-farm conversion, few examine the biodiversity consequences of converting grasslands. Many plants and animals inhabiting these grassy systems are restricted to these open habitats.

In this study, we assess how ant communities respond to land-use change across 28 sites in southeastern Madagascar, representing four land- use types: uncultivated grasslands, annual maize crops (3–9 years old), perennial crop plantations (eucalyptus, jatropha, geranium), and native savannah (Uapaca bojeri woodland). Using 1200 pitfall traps, we collected 2963 ant specimens representing 18 genera and 35 species. Species richness was highest in the savannah (25 species) and grasslands (23 species), and lower in cultivated lands, ranging from eucalyptus (15 species) to geranium (5 species). Savannah had also the greatest number of indicator species (3), while Maize (6 years) and Jatropha had only one species. Ant assemblages differed significantly across land uses, with a compositional shift from savannah to grasslands, then to perennial, and finally to annual crops.

The invasive Pheidole megacephala was present at all sites, but other invasive species showed no consistent land-use patterns. Our findings align with global evidence that intensive annual cropping reduces ant diversity, suggest that Malagasy grasslands support distinct ant communities, and provide new insights into grassland conversion, a neglected frontier of land-use changes in biodiversity hotspots.

SYMPOSIUM 24 · Social insect conservation
ORAL · Thu 20 Aug · 11:00 · K7 · Session 51 · Abstract ID 147815

Unknown allies in the grassland ecosystem. How the engineering of Lasius flavus benefits pollinators.

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The loss of semi-natural grasslands is a major contributor to the decline in pollinating insects, which rely on this habitat and the availability of floral resources. The restoration of grasslands has become an important focus in the efforts to conserve and recover pollinator populations and it is crucial to consider keystone species in restoration efforts. Lasius flavus (yellow meadow ant) is a keystone grassland species, influencing soil ecology, increasing heterogeneity of the grassland and creating microhabitats. We have been examining floral resources, bare soil availability and temperature on and off ant mounds in grasslands to consider what resources ant mounds may provide to pollinators. We also conducted insect behavioural surveys to examine interaction with mounds. The results will reveal how pollinators interact with ant mounds in grazed grasslands and how ants may benefit pollinators through ecosystem engineering. Could yellow meadow ants be an important species to consider in grassland restoration initiatives as both an ecosystem engineer and keystone species?

SYMPOSIUM 24 · Social insect conservation
ORAL · Thu 20 Aug · 11:15 · K7 · Session 51 · Abstract ID 148477

Big birds and ants: Interactions between Galliformes birds and Red Wood Ants—evidence from camera trapping, faecal analysis and their spatial overlap

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The dependence of Galliformes birds (capercaillie , black grouse, hazel grouse) on red wood ants has long been suggested by hunters and forest practitioners, and has influenced conservation practice, including capercaillie reintroduction programmes. However, direct scientific evidence remains scarce. Here, we present an integrated approach to test this interaction and report preliminary results. We deployed camera traps in the Czech Republic, Germany, South Tyrol and Italy, targeting active red wood ant nest mounds in areas with confirmed Galliformes presence. Cameras were operated for one year to quantify bird visitation and various types of bird/ant or bird/nest mound interactions. In addition, we tested capercaillie faecal analysis as a complementary method to assess ant consumption. Finally, we performed a landscape-scale spatial co-occurrence analysis to quantify habitat overlap between mound-building red wood ants and Galliformes birds. Together, these methods provide a complementary framework for evaluating the ecological relevance of this interaction and its implications for species conservation.

SYMPOSIUM 24 · Social insect conservation
ORAL · Thu 20 Aug · 11:30 · K7 · Session 51 · Abstract ID 148869

Examining the effect of urbanization on bumblebee movement through population genetics and agent-based modeling

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Bumblebees are some of the planet's most valuable pollinators but are declining worldwide due to anthropogenic change. One component of anthropogenic change is urbanization, with cities constantly expanding and more land becoming urbanized from sprawl. Cities have introduced many factors not previously seen in bees' evolutionary history, including impervious surfaces, heavy fragmentation, and the scattering of resources. Understanding more about how cityscapes affect movement to resources is paramount for conservation efforts. Our research examines movement of the common eastern bumblebee (Bombus impatiens) through two different approaches. The first is a genetic mark recapture study in different landscapes of St. Louis, Missouri, comparing gene flow and bumblebee movement between urban, suburban, and rural areas with whole genome sequencing. The second is an agent-based model simulating bumblebee queen dispersal in a variety of urban environments, incorporating city features, bumblebee energetics, and behavior rules to differentiate landscapes' effect on this movement process. From these studies, we can gain a better understanding of how urban environments facilitate and restrict movement to key resources for bumblebees, and how that contributes to their survival and health in cities.

Safeguarding locally adapted honeybee subspecies: Genetic Introgression and Health Risks in Apis mellifera sahariensis from Morocco

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The Saharan honeybee (Apis mellifera sahariensis) represents a locally adapted subspecies inhabiting the arid and semi-arid ecosystems of southeastern Morocco, where extreme temperatures and limited floral resources impose strong selective pressures. This subspecies is increasingly threatened by anthropogenic activities, particularly the introduction of non-native honeybee subspecies and emerging pathogens. In this contribution, we present an integrative synthesis aimed at assessing the conservation status and health condition of A. m. sahariensis using complementary approaches. Population structure and genetic diversity were investigated using microsatellite markers and geometric morphometrics, revealing significant introgression from non-native subspecies. Alarmingly, only a limited proportion of colonies retained high levels of genetic purity, indicating an advanced erosion of the Saharan honeybee's genetic identity, largely driven by migratory beekeeping. In parallel, the health status of Saharan honeybee populations was evaluated through molecular screening of major pathogens. Analyses revealed the presence of several honeybee viruses, as well as Nosema ceranae and bacterial agents responsible for European foulbrood diseases. Infection patterns varied geographically and occurred in mixed infections, suggesting interactions between pathogen pressure and environmental or management-related stressors. Overall, the combined evidence highlights a dual threat to the Saharan honeybee: genetic dilution through introgression and increased disease burden. These findings emphasize the urgent need for region-specific conservation strategies, including the protection of genetically pure populations, regulation of beekeeping practices, and continuous health monitoring. This work provides a scientific framework to support the long-term conservation of locally adapted honeybee subspecies in North African arid environments.

SYMPOSIUM 24 · Social insect conservation
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Effects of managed bees on flower visitor diversity and visitation patterns of Vitellaria paradoxa (shea)

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The introduction of managed bees into agricultural landscapes is increasingly used to supplement insect pollination services. Although this practice is less common in Africa, beekeeping is widely adopted in rural areas as an alternative livelihood activity. The establishment of apiaries can create unnaturally high honeybee densities within landscapes. This study examined the effects of aggregated honeybee colonies (apiaries) on the diversity and foraging behaviour of other bee visitors to Vitellaria paradoxa. Flower visitors were sampled from focal trees at four distances (100, 500, 1,000, and 4,000 m) from apiaries across six sites in three regions of Ghana. Visitation frequency of non-Apis bees to V. paradoxa flowers was recorded during 10-minute observation periods in the early morning (06:00–08:30 GMT) during peak flowering. The results showed that distance from apiaries did not significantly affect the richness, abundance, or visitation frequency of other bee visitors to V. paradoxa flowers. In contrast, visitation frequency of the honeybee (Apis mellifera adansonii) was significantly influenced by distance to the apiary. Overall, the study indicates that the presence of apiaries in shea parklands has minimal effects on other bee visitors. However, further research is needed to assess the long-term impacts of beekeeping on the biodiversity of florivorous insects at the landscape scale.

SYMPOSIUM 24 · Social insect conservation
ORAL · Thu 20 Aug · 14:30 · K7 · Session 57 · Abstract ID 148782

Genomic signatures of apiculture in the Western honeybee and their implications for conservation

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The Western honey bee (Apis mellifera) is a managed social insect. However, globally, wild/feral colonies are more than twice as abundant as managed ones. In their native range, wild colonies are an emerging conservation target since they can constitute valuable reservoirs of genetic diversity and exhibit ecological interactions that are absent in managed hives (e.g., interactions with nest commensals and predators). In Europe, the population status of wild honey bees varies strongly among regions, with colony survival rates not always passing the threshold needed for self-sustaining populations. Here, the question is whether population establishment is hampered by environmental factors alone or whether evolution under modern apiculture has generated genetic costs for living in the wild. Beekeepers increase admixture by importing non-native genotypes; they create genetic bottlenecks by mass-rearing queens; they relax natural selection by medicating and feeding hives, and they can exert directional selection through breeding. This study aims to quantify genomic signatures of modern beekeeping at a global scale by jointly comparing the genomes of pairs of wild/feral and managed honey bee populations from >15 regions worldwide. We analysed whether wild/feral and managed honey bee populations differ in genome-wide levels of genetic diversity, how the species' original geographic lineages are represented in each group, and whether there are any signatures of adaptation to managed conditions. The results will inform us about the conservation value of colonies that recently emigrated from apiaries in their native range and provide insights into whether beekeeping per se leads to honey bee domestication.

SYMPOSIUM 24 · Social insect conservation
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Effect Of Altitude On Bee Pollinator Communities Along A Tropical Elevation Gradient

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Social insects, especially bees, are essential pollinators that sustain ecosystem function across diverse terrestrial landscapes.Despite their importance, how pollination services and social insect assemblages respond to altitudinal gradients in tropical mountain systems remain poorly understood.This study investigates the effects of steep elevation on bee visitation to flowers in domestic agricultural habitats along the Bismarck Range of Papua New Guinea, sampled at 500 m intervals along the Mt. Wilhelm elevation transect from coastal to sub-alpine montane zones (200–3,700 m a.s.l.). At each gradient interval, bee collections from 10 village gardens (non-independent sites) are surveyed twice (morning and afternoon) at flowering plants via random-walk sweep-net sessions of 30-minute duration.Floral hosts visited by bees will be recorded to species or genus level.This standardized approach enables robust statistical comparison of bee abundance, species richness, composition of community assemblages, and plant–pollinator interactions across elevations.Results will address how physical environmental factors such as temperature influence tropical montane pollinator communities. The research aims to identify patterns of pollinator turnover, shifts in dominant pollinating groups (such as eusocial versus casteless or solitary nesting Apidae and Halictidae), and changes in the frequency of bee visitation to flowers across elevations. Outcomes will illuminate the ecological drivers of social insect foraging behaviour in tropical mountain ecosystems and improve understanding of pollination resilience and vulnerability to environmental change.This work represents the first comprehensive assessment of pollinators along the established Mt. Wilhelm biological transect to provide a baseline for future research and conservation in one of the world’s most biodiverse regions.

Assessing wild honeybee population trends in Europe: survival-based projections over IUCN time horizons and the contribution of citizen science

Benjamin Rutschmann; Patrick Kohl

The population trends of the western honeybee (Apis mellifera) in the wild have been neglected by conservationists because the species has been considered to consist of managed colonies only. New data suggest that wild honeybee colonies (still) make up one sixth to one fifth of the overall European honeybee population. Like other native wild taxa, these wild cohorts can be assessed demographically, but require methodological adjustments to account for immigration from managed colonies via swarming. We used data on wild colony survival rates from seven European countries to model their autonomous population changes over ten-year periods, the time frame considered for population evaluation by the International Union for the Conservation of Nature (IUCN). Populations of wild honeybee colonies currently represent demographic sinks in six out of seven countries with an estimated population decline of 56% per decade. Building on these results, we highlight the central role of citizen science for generating continent-scale demographic data on a species that is otherwise difficult to monitor. At the same time, citizen-science datasets can be affected by several biases (e.g. variable reporting effort, urban detection bias). We outline practical quality-control steps to address these limitations. Strengthening and harmonizing such citizen-science monitoring protocols —complementary to expert-led monitoring—will be critical for robust future IUCN reassessments and for evidence-based conservation of wild honeybee populations in Europe.

SYMPOSIUM 24 · Social insect conservation
ORAL · Thu 20 Aug · 15:15 · K7 · Session 57 · Abstract ID 146244

Translocating wood ants (Formica spp.): A systematic review of methods and outcomes

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Conservation translocations are used as a management tool to prevent biodiversity loss or restore ecological functions. Wood ants (Formica rufa group) are a focal group for translocation due to their roles as ecosystem engineers, increasing habitat heterogeneity and influencing nutrient cycling and invertebrate community composition. Many wood ant species have experienced population declines due to habitat loss and fragmentation, and their limited dispersal ability, which often relies on nest budding, means natural recolonisation of isolated habitats is unlikely. Although wood ant translocations have historically been motivated by biological pest control benefits, more recent efforts focus on loss mitigation, population reinforcement or reintroduction. However, documented outcomes are variable, highlighting the need for an evaluation of methods to identify those associated with long-term establishment of viable populations.

This systematic review analyses documented wood ant translocations identified from both academic and grey literature across Europe. Translocation techniques were compared, including hand-excavation, mechanical whole-nest translocation, partial colony translocation and release of mated queens. For each project, data were extracted on species, number of nests, time of year, collection and release methods, and post-release monitoring. Factors associated with successful colony establishment and persistence were then assessed.

By analysing historic and recent translocations, this review identifies approaches that are most likely to support the long-term establishment of wood ants, highlights knowledge gaps, and outlines ethical and practical considerations for future efforts. These findings will contribute to improving evidence-based conservation translocation methods, and emphasise the importance of preventing habitat loss and fragmentation as preferable alternatives to translocations.

Red Listing the Red Wood ants – conserving keystone species.

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University of York

Red Wood Ants (Formica rufa group) are keystone species, providing valuable ecosystem services such as habitat creation, seed dispersal and shaping carbon and nutrient flow. Their habitats are threatened by fragmentation and commercial forestry, but their extinction risk is not clear. A small subset of the Palearctic species of the Formica rufa group were last assessed for the IUCN Red List in 1996 while others have never been assessed. This project will assess this ecologically significant group of ant species using current data and IUCN Red List assessment criteria. We will apply IUCN Red Listing protocols to implement these assessments, but will also critically evaluate the applicability of the Red Listing process to social insects such as Red Wood Ants, in particular regarding calculation of generation time and population size in species that can be polygynous (multiple queens) and polydomous (multiple nests). Red List assessments are commonly used by a wide range of groups, including governments, NGOs and private companies in their decision making. An updated Red List assessment for Red Wood Ants will be valuable, as it can be used to inform decision making, for conservation policies, land management and land-use change, which might otherwise not take Red Wood Ants into account, resulting in further risk to these keystone species.

Altitudinal and ecosystemic distribution of Meliponini bees in the department of Cauca

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Stingless bees of the Meliponini tribe play an essential role in the pollination of tropical and Andean ecosystems, contributing to the maintenance of plant biodiversity and the stability of ecosystem services. The Cauca Department in Colombia, South America, is characterized by its altitudinal and ecosystemic heterogeneity, which favors a high diversity of pollinators. However, information on their spatial and ecological distribution remains fragmented. The objective of this study was to analyze the altitudinal and ecosystemic distribution of Meliponini bees in Cauca, identifying patterns of richness, abundance, and association with different types of ecosystems. Sampling was carried out along an altitudinal gradient between 200 and 3,200 m, encompassing tropical, sub-Andean, and Andean rainforests, as well as agroforestry systems, in 23 of the department's 42 municipalities. Data were obtained from direct observation of foraging and the search for natural nests. The results showed greater species richness and abundance at low and mid-altitudes, especially in well-preserved forests and agroforestry mosaics. Some species of the genera Nannotrigona, Trigona and Tetragonisca angustula exhibited broad altitudinal ranges, while others showed restricted distributions and a high dependence on specific ecosystems. The observed patterns suggest that ecosystem heterogeneity is a key factor for Meliponini diversity. This study provides relevant information for the design of conservation strategies, highlighting the need to protect entire altitudinal gradients and promote sustainable management practices that favor the conservation of native pollinators.

CONTRIBUTION OF SPECIES OF THE GENUS MELIPONA (APIDAE) TO FOREST CONSERVATION IN PIEDMONT, CAUCA, COLOMBIA

Hilda Rocío Mosquera Mosquera[1]; Elver Jaime Chapal Arcos[2]; Jhonny Cuellar[3]; María Cristina Gallego Ropero[4]

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The conservation of tropical forests depends largely on the ecological interactions that sustain their structure and function, among which pollination plays a fundamental role. In this context, stingless bees of the genus Melipona represent a key group for maintaining plant biodiversity, especially in tropical and subtropical ecosystems. These native bees not only contribute to the reproduction of numerous wild plant species but also promote natural regeneration, ecological connectivity, and forest stability. To understand the contribution of Melipona species to forest conservation in the municipality of Piamonte, in the department of Cauca (Colombia), honey samples from four species of the genus Melipona (M. nebulosa, M. eburnea, M. rufiventris, and M. grandis) were analyzed. These samples were collected between January and April 2025 and processed according to the melissopalynological method of Louveaux et al. (1978). The prepared slides were analyzed using a Primo Star Zeiss microscope with 40x and 63x objectives, photographed with an Axiocam ERc 5s camera, and edited with Zen software. Forty species from 30 genera and 20 botanical families were identified. The genera Bellucia, Melastoma, and Miconia (Melastomataceae) were the most represented, followed by the families Malvaceae (Pseudobombax and Ceiba), Myrtaceae (Sizygium and Eucalyptus), and Asteraceae (Piptocoma and Vernonanthura). These results confirm the interactions of these bees with plant species in forest remnants in Piamonte, Cauca, contributing with pollination to natural restoration and promotion of meliponiculture as a productive activity.

Pollen loads of bees of the tribe Meliponini (Apidae) in coffee systems, Department of Cauca, Colombia, South America

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Coffee (Coffea arabica L.) is an exotic species that has become widely naturalized in Colombia and is one of the country's main commercial crops. Although it has a self-pollinating reproductive system, several studies have shown that entomophilous pollination, especially by native bees, increases fertilization, fruit set, and seed quality. These interactions generate complex plant-pollinator networks that depend on agricultural landscape management and the availability of surrounding floral resources. Analyzing bee pollen loads is a key tool for understanding their role in crop pollination and for evaluating habitat use and the importance of associated flora in supporting these species. To determine the diversity of stingless bees and their interaction with the surrounding vegetation, seven diversified coffee farms were selected, each at three different flowering stages. Surveys were conducted in coffee plantations, and bees were collected using a net. These bees were individually separated into vials containing 96% alcohol, and pollen grains were extracted and identified. The bees were then processed at the Entomology Laboratory of the University of Cauca. Six bee genera were identified: Scaptotrigona, Paratrigona, Oxytrigona, Trigona, Tetragonisca, and Partamona. A total of 61 types of palynomorphs were also identified, primarily from the families Asteraceae, Lamiaceae, Malvaceae, Myrtaceae, Rubiaceae, Fabaceae, and Lauraceae, with genera such as Bidens, Ficus, Inga, Palicourea, Heliopsis, and Nectandra. The study highlights the importance of conserving native floral and bee diversity to ensure efficient coffee pollination and strengthen sustainable crop management strategies.

How urban green areas influence pollen morphotype diversity carried by bees in the Brazilian Cerrado

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Urbanization promotes changes in natural resource availability, influencing not only species composition but also the spatial and temporal distribution of floral resources and their pollinators. This study evaluated whether the richness of pollen morphotypes transported by bees differs between natural vegetation fragments and urban green areas, under the hypothesis that urban floral heterogeneity promotes higher pollen diversity. Pollen analysis consisted of removing pollen grains from the "safe sites" on the bodies of 536 bee specimens using fuchsin-stained gelatin, without acetolysis, followed by high-resolution slide scanning and morphotype classification. Differences in morphotype richness between environments were assessed using Generalized Linear Models (GLMs) with a Poisson distribution. A heatmap based on pollen morphotype richness was also generated to visually compare pollen richness among bee species shared between urban and natural environments, investigating potential environmental effects on bee foraging patterns. Bees collected in urban areas showed, on average, significantly higher pollen morphotype richness compared to those from natural areas, indicating a small but consistent increase in pollen diversity associated with urbanization, with species-specific variation evidenced by the heatmap analysis. The results indicate that urban green areas increase floral resource availability and pollen diversity carried by bees, especially generalist species, reinforcing the importance of green space connectivity and the maintenance of mixed plant communities for the conservation of pollination services.

Conservation strategies for native honey bee subspecies (Apis mellifera intermissa and Apis mellifera sahariensis) in Algeria under environmental change and anthropogenic pressures

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University of boumerdes

Through their central role in pollination and the maintenance of biodiversity, social bees are essential to ecosystem functioning. In Algeria, the Tellian and Saharan honey bees (Apis mellifera intermissa and sahariensis) represent a major biological and cultural heritage, particularly well adapted to contrasting climatic conditions ranging from humid Tellian regions to arid Saharan environments. However, these populations are currently facing increasing threats, including climate change, desertification, habitat loss and fragmentation, intensive pesticide use, as well as the emergence of diseases and parasites.

This communication aims to provide an overview of the conservation status of the Tellian and Saharan honey bees in Algeria, highlighting the main vulnerability factors affecting their survival and resilience. The approach is based on a synthesis of ecological, apicultural, and environmental data collected across different regions of the country, complemented by an analysis of local beekeeping practices and their impacts on honey bee populations.

The results indicate a gradual decline in colony diversity and stability in several sensitive areas, while also identifying refuge regions with high conservation potential. Finally, this study proposes integrated conservation strategies, including the protection of natural habitats, the promotion of sustainable beekeeping practices, the strengthening of sanitary surveillance, and the active involvement of local communities. The conservation of Tellian and Saharan honey bees thus emerges as a key issue for the sustainability of ecosystems and agriculture in Algeria.

Diversity and distribution of the Halictini tribe: an approach to the study of their social behavior in the department of Cauca, Colombia

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Bees of the family Halictidae represent a key group for studying social evolution due to the remarkable diversity of behaviors they exhibit, from solitary to primitive eusocial species and with polymorphic sociality. This diversity is particularly evident in the Halictini tribe, where studies suggest that social plasticity does not respond only to genetic factors, but also to environmental conditions, suggesting that regions with high environmental heterogeneity offer ideal scenarios to explore the relationship between environment and social organization.

The department of Cauca, with its wide diversity of climates and ecosystems, constitutes a representative model of environmental heterogeneity with high potential for the coexistence of multiple social strategies in halictids. The objective of this study was to characterize the diversity and geographic distribution of the Halictini tribe from georeferenced records of specimens deposited in the Entomological Collection of the Museum of Natural History of the University of Cauca. Patterns of spatial and altitudinal distribution of the genera present were analyzed, evaluating their regional coverage. 4 genera and 13 morphospecies were recorded in 10 municipalities of the department. Areas with contrasting environmental conditions that could favor different expressions of sociality were identified, highlighting their potential for future studies on social plasticity. The importance of entomological collections as a reservoir for ecological and evolutionary studies in local environmental gradients is highlighted, in addition to contributing to the knowledge of the diversity of Halictidae in the department of Cauca.

Protect Red Wood Ant’s populations to conserve Italian forest wildlife

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Red wood ants (RWAs) are a group of keystone species widespread in temperate and boreal forests of the Northern Hemisphere. Due to their large and long-lasting mounds, built by collecting plant materials and soil debris, they have a significant impact on the functioning of forest ecosystems and across several trophic levels. Their colonies are made up by millions of workers and their nest mounds host a rich invertebrate fauna, but they may also attract several vertebrates. Ant-vertebrates interactions are, however, still poorly known. Despite the key role and abundance in most of their distribution range, their conservation status (Near Threatened in the IUCN Red List) is raising increasing concerns as there is evidence of local decline and extinction.

This study aimed to assess the interaction between ants and their nest mounds with vertebrate species in different Alpine and Apennine Forests. We recorded nearly 80 nests (of Formica paralugubris, F. pratensis, F. aquilonia and F. rufa) belonging to 9 different populations for one year, using camera traps installed in front of the nests. We documented several behaviours, such as anting, predation, curiosity, and burrowing, displayed by different mammal and bird species at different times of day and year. Our results show the crucial role of RWA towards vertebrate species, pointing out their importance in preserving forest wildlife.

We suggest that emphasizing the important services ant provide to many protected mammals and bird species may help to further promote RWA conservation and protection at both local and national levels.

Beyond Species Counts: Biogeographical Regions and Evolutionary Diversity of Neotropical Swarm-Founding Wasps

FERNANDO NOLL; Marjorie da Silva; Gustavo Bellini Cortes
IBILCE/UNESP

Swarm-founding wasps of the tribe Epiponini are a major component of Neotropical insect diversity and play important ecological roles as predators and indicators of environmental integrity. Despite their relevance, large-scale distributional patterns of these social insects remain poorly documented, limiting their integration into conservation planning. Here, we present the first comprehensive biogeographical regionalization of Epiponini wasps and evaluate patterns of species richness and phylogenetic diversity with direct implications for conservation.

We compiled and curated more than 10,000 occurrence records for 248 Epiponini species from literature and museum collections across the Neotropics. Using a network-based clustering approach (Infomap Bioregions), we identified four major bioregions: Amazon, Central America, Atlantic Forest, and Mexico. Humid tropical forests, particularly the Amazon Basin, harbor the highest species richness and endemism, supporting nearly all evolutionary lineages of the tribe. Central America shows strong faunal affinity with Amazonia, whereas Mexican regions, despite low species richness, exhibit the highest phylogenetic distinctness, indicating the presence of evolutionarily divergent lineages.

Faunal similarity and taxonomic distinctness analyses reveal that regional assemblages differ markedly in evolutionary composition, even when species overlap is high. These results demonstrate that conservation strategies based solely on species counts may overlook areas of high evolutionary value. Our findings also highlight significant sampling gaps, reinforcing the need to improve distributional data for social insects.

By integrating biogeography and phylogenetic diversity, this study provides a robust spatial framework for identifying conservation priorities for Neotropical social wasps in rapidly threatened forest ecosystems.

SYMPOSIUM 25 · Social insect invaders around the globe
ORAL · Mon 17 Aug · 10:15 · K9 · Session 5 · Abstract ID 149950

Thermal tolerance of Sino-Indomalayan ants across latitude, ecological stratums and exotic status

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Abiotic conditions are an important component in shaping the distribution of species. For ectotherms, thermal limits strongly act as critical environmental and dispersal filters. Globalization has reduced geographical barriers, facilitating species introductions into new ecosystems and exposing them to new thermal ranges. Ants are major invaders, with ~310 species considered introduced worldwide. We hypothesize that exotic and tramp species might have greater thermal tolerance limits than native species which allows them to successfully establish within human disturbed habitats outperforming native species. Ecological stratum may also influence thermal tolerance, with canopy strata potentially experiencing greater extremes. In this study we assessed both critical thermal minima (CTmin) and critical thermal maxima (CTmax) of exotic and native ants across South-East and East Asia, including native species established outdoors (tramp). Using dynamic physiological assays, we tested 10,420 individuals representing ~200 ant species across eleven latitudinal regions. Generalized linear mixed model analyses revealed that CTmin shows a decreasing trend with lowest monthly mean of daily minimum temperatures values, while CTmax declines with elevation. Exotic ground-surface species exhibited higher CTmax than other groups, while litter-soil species displayed higher CTmin compared to other strata. In the Sino-Indomalayan region stratums play a role in the thermal tolerance limit capacities. On the ground surface, exotic species may establish by having greater upper limits and outperforming native species. CTmax appears critical for exotic success in certain strata, while CTmin functions as an effective dispersal filter.

SYMPOSIUM 25 · Social insect invaders around the globe
ORAL · Mon 17 Aug · 10:30 · K9 · Session 5 · Abstract ID 146501

Impact of two supercolonial species of the Tapinoma nigerrimum complex on soil epigeal fauna

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Invasive species are one of the major threats to biodiversity. Due to the central role of ants in ecosystem functioning, invasive ants can have strong negative impacts on native communities, human activities and health. The Tapinoma nigerrimum complex comprises five Mediterranean ant species recently distinguished, three of which have been introduced outside their native range by humans. Among them, T. magnum and T. darioi are both capable of forming supercolonies which enables them to efficiently monopolise resources to the potential detriment of other species. Despite the multiple introductions reported in Western Europe, their impacts on soil fauna have not been documented.

Our study aims to quantify the impact of the presence and intensity of activity of these two species on ground-dwelling arthropods, in particular ants, spiders, carabids and isopods.

We will use pitfall traps to sample arthropods in invaded and non-invaded urban French parks in Montpellier (mediterranean climate) and Lyon (continental climate) where T. darioi and T. magnum thrive respectively. Tapinoma activity levels will also be assessed in invaded parks using direct observation.

We expect an effect of Tapinoma on ground-dwelling arthropods in both cities, albeit less pronounced in Montpellier. Indeed, although T. magnum is exotic in Lyon, T. darioi is likely native in Montpellier, so that some local species might be adapted to its presence. Our results will contribute to evaluating the potential threat that these emerging supercolonial species represent to urban biodiversity.

SYMPOSIUM 25 · Social insect invaders around the globe
ORAL · Mon 17 Aug · 10:45 · K9 · Session 5 · Abstract ID 149174

Population genomics of Mediterranean Pheidole ants reveals complex patterns influenced by human history

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Ants are among the most successful and ecologically significant social insects, frequently interacting with human-modified environments. Throughout history, human activities such as land-use change and trade have profoundly altered species distributions, yet their long-term influence on the population structure of ants remains poorly understood. This is also evident in the Mediterranean Basin, a biodiversity hotspot characterised by strong environmental heterogeneity and a long history of human presence.

The AntTRAILS project aims to show how historical human activities have shaped population genomic patterns in Mediterranean ants, using the widespread and synanthropic Pheidole pallidula species complex as a model system. Using high-coverage whole-genome sequencing data from populations across the Mediterranean region, this project aims to disentangle natural dispersal processes from human-mediated connectivity and to reconstruct how population structure and gene flow have been shaped over time. Understanding these processes is essential for clarifying the origins of current distribution patterns and for assessing how historical connectivity may influence present-day responses to environmental change.

Preliminary explorations suggest pronounced geographic structuring accompanied by signals of gene flow and introgression. These patterns indicate a complex history that may not be fully explained by geography alone and is consistent with the long-term interaction between natural dispersal processes and human history in the Mediterranean region. These insights highlight the importance of considering historical connectivity when interpreting present-day population structure in easily translocated social insects.

Supercolony formation in invasive Tapinoma magnum ants

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Invasive social insects can rapidly colonise new environments and outcompete local species. A key factor in their dominance is their ability to form vast supercolonies. Individuals collaborate over distances of several kilometres. From a social evolution standpoint, this lack of boundaries between local nests is puzzling because local cheaters should be able to exploit global cooperation. The current spread of the ant species Tapinoma magnum in Germany enables us to observe the expansion of an invasive ant species in real time. This will help us to better understand how local invasions turn into large supercolonies. We collected ants from different locations in the Upper Rhine Valley where Tapinoma has become established within the last five years. We investigated the genetic structure of the population. At the same time, we conducted behavioural experiments and analysed nestmate recognition cues to determine whether a supercolony had formed. Our findings suggest that the Upper Rhine Valley has been invaded by ants of different origins. Some, but not all of the colonies are part of the same supercolony. Using these data, we have reconstructed the possible invasion history and propose different scenarios for how supercolonies can form from separate local invasions.

Behavioral mechanisms underlying competition between Lasius niger and Linepithema humile

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The Argentine ant (Linepithema humile) is an invasive species possessing several powerful competitive traits that confer superiority over other species, such as numerical dominance, mass recruitment, and high aggressiveness toward opponents. Despite this, some dominant ant species have occasionally succeeded in inhibiting the exploratory behavior or foraging activity of Li. humile, and thus may act as barriers to invasion. The present study aimed to assess whether the black garden ant (Lasius niger), a native and dominant species in Europe, can provide biotic resistance against invasion by Li. humile. Over three experiments we examined (i) resource exploitation during long-term competitive interactions between colony fragments of these species, (ii) avoidance by Li. humile of L. niger pheromonal markings after exposure to this native species, and (iii) individual aggressiveness in relation to numerical dominance and isolation from conspecifics. When facing L. niger, the foraging activity of Li. humile was strongly inhibited : for instance, we observed 40% reduction in the number of Li. humile workers foraging on the bait during the first hour of the resource competition experiment. Li. humile appeared to avoid repeated encounters with L. niger by avoiding traces of the latter’s presence. Numerical dominance by Li. humile did not reduce aggression in L. niger. These results suggest that L. niger is an effective competitor that could slow the invasion process of Li. humile in Northern Europe, not necessarily through direct interactions where numerical dominance can compensate the results observed, but possibly through the limitation of its foraging behavior.

SYMPOSIUM 25 · Social insect invaders around the globe
ORAL · Mon 17 Aug · 11:30 · K9 · Session 5 · Abstract ID 146258

Argentine ant invasion decreases seed dispersal but not other ant-dominated ecosystem processes

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Biological invasions can profoundly affect native communities, often leading to contrasting outcomes in ecosystem functioning. The Argentine ant (Linepithema humile) is among the most widespread invasive species worldwide and is known to strongly modify native communities and ecosystem processes. However, its effects are rarely assessed simultaneously across multiple ecosystem functions within the same ecological context, limiting our understanding of how invasion impacts vary among functions. Here, we applied a multi-process approach to quantify the effects of L. humile invasion on five ecosystem functions along an invasion front in Catalonia, Spain. We established 20 plots (10 × 10 m), with 10 located in invaded areas and 10 in nearby uninvaded areas approximately 2 km away. In each plot, we measured: (i) scavenging of dried Tenebrio molitor larvae; (ii) predation risk on live termites (Reticulitermes sp.); (iii) removal of myrmecochorous seeds (Euphorbia sp.); and (iv) removal and (v) predation of non-myrmecochorous seeds (Helianthus tuberosus). Invasion by L. humile had a significant negative effect on the removal of both myrmecochorous and non-myrmecochorous seeds, with removal rates of non-myrmecochorous seeds being four times higher in uninvaded areas. In contrast, termite predation, seed predation, and scavenging rates did not differ between invaded and uninvaded plots. Together, these results show that L. humile invasion strongly disrupts ant-mediated seed removal, with likely consequences for plant communities, while they seem to compensate functionally for other ant-dominated processes. However, the longer-term effects of this shift in functional actors on ecosystem dynamics need further investigation.

SYMPOSIUM 25 · Social insect invaders around the globe
ORAL · Mon 17 Aug · 11:45 · K9 · Session 5 · Abstract ID 149134

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

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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. Frist 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.

Large-scale invasive ant control with cognitive intervention of Linepithema humile in Spain

Lina Pedraza; Tiago Fernandes; Sílvia Abril; Tomer Czaczkes

The Argentine ant, Linepithema humile (Mayr, 1868), is a globally significant invasive species responsible for substantial ecological disruption and economic losses. Conventional large-scale insecticide applications have shown limited effectiveness and often cause collateral damage to native fauna and ecosystems. To address these limitations, we evaluated a novel, environmentally conscious management strategy that integrates a sustainable baiting system with a behavioral intervention to modulate individual and collective ant behavior.

The baiting system consisted of a biodegradable alginate hydrogel designed to reduce environmental impact while selectively targeting ant populations. In parallel, we applied a cognitive intervention involving caffeine and artificial odors, previously shown in laboratory conditions to influence ant behavior. Four treatments were deployed across 20 plots (10 × 10 m) within an invaded area. Ant communities were surveyed once prior to bait application and nine times post-treatment over two consecutive years.

The treatments caffeine and caffeine plus smell reduced the abundance of L. humile by nearly 60% in four months, compared with the negative control (sucrose solution). However, those results were highly similar to those of the positive control treatment (sucrose solution and poison). Interestingly, we observed the reintroduction of native species such as Crematogaster scutellaris and Pheidole pallidula at the monitoring stations after the treatments were applied. These findings suggest that while the tested approach did not suppress Argentine ant populations by 100%, it may influence community-level interactions and native species persistence. We discuss observed trends, potential ecological mechanisms, and implications for refining future intervention strategies targeting invasive ant populations.

SYMPOSIUM 25 · Social insect invaders around the globe
ORAL · Mon 17 Aug · 14:30 · K9 · Session 11 · Abstract ID 150021

Population Genetics of the invasive European paper wasp

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Social wasps are highly successful invasive species, capable of invading many diverse environments. In recent years, the rate of spread of invasive wasps has increased. Invasive social wasps often produce severe ecological and agricultural impacts. However, not every invasive wasp population is equally destructive. Some invasions form small, short-lived populations, with little impact to the local ecosystem. In contrast, other invasions are highly successful, reaching large, population sizes, and colonizing a range of different environments outside of their native distribution. This diversity of outcomes is exemplified in invasive populations of the European paper wasp (Polistes dominula). This species is native to Europe and regions surrounding the Mediterranean. An invasive population was initially detected in the USA in 1978 and shortly spread throughout most of the USA and Canada, rapidly adapting to novel environments, and negatively impacting the abundance of native paper wasp and butterfly species. Invasive populations of P. dominula have also been established in Australia (1980s), Chile (1980s), Argentina (2003), South Africa (2008), and New Zealand (2016) but in each of these cases, the invasive populations have spread more slowly. We used whole genome re-sequencing of P. dominula of invasive populations from the USA, South Africa, Argentina, and New Zealand, and samples from across the native range of this species to estimate the genetic diversity in each invasive population, and the source of each invasive population. Invasive populations of P. dominula provide a natural experiment to compare factors associated with invasion success.

SYMPOSIUM 25 · Social insect invaders around the globe
ORAL · Mon 17 Aug · 15:00 · K9 · Session 11 · Abstract ID 146506

Invasive social wasp inventory of the South Pacific isles

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Social wasps (Hymenoptera: Vespidae) are an ecologically successful, worldwide-distributed group of eusocial insects. Oceania, and more notably the Pacific islands, are unusual cold spot for social wasp diversity and research, having few native representatives and having being majorly overlooked by the scientific literature. Conversely, this global zone contains some of the most ecologically and socioeconomically severe social wasp invasions in recorded history. Here, we present a novel commentated inventory of the alien social wasp (Hymenoptera: Vespidae: Polistinae, Vespinae) of the South Pacific Oceanic islands, excluding Australia and Papua New Guinea. We include information on invasive social wasp distribution, known introductions and establishment dates, and notes on their invasive ecology. Introduced social wasps in the South Pacific consist of 11 species belonging to the Polistinae (Polistes: n=7) and Vespinae (Dolichovespula: n=1; Vespa: n=1; Vespula: n=2), nine of which are known to have established across the Pacific. Alien species were recorded on nine countries and teritories (Cook Islands, Easter Island, French Polynesia, Fiji, New Caledonia, New Zealand, Niue, Samoa, and Tonga), with earliest records having happened between the 19th and the 21st centuries, and the most recent (ongoing) incursions happening as late as 2026. This inventory provides a resource to further understand the invasion biology of social insects and to scaffold risk modelling and management efforts for a taxon of impactful invasive predators in a severely understudied area.

SYMPOSIUM 25 · Social insect invaders around the globe
ORAL · Mon 17 Aug · 15:15 · K9 · Session 11 · Abstract ID 146470

Investigating behavioral, ecological and abiotic factors influencing mating success in an invasive social yellowjacket wasp (Vespula pensylvanica)

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Yellowjacket wasps (Vespula spp.) can shape arthropod communities through predation and competition for resources. When yellowjacket colonies overwinter or become perennial, they can increase their ecological impacts on local ecological communities, especially in their introduced ranges. By understanding what behavioral, ecological and abiotic factors influence mate location, acceptance, and mating success, we may be able to better predict years with high wasp populations (“outbreak” years) and develop strategies for wasp control in their introduced ranges. Here, we report recent findings as to identifying which gynes will be attractive, which males are most likely to successfully mate, and additional factors that influence mating success in the western yellowjacket, Vespula pensylvanica. Such data provide insights into the queen joining process and the transition towards polygyny and perenniality in this invasive social wasp.

SYMPOSIUM 25 · Social insect invaders around the globe
ORAL · Mon 17 Aug · 15:30 · K9 · Session 11 · Abstract ID 148530

The continuing worldwide invasion of Vespa velutina hornets

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Of the five species of Vespa hornets that have successfully invaded exotic regions, Vespa velutina, the Yellow-legged Hornet (YLH), has emerged as the most successful of them. Since it was first detected in South Korea (2003) and France (2004), the YLH had been detected in 23 countries outside of its endemic range by the end of 2025. During 2025, notable range extensions occurred in New Zealand (the first colonization in Australasia and south of the Equator), Algeria (the first in Africa), Denmark, Northern Ireland, Sardinia, and the Azores, and populations grew explosively in Switzerland, the Netherlands, and Germany where the YLH has been established for several years. For example, in Switzerland and the Netherlands, the number of nests reported have increased by 6.5x per year. The population in southeastern USA is now well established: more than 150 nests were located and destroyed during 2025 within an area of ~8000 sq. km.

The several hundred gynes reared by each YLH colony disperse both naturally and with the assistance of humans, contributing to rapid population growth and creating high propagule pressure on regions not yet occupied. Genetic analyses suggest that the populations in continental Europe, the USA, and New Zealand were each initiated by a single inseminated foundress gyne. It is unclear how these populations thrive despite very low genetic diversity and single locus complementary sex determination. The effects of abundant V. velutina in various ecosystems are poorly documented, thereby limiting our understanding of its impact on ecosystems.

SYMPOSIUM 25 · Social insect invaders around the globe
ORAL · Mon 17 Aug · 15:45 · K9 · Session 11 · Abstract ID 148725

Incursion and early-stage management of the yellow-legged hornet (Vespa velutina) in New Zealand, with a focus on eradication

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The yellow-legged hornet (Vespa velutina) was detected for the first time in New Zealand in spring 2025, when queens with small primary nests were observed in suburb of Auckland. Genetic and phenological inference suggest that a single mated queen likely arrived in the previous summer, successfully founded a nest, and produced new dispersing queens. A national biosecurity response was initiated, led by the Ministry for Primary Industries, with the explicit goal of eradication. The programme comprised three integrated phases: (i) systematic surveillance and destruction of primary nests, including visual search and public reporting; (ii) localisation and elimination of secondary nests using baited traps, tagging, and radio-tracking; and (iii) deployment of protein-based toxic baits containing fipronil, developed originally for Vespula spp. wasps. More than 50 queens or nests were found and destroyed, with 60% were identified by government teams and 40% through members of the public. Public engagement was extensive nationwide, with >12,000 photographic reports submitted from throughout the country. This presentation details the incursion chronology, operational decisions, surveillance analytics, and lessons learned from the first season. Multiple hornet-free years will be required to demonstrate successful eradication, but early indicators suggest strong feasibility.

SYMPOSIUM 25 · Social insect invaders around the globe
ORAL · Mon 17 Aug · 16:00 · K9 · Session 11 · Abstract ID 149271

Naivety in the face of invasion: Western honeybee behavioural and molecular responses to the Asian hornet

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The western honeybee (Apis mellifera) is a key pollinator worldwide but is threatened by predators, including the invasive Asian hornet (Vespa velutina), which has caused major apicultural losses in parts of southern Europe. While honeybee responses to familiar predators are well studied, we know much less about how bees respond when confronted with a novel threat.

In this study, we examined honeybee behaviour foraging at a sugar feeder in southwest England in the presence of three different cuticular hydrocarbon stimuli: a non-nestmate conspecific, a known predator (Vespula germanica), and the invasive Asian hornet V. velutina. We quantified behavioural responses at the sugar feeder and combined these observations with analyses of gene expression in the antennae of bees following exposure to explore how they detect and discriminate between threats.

The bees responded strongly to both the non-nestmate and the known predator, showing clear changes in behaviour accompanied by shifts in antennal gene expression. In striking contrast, the presence of V. velutina elicited little to no behavioural or molecular response. This suggests that honeybees may not readily recognise this invasive hornet as a threat.

Overall, our results highlight how honeybee defensive responses depend on prior evolutionary experience, and suggest that a lack of recognition may leave bees particularly vulnerable to emerging invasive predators.

SYMPOSIUM 25 · Social insect invaders around the globe
ORAL · Mon 17 Aug · 16:15 · K9 · Session 11 · Abstract ID 149467

Activated Charcoal: A Highly Potent Legal Alternative for Vespa velutina Nest Destruction

Andreas Presuhn; **Ulrich Ernst[1]**

[1] *Independant Scholar*

The invasive yellow-legged hornet Vespa velutina nigrithorax has spread across Europe following its accidental introduction into France in 2004. This species adversely affects biodiversity, apiculture, pomiculture and viticulture, and human health. Current management relies predominantly on nest destruction; however, manual removal is often logistically challenging and costly because nests are typically located high in trees (up to 30 m), frequently necessitating vehicle-mounted lifts. Ground-based application of biocides using long injection lances is comparatively rapid and inexpensive, but in many countries insecticides are not permitted because products are not specifically authorized for hornet control. Consequently, alternative approaches are needed. Here, we evaluated the efficacy of activated charcoal for nest destruction in V. v. nigrithorax. We injected 150 nests with 50–100 g of activated charcoal and subsequently destroyed the nests. One week later, we assessed worker survival and the establishment of new nests. Emergency nest construction by surviving workers was observed in 3 of 150 cases (2.0%). This rate was comparable to that observed following insecticide treatment (2 of 136 cases; 1.5%). Activated charcoal therefore appears to be similarly effective to insec-ticide-based control while offering advantages in terms of environmental compatibility, user safety, ease of handling, and legal applicability in Europe. Activated charcoal may represent a practical alternative to manual nest removal and unauthorized insecticide use.

Nest mound damage reduces subsequent venom delivery by red imported fire ant colonies

Kevin Haight
Arizona State University

The imported fire ant, Solenopsis invicta, is a widespread and spreading South American ant species, now also found in areas of continental North America, the Caribbean, Asia, Australia/Oceania, and Europe. It thrives in disturbed habitats and often nests in lawns, gardens, fields, pastures, and along roadways and sidewalks where it builds subterranean nests with above-ground mounds. Their affinity for areas of human habitation exposes their chamber-filled mounds to damage by human activities. Coupled with their aggressive stinging behavior, this results in an estimated 1/3 or more of the human population in affected areas being stung each year. Here, I investigate whether previous nest mound damage affects the subsequent defensive stinging behavior of S. invicta colonies to determine whether mound condition affects the severity of envenomation people face during interactions with fire ants. I repeatedly sampled field colonies under intact, razed, and rebuilt nest mound conditions and found the average venom dose delivered when defending from razed nest mounds was reduced to 54% of that delivered from intact mounds and returned to previous levels after mounds had been rebuilt. Also, the extent of mound damage and venom dose from razed mounds were negatively correlated. Thus, fire ant colonies appear to vary their defensive effort in response to mound condition. Because the pain and tissue damage caused by their venom is dose dependent, these results suggest that by purposefully damaging S. invicta mounds people who live among them may be able to reduce the severity of envenomation they face from future stings.

Applied research to improve the management of the invasive termite Reticulitermes flavipes in Canary Islands, Spain.

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Reticulitermes flavipes (Kollar, 1837) is a subterranean termite species native to eastern and central parts of North America. Globalisation and international trade have led to its introduction and establishment in many countries, both in America and Europe.

This termite is one of the most harmful subterranean termite pests in both its native and introduced ranges. Its populations cause damage to buildings, trees and shrubs around the world, causing severe economic losses.

It is a social insect with considerable reproductive and ecological plasticity and complex population and colony structures that enhance their ability to colonise and invade new environments.

Its presence on the island of Tenerife has been reported since 2009, although it is thought to have arrived in the early 2000s. During this period, it has spread through various municipalities, affecting buildings, street furniture, crops and native and ornamental plant species.

Faced with this problem, various public institutions have joined forces to contain and try to eradicate this invasive termite. As part of the strategy for the management, control and eventual eradication of this species on the island, research has been undertaken to improve our knowledge of the species, of control measures and their potential side effects. The results confirm the existence of large and extensive colonies on the island, an absence of aggression between colonies, the capacity to establish new colonies through primary reproductives and neotenics, the efficacy of treatments and that no severe side effects have been detected in the environment.

The Cutting edge of early detection and management systems for invasive alien social insects in Japan

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Unintentional introductions of invasive alien species have caused severe negative impacts on native ecosystems worldwide. Among them, social hymenopteran insects include many invasive species that can cause extensive damage by rapidly increasing their populations in newly invaded areas. The red imported fire ant, Solenopsis invicta, is one of the most notorious examples, having produced serious impacts in invaded regions such as the United States and China. Since its first detection in Japan in 2017, a cumulative total of 171 invasion cases had been confirmed by December 2025. Although the establishment of S. invicta has so far been prevented in Japan, the number of invasion cases reached a record high of 36 in 2025, indicating a critical warning stage. Against this increasing risk of establishment, there is an urgent need to enhance early detection and control systems. In addition, the development of efficient management methods for already established invasive alien social insects—such as the yellow-legged hornet Vespa velutina and the Argentine ant Linepithema humile—has become an important social and environmental priority. To address the invasion and spread of these invasive alien social insects, we have been advancing early detection and control technologies and building cooperative management systems in collaboration with local governments. In this presentation, we introduce the current status of invasion and spread of invasive alien social insects in Japan and the latest progress in the advancement of detection and control systems.

Guiding management strategies of the yellow-legged Asian hornet through results of citizen science

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The yellow-legged Asian hornet Vespa velutina nigrithorax is a predator of honeybees and other pollinators that has been found for the first time on the European continent in 2004 in France. Since then, the hornet invaded all of France and neighbouring countries before continuing eastwards, reaching Switzerland in 2017. Recently, the same subspecies also became invasive in the US and New Zealand. The first response to the hornet's presence has been widely rushed and rather based on half-truths than scientific facts. Thus, there is at the same time a need to educate the public with science-based information and to generate data about the specie's biology, ecology, and behaviour to develop effective management strategies. The hornet being a relatively big and easy to identify species, generates a strong engagement by the public in Switzerland, making it a great opportunity to conduct citizen science. Here, we present results of data gathered with help of citizens through multiple means, including an online reporting platform, observations done by beekeepers, data gathered during searches of nests, dissection of nests brought to us by various people, and scientifically guided trapping campaigns. The results are a great well of information about the hornet's behaviour, phenology and feeding habits, efficacy of nest searching and elimination methods, as well as the (in)efficiency of trapping campaigns. As such, citizen science can be used to refine and develop effective management strategies and give recommendations about the dos and don'ts in the fight against this invasive hornet.

SYMPOSIUM 26 · The role of citizen science in social insect research
ORAL · Wed 19 Aug · 10:30 · K10 · Session 36 · Abstract ID 145143

Citizen science reveals caste-specific seasonality and unexpected winter activity in invasive New Zealand wasps

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[1] *Te Herenga Waka - Victoria University Wellington*

Invasive social wasps pose significant ecological and economic risks in New Zealand, and long-term datasets on their phenology would be valuable for effective pest management. Citizen science offers a growing opportunity to generate broad-scale ecological information. In this study, we analysed caste-specific seasonal activity and spatial patterns of three invasive wasps, Polistes dominula, Vespula germanica, and V. vulgaris, using online citizen science records. We used a dataset from the Global Biodiversity Information Facility, which had 3554 observations spanning from 1945–2024. Species identifications submitted by the public were generally accurate, and expert review substantially improved the dataset by adding caste-level information. Seasonal patterns of reproductive castes matched expected phenology, including a clear autumn peak in drone activity. Records were concentrated in urban and lowland areas, reflecting known citizen-science sampling biases. An ecologically notable finding was the observation of winter-active workers across all three species, recorded on both islands and throughout every winter month. Their presence outside major urban areas suggests that some colonies may persist through winter, likely indicating potential perennial nesting. Overall, the value of citizen science was emphasised in this study, particularly for identifying caste-specific seasonal patterns in invasive species. The unexpected prevalence and distribution of winter-active workers demonstrate the potential of public datasets to reveal unusual behaviours and inform targeted wasp management in New Zealand.

SYMPOSIUM 26 · The role of citizen science in social insect research
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MonitAnt Citizen Science Project: Europewide assessment of mound-building Formica ants

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Mound building Formica ants of the Formica rufa group, commonly referred to as red wood ants (RWA), are a Holarctic group widely distributed in temperate and boreal forests and natural grasslands. As keystone and umbrella species, RWA provide numerous ecosystem services, yet many populations are currently in decline, raising increasing conservation concerns. Within the framework of the EU Biodiversa+ project MonitAnt, we established a citizen science component to improve large-scale knowledge of the distribution and ecology of red wood ants across Europe.

Through this citizen science initiative, participants record the geographic locations of RWA nest mounds and provide additional ecological information, including photographs, mound dimensions, habitat characteristics, tree species used for foraging, and, where possible, ant species identification. Since its launch in May 2024, more than 2,600 observations have been submitted via the MonitAnt platform and iNaturalist, covering six red wood ant species across 16 European countries. Preliminary analyses indicate that 39% of nests are part of polydomous colony systems, with a mean mound height of 61 cm and a mean diameter of 108 cm. Most nests were located in forest interiors (48%) or at forest edges (34%), while occurrences in open or urban habitats were rare.

By combining citizen science data with environmental information, MonitAnt provides new insights into the habitat preferences and large-scale distribution patterns of red wood ants. These findings contribute to a better understanding of their ecological requirements and support the development of evidence-based recommendations for conservation, forest management, and policy.

The Ant-Free Atacama Desert: Distributional Limits of Native Ants in Northern Chile

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Ants are widely regarded as one of the most ubiquitous and abundant animal groups on Earth, occupying nearly all terrestrial habitats. Apart from the polar regions, only a small number of remote islands are known to lack native ants, and ants are typically considered dominant even in desert ecosystems. In this study, we tested whether this holds true for the Atacama Desert, one of the driest and oldest deserts on Earth. Through intensive field sampling combined with extensive citizen science data and a comprehensive literature review, we examined ant distributions along pronounced aridity and elevational gradients in northern Chile.

The integrated dataset reveals a contiguous, ant-free region for native species spanning the hyperarid desert core. Native ants occur only in two marginal zones: a narrow coastal strip associated with fog-fed lomas south of the Mejillones Peninsula, and the Andean slopes that receive seasonal summer rains. These habitats mark the extreme limits of ant occurrence in arid environments. Together, these results identify the Atacama as one of the largest continuous land areas on the South American continent without native ant fauna, with interior records restricted to invasive species established in human settlements within the desert interior.

Methodologically, this study demonstrates the utility of integrating citizen science data with targeted field sampling in remote areas and highlights the potential of citizen science to help evaluate whether apparent absences reflect true limits or undersampling, while also strengthening early detection of invasive ants in desert landscapes.

Atta Leafcutter Ants are Climate-Sensitive Bioindicators: Integrating evidence from iNaturalist, literature, and expert researchers

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We developed Atta leafcutter ants as bioindicators that respond at fine scales to geographic and seasonal changes in precipitation and temperature in both the Southern and Northen Hemispheres. We first elucidated biogeographic patterns of mating-flight phenologies of Atta leafcutter ants across the entire Atta range from Uruguay/Argentina to the USA, using 2335 records of Atta reproductives from the community database iNaturalist, then ground-truthed these biogeographic pattens by comparison with (i) mating-flight records (n=806) reported in the Atta literature; and (ii) mating-flight observations (n=836) accumulated by a consortium of 50+ experts who have researched Atta biology for a combined 1000+ work-years across the Atta range. Mating-flight information of Atta reproductives deposited in two museum collections covering Colombia (Universidad Nacional Agronomía Bogotá) and north-east Brazil (CEPLAC Ant Collection) complement the iNaturalist data, together elucidating two regions of special biogeographic interest. Overall, the iNaturalist data outperform the data from the literature and from the Atta experts, documenting for example so-far unknown gradients in mating-flight phenologies (e.g., Colombia to the USA) that correspond to geographic gradients in precipitation and temperature; and transitions over short distances (e.g., 100 km) from mating flights predominantly early in the year to predominantly late in the year, particularly across the biogeographically complex Andean region of Colombia. Combined, these findings recommend Atta as an insect bioindicator to monitor impacts of climate change with detailed spatial and temporal resolution. We outline future research directions using the continuously growing, and now ground-truthed, information on Atta reproductive phenology available at iNaturalist.

SYMPOSIUM 26 · The role of citizen science in social insect research
ORAL · Wed 19 Aug · 11:30 · K10 · Session 36 · Abstract ID 145595

Is climate change shrinking bees?

Madeleine Ostwald[1]; Charles Thrift[2]; Robert Guralnick[3]; Julie Allen[4]; Colleen Smith[2]; Adrian Carper[5]; Peter Oboyski[6]; Giar-Ann Kung[7]; Pamela Horsley[8]; Sagmi Lee; Katja Seltmann[2]

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Declining body size has been proposed as a possible ‘universal response’ to climate warming. For bees, evidence for size declines is emerging but fragmented, due in part to challenges of measuring body size across large geographic, taxonomic, and temporal scales. We addressed this challenge by leveraging citizen/community science to crowd-source body size measurements from specimen images arising from museum digitisation efforts. Citizen scientists showed high engagement and accuracy in the measurement task, with only a 2% measurement error compared with trained researchers. Using this approach, we generated replicated size measurements for thousands of bee specimens across California, spanning all North American bee families and more than a century of climate and land use change. We use this data to evaluate roles of climate and land use as possible drivers of size change over time. Because size is implicated in bee social interactions, pollen transport, thermoregulation, and more, these effects may have consequences that scale from individual fitness to population persistence and ultimately to ecosystem functioning.

Citizen Science as a Tool for Quantifying Insect-Plant Interactions and Network Dynamics

Morgan Morrison

Ecological interactions can provide valuable insights into the structure, dynamics and function of ecological systems. The use of interactions has aid understanding of insect–plant communities. However, interaction data is labour intensive to collect and require repeated sampling across space and time to capture their inherent dynamics. Citizen science has increasingly become a key tool in gaining information of the occurrence is species, yet its potential contribution to monitoring ecological interactions remains less well explored.

Here, we assess whether citizen scientists can contribute meaningful plant–pollinator interaction data. To answer this, we mirrored opportunistic monitoring by citizen scientists with observation generated through regular, standardised monitoring conducted by researchers. Here, we use the context of urban garden which have been identified as a key refuge for insects. We evaluate the statistical and ecological implications of citizen-generated data for biomonitoring pollinator interactions and diversity.

In addition to ecological outcomes, we examine the social impacts of participation in interaction-focused citizen science. By engaging gardeners as active contributors, we explore changes in relationships between people and nature at both the scale of individual gardens and the broader network of urban green spaces within towns. This study aims to inform the use of citizen science generated interaction data in ecological monitoring while supporting nature-positive actions and relationship in fragmented urban landscapes.

When stingless bees and ants bewitch: an approach to the myths and realities of four ethnic groups in the Peruvian Amazon

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Stingless bees (Apidae: Meliponini) have attracted increasing research interest across several Latin American countries, particularly due to the recent expansion of their management and rearing, known as meliponiculture. Unlike the well-documented Maya meliponicultural tradition, there is no evidence of comparable ancestral practice in the Amazon Basin. This study examines cultural expressions related to stingless bees among Amazonian peoples of the Peruvian Amazon. We reviewed ethnohistorical and socioeconomic references for 30 Indigenous groups and conducted in situ documentation of traditions and myths among three ethnolinguistic groups: Kichwa Lamas, Yánesha (Arawak), and Kampu Piyawi (Shawi-Cahuapanas). A symbolic interpretation of myths, social conventions, and practices governing human–bee relationships was undertaken using an ethnographic approach. Across the three groups, we identified convergent myths, roles, and traditions that attribute an ambiguous, magical-spiritual role to stingless bees and other social insects, in which their “bewitchment” is perceived as harmful, while their use as a remedy is considered beneficial. This duality is consistent with oral traditions reported for other Amazonian societies. Our findings suggest the presence of ideological factors—beyond practical considerations—that may help explain the absence of stingless bee domestication, as well as the links between subsistence conditions and the persistence of these cultural expressions. These relationships are discussed within a broader context of rapid changes in subsistence strategies, ecosystem loss, and the erosion of community cohesion.

Rate your bugs: using a mobile app to map public attitudes towards invertebrates

Heikki Helanterä
University of Oulu

We live in a world where conservation needs are dire, but sustainable conservation needs public support and acceptance. In this project we use a mobile app to collect data on public attitudes towards insects and other invertebrates. In the app users rank images on attractiveness, interest, familiarity and willingness to conserve. Combined with background data on users, this allows an exploration on how exposure to nature and previous knowledge on insects, as well as species level traits affect feelings of attraction and curiosity, and ultimately the motivation to conserve.

This is an interdisciplinary collaboration between entomologists, ecologists and environmental social scientists, and part of broader science communication efforts by Finnish insect researchers across several institutes.

Come and see my poster and share your citizen science and outreach experiences!

SYMPOSIUM 26 · The role of citizen science in social insect research
POSTER · Abstract ID 149954

How To Take Better Insect Photographs for Citizen Science

Alexander Wild
University of Texas at Austin

A brief tutorial and discussion of how scientists and citizen scientists can create images tailored for identification, for ecology, and for behavioral observation using just a cell phone.

Genetic diversification of ectoparasitic mites (Varroa spp.) across honey bee species and populations

Alexis Beaurepaire

Bee Research Centre, Agroscope

Parasite host shifts represent a growing global threat to biodiversity. The ectoparasitic mite Varroa destructor is considered the most devastating parasite of European-derived western honey bees (Apis mellifera) and plays a major role in the transmission of viruses to both managed and wild pollinators. Despite its severe impact worldwide, our understanding of the mechanisms that have enabled some mite populations to shift from the eastern honey bee (Apis cerana) to introduced colonies of A. mellifera in Asia, while most mite populations did not, remains limited. Additionally, how invasive mite populations managed to rapidly adapt to new western honey bee populations across the globe, despite low genetic diversity caused by population bottlenecks and an inbred life cycle, remains poorly understood. To address these knowledge gaps, I will present results from population genetic studies conducted over the past decade that elucidate host-shift events of Varroa spp. in Southeast Asia and examine patterns of genetic differentiation among mite populations associated with their original and new hosts. Taken together, these findings highlight the complex interplay among mite and honey bee traits, environmental factors, and human management practices. As additional ectoparasitic mite species continue to spread globally, understanding the factors that drive host-range expansion is increasingly urgent to prevent future host shifts and biological invasions.

Who is the host and who is the vector? Bacterial communities and pathogens in wild bees and honey bees of a mountain region.

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Wild bees are declining in abundance and species richness due to human impact. In contrast, the numbers of the domesticated Western Honey Bee (Apis mellifera) have been increasing in recent decades. However, particularly wild bee diversity and specialization are essential for successful pollination in both agricultural and natural ecosystems. Whether high honey bee densities could pose a further threat to wild bees due to competition, pathogen transmission, and microbiome alteration, as some claim, remains to be determined. We explored the bacterial community structure and the distribution of common bee pathogens (viruses, microsporidian, trypanosomatids) in various habitats in the Austrian Alps. Bumble bees (Bombus spp.), as key pollinators and major eusocial bee group in Alpine environments, were sampled as well as three solitary wild bee species (Andrena hattorfiana, Andrena vaga, Osmia cornuta) and honey bees. Bacterial communities differed little among honey bee individuals, while bumble bees had the most differentiated bacterial communities. High honey bee densities corresponded with lower bacterial diversity in wild bees and a higher bacterial similarity between honey bees and wild bees. All pathogens examined were detected in honey bees and bumble bees, but not every pathogen in every solitary bee species. Concluding, we found hints that high honey bee density may negatively impact wild bees through alterations of wild bee microbiomes and pathogen transmission. Nevertheless, we need more precise methods to assess honey bee density and a better understanding of transmission mechanisms and their consequences for wild bees to ultimately preserve the diversity of these key pollinators.

SYMPOSIUM 27 · Host-microbe interactions in social insect
ORAL · Mon 17 Aug · 11:00 · Halle 4 · Session 1 · Abstract ID 148529

Pathogens and Ants: Does antimicrobial investment across ant species predict susceptibility against fungal entomopathogens?

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Social insects live in dense, highly interactive colonies where the risk of disease transmission is much higher than in solitary animals. To mitigate this risk, ants employ a range of external immune defenses, including antimicrobial compounds that prevent infection following pathogen exposure. However, not all ant species invest in external antimicrobial defenses and may instead rely more heavily on internal immune mechanisms. Here, we tested whether ants that vary in external antimicrobial investment differ in their susceptibility to entomopathogenic fungi. First, we compared multiple strains of the generalist entomopathogenic fungus Beauveria bassiana against the red imported fire ant, Solenopsis invicta. We then selected the most virulent strain and conducted a cross-species comparison across 12 ant species exposed to six concentrations of B. bassiana. We predicted that species investing in external antimicrobials would show greater resistance at low pathogen doses but would be overwhelmed at high doses relative to species lacking such investment, which we expected to be comparatively more resistant at high doses due to higher investment in internal defenses. Our results showed that ant species do vary broadly in their pathogen susceptibility, but this was not related to antimicrobial investment. We further examined additional traits, including body size and cuticle thickness, and found support for an effect of body size but not cuticle thickness. These results suggest that factors other than external antimicrobial investment shape ant susceptibility to fungal pathogens.

Interacting Parasites, Host Genetics, and Gut Microbiomes Shape Contrasting Population Trajectories in Wild Bumblebees

Miles Liam Nesbit[1]; Ryan Ellis[1]; Natasha Ramsden[1]; Seirian Sumner[2]; Claire Carvell[3]; Peter Graystock[1]

[1] Imperial College London; [2] University College London (UCL); [3] UK Centre for Ecology and Hydrology

We investigate how interactions among parasites, host population genetics, and the gut microbiome contribute to population persistence or decline in wild bumblebees. We sample 255 individuals from four sites across the United Kingdom, spanning three species with contrasting trends: Bombus ruderatus (declining), Bombus hortorum (stable or increasing), and Bombus terrestris (widespread and abundant).

For each bee we quantify infection by three common gut parasites (Nosema, Crithidia, and Apicystis) using absolute parasite counts per individual. This captures infection prevalence, infection intensity, and patterns of co-infection. For a subset of individuals (n = 206), we generate genome-wide RAD-seq data to characterise population structure and selection pressures. For a smaller subset (~ 90 bees), we sequence the gut microbiome to describe microbial diversity and community composition.

By integrating these datasets, we move beyond single-factor explanations for species decline. Parasites, host genetics, and microbiomes do not act independently; instead, they form a tightly interacting system in which indirect effects may be as important as direct ones. Closely related species that share environments but differ strongly in population trajectory provide a powerful comparative framework for identifying underlying mechanisms rather than simple correlates of decline. By comparing a declining species with a stable sister species, we identify biological interactions that increase vulnerability to population decline. This work offers a systems-level perspective on disease ecology in social insects, with relevance to host–pathogen barriers, microbiome-mediated resistance, and pollinator conservation.

Beyond eusocial hosts: metagenomic evidence of trypanosomatid spillover in a bee community

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Social insects provide ideal environments for parasite establishment and transmission; nevertheless, many pathogens circulating within these systems may exhibit host ranges that extend beyond eusocial boundaries. In bee communities, trypanosomatid parasites are recognized as important pathogens infecting principally eusocial hosts, such as Apis and Bombus. However, how these parasites circulate among phylogenetically and ecologically distinct bee species within a community remains poorly understood. Identifying the mechanisms that allow or restrict pathogen transmission across host species is therefore essential for understanding spillover dynamics in bee communities. Using a shotgun metagenomic approach, we generated deep sequencing data from a bee community located in the Northeastern U.S., composed of gut samples from more than ten bee genera (n = 137). We are currently investigating patterns of trypanosomatid diversity, prevalence, and host association across this bee community. Our investigation aims to assess whether shared trypanosomatid strains occur across multiple bee species, which would suggest pathogen spillover, and to evaluate how host-related factors, such as gut microbiome composition, may contribute to pathogen prevalence across hosts. We expect to detect signatures of host specific and generalist trypanosomatid strains that correlated with changes in host species, as well as differences in microbiome composition across bee species that could explain trypanosomatid prevalences in this bee community.

Changes in Floral Traits and Pollinator Behavior Induced by Plant Virus Infection

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The relationship between plants and their pollinators is a classic example of mutualism, having co-evolved over long timescales. Pollinators assess a combination of floral signals (e.g., morphology, color, and scent) and rewards (e.g., pollen and nectar) to decide which flowers to visit. Bumblebees, eusocial insects belonging to the family Apidae, exhibit high learning abilities and floral constancy and are key pollinators for many crops and wild plants. Recent studies have revealed that bumblebee foraging behavior can contribute not only to pollination but also to the transmission of plant pathogenic viruses. In this study, we aimed to examine whether plant viruses exploit pollinators as potential vectors and how viral infection alters plant traits and pollinator behavior to facilitate viral spread. We inoculated snapdragon plants with a primrose isolate of Plantago asiatica mosaic virus (PlAMV) and quantified floral traits—including color, nectar volume, and sugar concentration, and volatile profiles—followed by a Y-tube olfactometer assay to test pollinator preference. Our results indicate a potential for horizontal transmission of PlAMV from infected to healthy flowers via pollinators. We also found that PlAMV infection caused pronounced changes in floral scent, which increased the attraction of bumblebees to infected flowers.

Nosema ceranae infection alters honey bee (Apis mellifera) queen behavior and reproductive capacity

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The takeover of Nosema ceranae over N. apis as the primary honey bee (Apis mellifera) gut pathogen in

the United States has revealed a knowledge gap regarding how N. ceranae affects the reproductive health of queens and drones. While the general consequences of intense Nosemosis are well substantiated, the long-term effects of Nosema infection, specifically on queen behavior, are understudied. In this study, we explored the effects of N. ceranae infection on queen egg-laying capacity, mobility, and retinue behavior. We hypothesized that queens would lay fewer eggs, be less mobile, and elicit a smaller worker retinue after inoculation with N. ceranae compared to the baseline values for these behaviors prior to infection. We set up observation colonies headed by sister queens and fed each a sucrose solution. We monitored the queens' egg-laying capacity, mobility, and retinue behavior in the observation colonies for six consecutive days. Then, each queen was inoculated with 200 µL of sucrose solution containing roughly 200,000 N. ceranae spores and measured the same parameters from each queen starting one day post infection, and doing so for six consecutive days. We found a significant increase in mobility and egg-laying capacity with a significant decrease in retinue size in queens

post infection. Our results indicate that honey bee queens infected with N. ceranae suffer physiological consequences that is likely to be translated to an overall decline in colony productivity over time.

Bumble bee hygienic behaviour induced by colony exposure to a bacterium-based biopesticide

Michelle Scheffler; Karoline Wueppenhorst; Doreen Babin; Abdulrahim T. Alkassab; **Silvio Erler**

Julius Kühn Institute (JKI) - Federal Research Centre for Cultivated Plants

Social immunity, the behavioural defence in social insects, includes the removal of sick or diseased individuals (e.g., adults, pupae, larvae) from their colonies. This specific behaviour, to reduce disease spreading within colonies, is well described for ants, honey bees and termites. However, for bumble bees only limited information about corpse removal is known so far. Here, we used full-size colonies of the model bee species Bombus terrestris to investigate if brood exposed to a bacterial biopesticide (Bacillus thuringiensis ssp. aizawai, strain: ABTS-1857), especially larvae, will be actively removed by worker bees. Bacteria-exposed colonies removed the most larvae within 24 days post-exposure compared to both: (1) colonies that received untreated sugar solution and (2) colonies with mechanically wounded larvae. Larger colonies of all treatment groups removed more larvae than smaller ones. The majority of the removed larvae were of light weight (< 100 mg) and of white colour. Few removed larvae of all treatment groups showed signs of coloured dots or were desiccated. All experimental manipulations had no impact on colony development or the production of new sexuals. We could show that bumble bee colonies might regulate larvae removal behaviour to guarantee successful colony development and to reduce potential burden by affected individuals. However, underlying mechanisms, especially the chemical ecology of brood-worker interaction and trigger substances initiating brood removal, need further investigation.

SYMPOSIUM 27 · Host-microbe interactions in social insect
ORAL · Mon 17 Aug · 15:00 · Halle 4 · Session 7 · Abstract ID 146432

Transmission in Action: What pathogen mimics can show about disease spread

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Disease can easily spread in social insect colonies due to the close interactions between colony members. However, our understanding of which host behaviors most affect infection dynamics has so far been limited to retrospective, correlative evidence of infectious particle transfer after observing specific behaviors. Moreover, many pathogens can transmit through both direct host-to-host contact and indirect transfer via a contaminated environment. Even for highly studied model systems like the fungal pathogen Metarhizium infecting ant colonies, it therefore remains unresolved which interactions most promote cross-contamination, and how important indirect transmission is for disease spread through the colony.

To address these questions, we have developed a highly fluorescent artificial pathogen mimic with adhesive properties and chemical cues similar to Metarhizium spores. After exposure of Lasius ants to these mimics, we use our real-time imaging setup to simultaneously record the interactions between the exposed ant and its nestmates, the pathogen mimics, and the nest environment, allowing us to observe particle transfer as well as grooming events in action.This visualization of removal and transmission in the context of specific host behaviors fills current knowledge gaps that cannot be addressed with natural pathogens alone. It helps shed light on the mechanisms underlying both the efficiency and the risk of social immunity emerging from the close interaction between infectious ants and their colony members.

Immune heterogeneity shapes disease spread in clonal ant societies

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Classical epidemiological models often assume homogeneous susceptibility among hosts, yet growing evidence shows that individual heterogeneity in immune competence and behaviour can strongly shape transmission dynamics. In social organisms, such heterogeneity interacts with collective defences, or “social immunity,” but how variation among individuals scales up to influence group-level disease outcomes remains poorly understood. To investigate this, we used the clonal raider ant Ooceraea biroi. We combined CRISPR/Cas9-mediated knockout of a key immune pathway with immune priming to generate immune-suppressed, immune-enhanced, and wild-type individuals within otherwise genetically identical groups. These were used in controlled ratios to assemble colonies with low and high levels of immune heterogeneity and exposed to bacterial and fungal pathogens. We quantified infection outcomes and assessed how immune heterogeneity reshaped social interactions and networks.

At the colony level, our data will allow us to test two alternative and non-mutually exclusive outcomes. First, increased immune heterogeneity may elevate pathogen transmission if highly susceptible individuals contribute disproportionately to spreading, acting as super-spreaders. Alternatively, transmission may be buffered by social immunity, with resistant individuals compensating through changes in behaviour, such as altered contact patterns, increased care, or social exclusion of susceptible nestmates.

Our results will provide a causal experimental framework linking individual immune heterogeneity to collective disease outcomes in a social system. By integrating immune manipulation, behaviour, and controlled group composition, this study moves beyond correlative approaches and advances our understanding of how individual variation scales up to group-level epidemiology, with implications from wildlife conservation to public health.

Evasion of behavioural disease barriers facilitates cross-species virus spillover

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Predicting which disease spillover events lead to sustained transmission in new hosts represents a major challenge in disease ecology and epidemiology. Although cross-species virus transmissions occur frequently, successful host shifts with subsequent disease emergence are rare, suggesting that host barriers limit infection success. In social insects, high contact rates may amplify transmission risk, while collective disease-defence behaviours (social immunity) are expected to mitigate disease risks. Here, we investigate whether social immunity restricts virus transmission following a host shift from honey bees to ants. Using the acute bee paralysis virus (ABPV) and Lasius niger ants, we tested whether ants avoid virus-contaminated food and restrict its distribution within the colony. We combined binary food-choice assays offering ABPV-infected versus control honey bee pupae with automated behavioural tracking of entire colonies to reconstruct trophallactic contact networks and food flows. Contrary to expectations, colonies exploited ABPV-infected food more than control food. This pattern was driven by earlier discovery of infected resources and reinforced by higher feeding frequencies and durations. Tracking data further revealed that virus-contaminated food was shared more rapidly and widely among nestmates than control food, with no evidence for social compartmentalisation. Together, these results demonstrate that key behavioural barriers expected to restrict pathogen transmission in social insects are ineffective against this virus following cross-species transmission to a novel host. Instead, the presence of infectious virus in the food appears to promote its exploitation and distribution, increasing the likelihood that spillover progresses towards sustained transmission.

From Entrance to Queen, Spatial Organisation of Sanitary Behaviours in Ant Colonies

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Ant colonies are highly vulnerable to pathogens due to their dense, genetically related populations sharing a common nest. The spatial organisation of grooming behaviours is therefore critical, as it shapes local exposure risk and influences pathogen transmission dynamics. We hypothesised that colonies adjust both the nature, frequency and spatial distribution of grooming behaviours in response to pathogenic risk. To test this, we designed an experimental nest composed of 60 hexagonal zones and quantified grooming events, worker density, and activity levels within each zone. Using seven Myrmica rubra colonies, we examined how grooming patterns changed first following the introduction of non-infectious corpses and subsequently after exposure to cadavers sporulating from the generalist entomopathogen Beauveria bassiana. Our results indicate that, under baseline conditions, the nest entrance functioned as a hub for social, extensive, and self-grooming behaviours. Furthermore, baseline levels of extensive and social grooming increased specifically in response to entomopathogenic threat, but not after the introduction of non-infectious cadavers. In contrast, the queen's vicinity consistently exhibited high worker densities but low activity and grooming levels, even after pathogen exposure. These findings reveal distinct sanitary strategies inside the ant colony: the nest entrance is protected through intensive grooming behaviours that limits pathogen establishment in this high-traffic zone, whereas queens are safeguarded by dense clusters of low-activity workers that reduce local transmission of pathogens. Overall, this study provides new insights into the functional role of inactivity in ant colonies and demonstrates how social immune strategies are spatially organised within the nest.

Do bumblebees care? Wound care and social immunity in social bees

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Social immunity enables eusocial insects to mitigate the high risks of pathogen transmission inherent to group living. Although hygienic behaviours are well-studied in ants and honeybees, comparatively little is known about how bumblebees limit pathogen uptake and spread. Here, we investigated the influence of injuries and wound infections on survival and behavioural responses in Bombus terrestris. Workers were experimentally injured and their wounds were either left uninfected or infected with the opportunistic bacterium Pseudomonas aeruginosa. We quantified behaviours using ethograms, measured survival in isolation and in the presence of nestmates, and assessed injury rates in wild-caught bees.

Injured workers did not suffer an increase in mortality, but increased their presence in the nest compared to the uninjured control workers. In contrast, infections caused substantial mortality and induced the opposite behavioural shift. Infected workers were less likely to be present in the nest and instead predominantly remained and eventually died in the foraging arena. This behavioural pattern was consistent in both wild and lab-reared colonies. Field data showed that natural injury rates are low among foraging wild bees, suggesting that injuries are unlikely to occur in the wild.

Overall, our findings reveal opposing behavioural responses to injury and infection: injury promoted increased nest affiliation, whereas infections led to social isolation. This exclusion-like behaviour may represent a simple but effective component of social immunity, reducing the risk of pathogen introduction into the nest.

SYMPOSIUM 27 · Host-microbe interactions in social insect
ORAL · Tue 18 Aug · 10:15 · Halle 4 · Session 13 · Abstract ID 148948

Manipulation of carpenter ant social behaviours by a specialized fungal parasite

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Ophiocordyceps fungi have evolved to infect and manipulate the behaviours of social insects such as ants and wasps. The so-called “zombie behaviours” that are induced are thought to aid the fungal parasite in evading social immunity, promote fungal development, and increase transmission rates. To unravel the underlying parasite and host mechanisms that give rise to these parasite-adaptive behaviours, we study the interaction of Ophiocordyceps camponoti-floridani with its carpenter ant host Camponotus floridanus. In these host-microbe interactions we have observed significant changes in host daily activity rhythms, locomotion and communication, followed by summiting behaviour, which is highly characteristic for Ophiocordyceps infections. To investigate the interacting fungal molecules and ant host pathways that elicit these behavioural changes, we integrate omics technology with functional genetics techniques and quantitative behavioural assays.

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 ant circadian clock is significantly affected during Ophiocordyceps infection. These are some of the first results to connect Ophiocordyceps genomes with carpenter ant phenomes, thereby answering how these specialist fungi hijack ant behaviour and how those behaviours are regulated at a molecular level.

SYMPOSIUM 27 · Host-microbe interactions in social insect
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Age-controlled effects of cestode infection on different castes and age classes of the ant Temnothorax nylanderi

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Parasites frequently manipulate host immunity and behavior to enhance their transmission, often by altering host phenotypic plasticity. Helminths are well-known for inducing stage-specific morphological and functional changes, including immunomodulation and host metabolic alterations. In the ant Temnothorax nylanderi, infection by the cestode Anomotaenia brevis reduces cuticle melanization and sclerotization, lowers activity, and markedly extends host lifespan. Previous transcriptomic studies identified infection-associated gene expression changes, but interpretation was limited by age differences, as infected ants live much longer than uninfected individuals.

To separate infection effects from age, we compared brain and fat body transcriptomes of newly emerged (callow) and older infected and uninfected workers and queens. Infection was the dominant factor influencing gene expression in workers across both tissues. Only the fat body showed minor age-dependent changes. These results demonstrate that age-controlled sampling reveals a distinct transcriptional signature of A. brevis infection and that age contributes little to expression variation in this system. Ongoing analyses will expand these comparisons across additional age classes and castes.

We further characterized the transcriptomic profile of intercastes, individuals displaying both queen- and worker-like traits and commonly found in T. nylanderi colonies. Using RNA-seq data from mated queens, unmated queens, intercastes, and workers, we examined caste-level expression patterns. Intercastes were transcriptionally more similar to workers than to either queen type, indicating a primarily worker-like molecular phenotype despite their partial morphological resemblance to queens.

Nematode infections provoke aggression in ants

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Maintaining group integrity by excluding outsiders and pathogens is a fundamental requirement and challenge of social living. In social insects, these defences rely heavily on chemical communication, with cuticular hydrocarbons (CHCs) mediating both nestmate recognition and infection-related social responses. In ants, CHCs are stored and homogenised in the pharyngeal gland (PG), contributing to the formation of a shared colony odour that enables nestmate recognition. Nematodes of the Diploscapter genus specifically infect the PG of ants. In the clonal raider ants (Ooceraea biroi), infections reduce host survival, disrupt division of labor and alter host CHC profiles. Based on the role of CHCs in nestmate recognition and the social detection of infections, we asked whether Diploscapter infections are detected by social partners and what behavioral responses they elicit.

Using controlled behavioural assays, we quantified the behavior of uninfected colonies toward both infected and uninfected nestmates and non-nestmates. We then performed chemical analyses to identify the chemical basis of these responses. Our behavioral and chemical analyses together show that 1) infected ants elicit increased aggression from uninfected nestmates and non-nestmates, which infection-specific changes in CHC profiles may drive and 2) infections do not compromise nestmate recognition, which acts through different CHCs. Thus, while many parasitic nematodes can evade host immune recognition, Diploscapter fails to evade the social recognition system of its host. The efficient detection and exclusion of infected individuals likely reduces parasite introduction and transmission both within and between colonies.

Mycobiota of Formica polyctena ants and their nests: insights into hidden interspecies interactions

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Fungi and ants can form diverse mutualistic interactions, with fungi serving as food sources (e.g. fungus-farming ants) or contributing to nest stability (e.g. carton-nesting ants). However, while most research on non-antagonistic ant-fungus interactions has focused on tropical systems, temperate regions remain poorly understood. Red wood ants are among the dominant ecosystem engineers in Eurasian forests, but despite their significance, their mycobiota have received little attention. In our studies, we characterized the fungal community associated with Formica polyctena ants and their nests, focusing on six colonies from Central Poland. Culturing-based analyses of the ant mounds' mycobiota showed a distinct Mucoromycota community, more stable than that of the surrounding forest litter, with Entomortierella lignicola strongly associated with the mound environment. Characterization of the fungal community of the infrabuccal pockets of 135 workers using microscopy, culturing, and DNA metabarcoding revealed a diverse mycobiota, with a core community comprising 15 fungal genera, including insect-associated yeasts as well as filamentous saprotrophs and endophytes likely acquired from the environment. Finally, based on isolates from infrabuccal pockets and combining phylogenetic and morphological approaches, we described a new species, Formicomyces microglobosus (Trichomeriaceae), indicating an independent evolutionary transition toward association with ants within the Trichomeriaceae family. Overall, our results show that while F. polyctena hosts a diverse mycobiota, several taxa appear to be strongly associated with these ants.

Ecological traits of Hypocreaceae fungi in the fungus-growing ant symbiosis

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Ecological traits of Hypocreaceae fungi in the fungus-growing ant symbiosis

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The symbiosis of fungus-farming ants (Attini) constitutes a multipartite interaction involving multiple microbial partners. A novel fungal genus currently under description – Manidigitorum Ad. Int. (Hypocreaceae), was found in colonies of the Apterostigma pilosum grp. The ecology of this fungus remains poorly understood. Here, we investigated the interactions between Manidigitorum and different members of this symbiosis. Dual-culture assays on solid medium were performed using two species of Manidigitorum against: Myrmecopterula, the mutualistic fungus cultivated by Apterostigma pilosum; Leucocoprinus, a mutualist of other attine ants; Escovopsis, a sister group of Manidigitorum and an antagosnist of attine fungal mutualists; and Streptomyces from worker body. In addition, in vivo experiments using Apterostigma subcolonies were performed to assess worker ant behavioral responses to Manidigitorum. Isolates of Manidigitorum showed strong antagonism just against Escovopsis and Leucocoprinus. In contrast, Streptomyces isolates completely inhibited the growth of Manidigitorum spp. In behavioral assays, Hypocreaceae fungi elicited self-grooming and fungus-weeding behaviors by worker ants; however, these responses were not specifically triggered by Manidigitorum. Then, the unique interaction profile of Manidigitorum within the fungus-growing ant symbiosis presented here adding further complexity to this symbiotic system.

Key-words: Formicidae, insect-fungi interaction, antagonism.

Paper wasp caste plasticity and sex mediate the extent of parasitic manipulation

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Successful manipulation by parasites is constrained not only by host species boundaries, but also by plasticity within a species. For instance, when a host exhibits plasticity, the extent of parasitic manipulation may be facilitated or constrained by alternative host phenotypes. The twisted-wing parasite Xenos peckii (Strepsiptera) and its infection of the social wasp Polistes fuscatus provide a powerful system for examining such barriers imposed by varied levels of plasticity. Female wasps with non-permanent castes exhibit high plasticity in behavior, reproduction, and lifespan, while males without castes show less plasticity in these traits. Additionally, X. peckii shows a striking sexual dimorphism. Males begin as endoparasites and only need short-term hosts to develop and emerge as adults, whereas females are permanently endoparasitic and need a long-lived host. We hypothesized that these within-species differences result in asymmetric manipulation outcomes. First, we confirmed that parasites of both sexes can survive and reproduce in worker hosts. In contrast, male parasites can develop and emerge from male wasps, but female parasites cannot survive in these short-lived hosts. Using transcriptomic data, we are comparing co-expression patterns across female primary host brains, male secondary host brains, and whole bodies of the male and female parasites infecting these hosts. We are now identifying molecular pathways associated with successful or limited exploitation, with particular emphasis on caste-related host plasticity. Our initial results support that host and parasite sexes jointly facilitate or constrain reprogramming of the host as an extended phenotype to secure parasite survival and fitness.

Paenibacillus melissococcoides: a new pathogen of honey bee brood?

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Agroscope Liebefeld

Due to the high number of individuals in close proximity, honeybee colonies represent fertile grounds for pathogens. The two globally distributed brood bacteria Paenibacillus larvae and Melissococcus plutonius are the causative agents of the economically important American (AFB) and European foulbrood (EFB) diseases, respectively. In Switzerland, an outbreak led to increased research into the epidemiology and control of EFB. During such research, an unknown bacterium was found in an EFB-affected apiary. This new species was named Paenibacillus melissococcoides. We investigated whether it was present in larval jelly and in larvae, and tested, in vitro, whether it was pathogenic to the brood. To determine its prevalence, we screened 939 EFB-diseased and healthy honeybee colonies sampled between 2005 and 2021 in Switzerland and genome databases for misidentified sequences. To better understand the interaction between Paenibacillus spp. and A. mellifera honeybees, we compared the virulence of P. melissococcoides with that of two Paenibacillus species previously found associated with honeybees. Their virulence was associated with their resistance to the antibiotic effect of the nutritive jelly larvae are fed with, which acts as an immunological barrier to infection by Paenibacillus spp. In this presentation, we review what we have learned on the ecology, distribution and pathogenicity of P. melissococcoides and discuss whether this species is a new honeybee pathogen. The discovery of this species brings new insights into EFB epidemiology and the suite of bacteria associated with it, as well as a better understanding of the ecology of Paenibacillus species when they encounter honey bees.

SYMPOSIUM 27 · Host-microbe interactions in social insect
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The microbiome of leaf-cutting ants reveals the prevalence of Tsukamurella and a Floricoccus-like bacterium, a link between ants and stingless bees.

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The microbiome of social insects is shaped by social transmission. Leaf-cutting ants of the Attini tribe associate with the fungal symbiont Leucoagaricus gongylophorus, cultivated in fungus gardens and used as a food source, yet less is understood about their associated bacterial microbiota. We earlier reported a high prevalence of the Actinobacteria Tsukamurella in Atta sexdens ants, sharing amplicon sequence variants (ASVs) with an Atta laevigata outgroup, suggesting a widespread but non-host-specific association. Here, we expanded sampling and investigated A. sexdens bacterial communities across six Brazilian states using 16S rRNA gene metabarcoding. As expected, Tsukamurella, when present, tends to dominate the ant microbiome and reduce overall alpha diversity. Interestingly, a Floricoccus-like Streptococcaceae (FLS) ASV was also very abundant and widespread across samples. Phylogenetic analyses did not resolve Tsukamurella taxonomy and origin, but an ant-specific clade was observed for the FLS ASV, consistent with patterns observed in stingless bees, which also harbor bee-specific FLS clades. Together, our findings reveal Tsukamurella as a dominant, non-obligate ant symbiont and Floricoccus-like Streptococcaceae as a putative insect-specialized taxon, with ant- and stingless bee–specific clades. These results expand our understanding of bacterial symbioses in leaf-cutting ants and provide a foundation for the isolation, functional and genomic characterization of these bacteria—including the description of new taxa, elucidation of their biotechnological potential, their benefits to the host, and their use as targets for ant biological control.

Effects of direct and indirect antibiotic-induced gut dysbiosis on bumblebee health

Svea Lindeboom

Bees host a highly conserved, coevolved gut microbiome that is socially transmitted and provides essential protection against pathogens. Disruption of this microbiome, such as through antibiotic exposure, has been linked to reduced survival and increased pathogen susceptibility. However, the specific mechanisms underlying these negative effects remain unclear; they could stem from direct antibiotic toxicity or, alternatively, from the disruption of the gut microbial community.

To disentangle these effects, naive bumblebees (Bombus terrestris) were extracted from cocoons and inoculated with either a healthy microbiome or a dysbiotic microbiome (sourced from oxytetracycline-exposed bees), allowing bees to acquire an altered microbiome without direct antibiotic exposure. A separate group received a healthy microbiome followed by direct antibiotic treatment. Bees were subsequently challenged with Slow Bee Paralysis Virus (SBPV).

Our results demonstrate that both direct antibiotic exposure and the transmission of a pre-disrupted microbiome significantly affect host health and viral defense. qPCR analysis revealed elevated SBPV titers in both treatment groups compared to controls. In addition, 16S rRNA sequencing showed that these treatments significantly altered gut microbiota composition, specifically reducing alpha diversity. These shifts in the microbial community were also associated with reduced ovary development, indicating broader physiological costs of dysbiosis. Together, these findings suggest that loss of a diverse, stable microbiome—rather than antibiotic toxicity alone—is a key driver of increased viral susceptibility in bumblebees, highlighting the critical role of the gut microbiome in mediating bee health.

Integrating microbiome and host genomic data to improve selection of Apis mellifera resistance to Varroa parasites

Victor Rossier; Markus Neuditschko; Vincent Dietemann; Benjamin Dainat

The honey bee microbiome can enhance host defences against pathogens and parasites by forming protective biofilms or modulating the immune system. The ectoparasitic mite Varroa destructor is the main biotic factor threatening honey bees in the Northern Hemisphere. However, the honey bee microbiome has so far been overlooked as a potential confounding factor in heritability estimates used for selecting honey bees for Varroa resistance. This could explain the low heritability of resistance phenotypes and the poor success of selection programs. In this study, we characterised the microbiome and queen genotypes of 1442 colonies using metagenomic data from pools of 500 workers per colony. Geography, sampling date and, to a lesser extent, Varroa load emerged as major drivers of microbiome variation. We also detected numerous taxa that were significantly associated with Varroa load. Notably, the core symbiont Lactobacillaceae was found to be negatively associated with Varroa, whereas opportunistic bacteria such as Morganellaceae and pathogens such as Trypanosomatidae showed positive correlations. These results suggest that Varroa either disrupts the microbiome or proliferates preferentially in colonies harbouring particular microbial communities. Finally, we report increased genomic heritability estimates for Varroa load and resistance traits when the microbiome was included as a covariate. Overall, integrating microbiome information into breeding frameworks could strengthen selection programs for Varroa resistance and contribute to improved honey bee health.

SYMPOSIUM 27 · Host-microbe interactions in social insect
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Microbiome influences on gene expression, social organization and behaviour in a facultatively social bee

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The bee microbiome is intricately connected to bee physiology, behaviour, sociality, and their external environment. Although the relationship between microbiota and bee health is increasingly studied in obligately eusocial bees, examining nests of a facultatively social bee unveils the impact of varying social roles on microbial acquisition and its influence on behaviour. We utilized a multi-faceted approach to characterize the microbiome, gene expression, and both in-nest and foraging behaviours of a small carpenter bee, Ceratina calcarata, reared on microbially diverse, sterile, and probiotic supplemented diets. Through examining the associations between larval microbial diets and social role in determining bacterial and fungal microbial communities, we found that adult bee microbiomes vary with pollen provision microbial composition and levels of exposure to the external environment. Furthermore, we found positive effects of introducing a bacterial symbiont to the pollen provisions on development and survivorship. We found an increased number of uniquely upregulated genes in bees reared on a sterile diet and on sterile pollen supplemented only with Apilactobacillus kunkeei as a probiotic. Bee reared on these diets lacking diverse microbiota had upregulated genes involved in olfactory receptor activity, sensory perception of smell, and protein processing. By further integrating behavioural characterizations with the microbiome and transcriptome, we highlight a network of host-microbe-social interactions with important implications on bee health at the individual and nest level.

SYMPOSIUM 27 · Host-microbe interactions in social insect
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Bacterial symbionts of aphids as hidden modulators of their partnership with ants

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The multitrophic plant–aphid–ant system is a well-established model in ecology and evolutionary biology. Within this system, bacterial symbionts can circulate among partners and modulate their interactions. The aphid-associated bacterial symbiont Serratia symbiotica comprises multiple strains with diverse lifestyles, including a free-living strain found in the gut of Aphis fabae aphids. While S. symbiotica is known to influence aphid development and to reduce selective pressure imposed by parasitoids, its effects on aphid mutualisms with ants remain poorly understood.

We show that aphids infected with S. symbiotica exhibit reduced population growth, an effect that is partially alleviated in the presence of tending Lasius niger ants. Although ants were initially more attracted to infected aphids, this did not result in increased collective recruitment or enhanced trail reinforcement. Instead, bacterial infection led to a progressive decline in ant interest over time, likely due to reduced honeydew palatability. These findings suggest that the free-living S. symbiotica strain may promote the gradual abandonment of infected aphids by ants, ultimately threatening the stability of the ant–aphid mutualism. We further speculate that reduced ant attendance could have cascading consequences, including diminished aphid protection against natural enemies and increased host-plant defense resulting from the redirection of ant foraging toward extrafloral nectaries.

Reassembly of the termite gut microbiome across the molting cycle in Cryptotermes secundus

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Termites are eusocial insects that rely heavily on their gut microbiome for lignocellulose digestion and survival. However, in lower termites, molting represents a critical physiological challenge to this symbiosis. The molting cycle involves gut voiding and the loss of a large fraction of gut symbionts, which are later re-introduced through proctodeal trophallaxis from nestmates. This process provides a unique opportunity to investigate the critical role of social interactions in maintaining the stability of the host microbiome.

In this study, we used shotgun metagenomics to investigate gut microbiome dynamics in the wood-dwelling termite Cryptotermes secundus. We collected gut samples from workers at five time points across the molting cycle (day 0, 1, 2, 5 and 7 after molting), as well as from individuals with a full gut prior to molting. Metagenomic libraries were sequenced on an Illumina NovaSeq and analysed using fully reproducible Galaxy workflows (FAIRyMAGs and associated pipelines). Our analyses include taxonomic and functional profiling, recovery of high-quality metagenome-assembled genomes (MAGs), and screening for viral, archaeal, fungal and other micro-eukaryotic components.

Preliminary results suggest that a small fraction of microbial taxa may persist immediately after molt (day 0). Across days 1–7, the gut communities appear to regain diversity and functional potential, though the specific timeline of symbiont restoration via social transfer is still being evaluated.

Overall, our study provides an initial genome-resolved view of microbiome dynamics across the molting cycle, offering insights into the resilience of the host-microbiome relationship and the maintenance of homeostasis in a social insect.

SYMPOSIUM 27 · Host-microbe interactions in social insect
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Social Microbiomes and Colony Fusion in Pacific Dampwood Termites (Zootermopsis Angusticollis)

Kingsley Hunt
University of Exeter

Group living is thought to evolve when the benefits of sociality outweigh the costs. It's long been recognised that acquiring pathogens from social partners can be costly, but only recently has this argument been flipped on its head to consider the exchange of beneficial mutualistic microorganisms as a driver of social evolution. This concept, of an adaptive 'social microbiome', is most likely to occur in species that have high levels of interaction, resource exchange and where the microbiome is of high functional importance, such as in wood-eating termites. Social structure is highly variable in dampwood termites, ranging from simple colonies formed from single founding pairs to mixed colonies formed from the fusion of multiple, unrelated colonies. Here I use 16S rRNA sequencing to describe the community composition of the bacterial microbiome of 35 wild colonies of Pacific dampwood termites (Zootermopsis angusticollis). This information is combined with microsatellite genotyping of each colony, providing information on their social structure and likelihood of prior fusion. I show evidence for unique colony-specific social microbiomes and changes in the microbiome that occur following colony fusion. My work suggests that the acquisition of a beneficial microbiome can play an important role in social evolution, including in the fusion of termite colonies.

SYMPOSIUM 27 · Host-microbe interactions in social insect
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Characteristic microbe communities in vespid wasps facilitated by diet, not just social transmission

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Honey bees and bumble bees have host-restricted gut symbionts that provide benefits such as resistance to pathogens and metabolism of ingested carbohydrates and pollen. Social interactions among nestmates facilitate transmission. Consequently, solitary bees have smaller, more variable, and less diverse gut communities.

In contrast to bees, the microbial communities of wasps are poorly known. We characterized gut communities of social vespids including five species of Polistes paper wasps and the Mexican honey wasp, Brachygastra mellifica. Polistes are predators that consume some nectar, whereas honey wasps feed primarily on stored honey and small invertebrate prey. Wasps were collected from sites in Texas, their gut bacterial communities were characterized using 16S rRNA sequencing, and absolute bacterial loads were quantified with qPCR. For comparison, we also investigated solitary predatory wasps from six families. Honey wasp gut bacterial communities were highly consistent among individuals and across localities. Almost all individuals harbored novel species of Bifidobacterium and an uncultured Lactobacillus, both related to lineages in honey-feeding social bees. In contrast, Polistes individuals lacked consistent bacterial associates, although communities were more similar within nests than between nests, suggesting some transmission among nestmates. The bacterial communities of solitary wasps were also variable and were smaller on average. Our findings show that social interaction alone does not lead to the evolution of host-restricted gut symbionts. Further, the transition to a honey-feeding diet is linked to the establishment of a distinctive gut community with similarities to communities of honey-feeding bees.

SYMPOSIUM 27 · Host-microbe interactions in social insect
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Temperature optima overlap in an ant host and its specialist symbiont

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Temperature-induced death of symbiotic bacteria can have detrimental effects on insect fitness. Specialist bacteria, which provide essential services to hosts, may be especially vulnerable to heat. Ants are the dominant insect taxon in many ecosystems but how temperature change impacts their specialist and generalist symbionts has not been studied. We investigate how temperature affects fitness in the ant Cardiocondyla obscurior and its generalist Wolbachia and specialist Cand. Westeberhardia cardiocondylae symbionts. We find a clear overlap in the temperature optima of the ant host and its specialist, but not its generalist, symbiont. We furthermore find that symbionts react differently to temperature treatment according to host phenotype, demonstrating flexibility in symbiont temperature sensitivity. Together, these results support the idea that specialist symbionts are more highly constrained in their temperature niche and contribute to a better understanding of how human-induced temperature change influences ecologically important insect taxa.

Venom Exposure Without Collapse: Stability of Fungus-Growing Ant Microbiomes Under Social Parasitism

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Symbiotic relationships are foundational to biological systems yet understanding them remains challenging due to complexities introduced by multi-species interactions. The fungus-growing ant Sericomyrmex amabilis is a model example of multi-species interactions, as they cultivate mutualistic fungal gardens that contain bacteria with important functional roles (e.g., nutrient processing, pathogen defense). Megalomyrmex symmetochus is an obligate social parasite of S. amabilis, living within host colonies, consuming brood and fungus garden over the lifetime of the colony. While the parasite's alkaloid-based venom is used in communication between parasites and their hosts, M. symmetochus also dispenses it upon their brood and the fungus garden. Alkaloidal venoms are known to have antibacterial properties, but the specific effects of M. symmetochus venom on the garden microbiota are unknown. The objective of this work aims to determine how M. symmetochus venom influences the bacterial communities within S. amabilis fungus gardens, by employing two complementary approaches: (1) comparing bacterial diversity of parasitized and non-parasitized gardens using 16S rRNA high-throughput amplicon sequencing; (2) assessing susceptibility of cultured isolates to biologically relevant concentrations of raw venom alkaloids using minimum inhibitory concentration assays. Our findings indicate that parasitized gardens exhibit reduced bacterial richness and diversity, yet bacteria with potential functional roles persist. These results suggest that while the venom affects the bacterial community, it does not eliminate key symbiotic bacteria. Understanding these interactions enhances our knowledge of the complex dynamics within ant-microbe symbioses and reveals how multi-species symbiotic systems can persist and function.

Host-Symbiont Interactions across a Sociality Continuum in Halictid Bees

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Most studies of parasitism and disease in pollinators are focused on a small number of eusocial, commercially important honeybees and bumblebees. As a result, little is known about how parasitism varies across the social landscape of the nearly 20,000 other bee species. My goal is to understand how social structure impacts where symbionts fall on the mutualist-to-parasite continuum, and how virulence and transmission optimums are influenced by variation in social behavior. Halictid bees (‘sweat bees’) provide an ideal system for such comparative studies – this species-rich family includes species whose life histories range from solitary individuals to eusocial colonies of ~400 workers. Some halictid species host over 4500 non-feeding Acrostichus spp. nematode dauers in an exocrine organ called the Dufour’s gland. These host-specific nematodes are vertically transmitted from the Dufour’s gland into the brood cells, where they feed and reproduce sexually. Juvenile nematodes will molt into dauer and enter the bee shortly before eclosion. Despite their high numbers, these nematodes are generally considered commensal, and their impact on their hosts remains poorly understood. Here, I compare four solitary, social, and socially flexible sweat bee species within the tribe Augochlorini (Hymenoptera: Halictidae) and assess how nematode burden impacts host body condition, reproductive capacity, and immune response across different bee species and social forms. This work provides new insights into how nematode prevalence, infection intensity, and virulence vary across social scales and highlights how key aspects of disease ecology can be influenced by the social structure of the host.

SYMPOSIUM 27 · Host-microbe interactions in social insect
ORAL · Tue 18 Aug · 17:45 · Halle 4 · Session 25 · Abstract ID 146362

Field-realistic stressors alter the bumblebee gut microbial community

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The gut microbial community is increasingly recognised as an important component of bee health. In bumblebees, key pollinators in the natural environment and in agriculture, the specialised gut microbial community, ubiquitous across Bombus species, is thought to contribute to host digestion, metabolism, pathogen defence, and drive how bees respond to stressors. However, the effect of stressors such as pesticides and pathogens on the gut microbial community of bees remains largely undetermined. Here, we investigate the relationship between the bumblebee Bombus terrestris, their gut microbial community, and field-realistic combinations of pesticides and pathogens, including the neonicotinoid insecticide thiamethoxam, the pyrethroid insecticide ➔-cypermethrin, the fungicide tebuconazole, and the gut pathogen Nosema ceranae. Forty B. terrestris colonies were exposed to different field-realistic combinations of these stressors under controlled laboratory conditions, and the gut bacterial communities of the bees were subsequently determined using amplicon sequencing (16S rRNA gene). We show that some non-core taxa of the Bombus microbiome, including members of the Burkholderiaceae, exhibit significant decreases in relative abundance in bees exposed to pathogens and pesticides compared to controls. In contrast, the core gut bacterial taxa show no significant differences in relative abundance between the treatments. These findings suggest that exposure to field-realistic combinations of stressors influence non-core bacterial taxa in bumblebee gut microbial communities, and that these often over-looked non-core taxa may play important roles in bee host adaptation to the environment.

SYMPOSIUM 27 · Host-microbe interactions in social insect
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Engineering resistance: in situ microbiome engineering to increases bee tolerance to pesticide exposure

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Pollinating insects are essential for global food production and ecosystem stability, yet many species are chronically exposed to agricultural pesticides that reduce survival and reproduction. Although gut microbial communities influence host metabolism and stress responses, it remains unclear whether they can be shaped to alter host tolerance to chemical exposure. Under typical field conditions, the native bee gut microbiome appears to offer little or no protection against pesticides, leaving pollinators vulnerable to non-target effects of agrochemicals.

Here, we test whether gut microbial communities can be engineered through repeated transmission under pesticide selection to enhance host tolerance. Using successive cohorts of germ-free bumblebees, we serially passaged gut microbiomes harvested from nestmates exposed to LC50 concentrations of the neonicotinoid imidacloprid. Microbiome transplantation was repeated across multiple passages, with each round introducing selected microbial communities into newly emerged hosts. Across passages, gut microbiome composition shifted dynamically under selection, leading to divergence in host survival when bees were challenged with pesticide exposure. Pesticide-selected microbiomes exhibited substantial compositional restructuring, indicating that chemical exposure can drive rapid and repeatable changes in community assembly. Joint host–microbiome transcriptomic analyses revealed coordinated changes consistent with altered metabolic investment, redox balance, transport processes, and xenobiotic-associated functions, suggesting an emergent, system-level response to chemical stress. Together, these findings demonstrate that bee gut microbiomes can be experimentally engineered to modify host pesticide tolerance, identifying the microbiome as a dynamic and selectable component of pollinator resilience. This work highlights the importance of considering host–microbiome interactions when predicting the biological impacts of agrochemical exposure,

SYMPOSIUM 27 · Host-microbe interactions in social insect
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Characterising effects of Pantoea bacteria on pathogen infection in bumble bees

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In addition to their core symbiotic gut microbiota acquired within their nest, bees can become colonized by other facultative microbes from their environment. Although the function of the core microbiota has been extensively studied, that of environmentally acquired microbes often remains unclear, even when those microbes are of high prevalence across bee populations. While Pantoea can cause disease in their plant hosts, they have also been proposed as a biological control for agricultural pests of crops given their antifungal and antibacterial activity. These bacteria are also commonly found in the gut microbiota of bees, and we propose they may have protective effects on their bee host. To test this hypothesis, we conducted laboratory experiments comparing survival of gnotobiotic-reared bumble bees (Bombus terrestris) fed Pantoea, gut homogenate spiked with Pantoea, and microbe-free controls, challenged with the fungal entomopathogen Beauveria bassiana. We assessed bumble bee survival, and tested association with bee gut microbiota communities characterized through 16S and ITS metabarcoding. Our results provide insight to the role of a common, environmentally-acquired gut-associated microbe in bee health.

SYMPOSIUM 27 · Host-microbe interactions in social insect
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The Two-Tier Dose-Response: Bumblebee Survival and Microbiome Shifts Under Contaminant Stress

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Imperial College

Environmental contaminants are known to impact bee health, but their impact on important gut microbial communities are poorly understood. This work quantifies a holobiont-level dose response in bumblebees by comparing toxicity thresholds for the host alongside disruption thresholds for the gut microbiome across a selection of contaminants with distinct modes of action. Cohorts of adult bumblebees were exposed to concentrations of five stressors across environmentally relevant gradients. The stressors tested were included a miticide, fungicide, insecticide, heavy metal, and a so called forever chemical. For each, we quantified consumption, dose-dependent changes in both host survival and microbiome stability thresholds. We test the hypothesis that microbiome disruption is asynchronous with host mortality, creating a separation between “sublethal” holobiont disruption and host mortality. We further predict that the separation between mortality and microbiome stability thresholds will differ among the tested contaminants, reflecting different primary targets (host neurotoxicity, microbial inhibition, or broad physiological stress). By separating host and microbiome sensitivity, this approach can reveal effects missed in host-only assays and evaluate how the gut microbiome shifts and contributes to detoxification.

Fungus-farming termites can protect their crop by confining weeds with fungistatic soil boluses

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Fungus-growing termites are canonical examples of the evolution of agriculture in insect societies. They grow a fungus Termitomyces sp. for food on spongy structures known as fungus comb. However, just like human agricultural fields, these fungal crops are also prone to invasion by other weedy fungi. Pseudoxylaria is the most dominant weed in termite fungal gardens. Since termites cannot subsist on any fungi other than Termitomyces, it is essential for termites to detect and suppress any weedy fungi. The precise mechanisms by which termites prevent Pseudoxylaria remains unknown. Previous studies suggest the role of symbiotic fungistatic microbes in bringing about weed control. However, how termites employ these microbes to suppress the fungal-weeds, without affecting the fungal-cultivar, remains unknown. Here we show that the fungus-farming termite, Odontotermes obesus, uses specific behaviors to remove, isolate and suppress the growth of the fungal weed Pseudoxylaria, by primarily encasing them with soil boluses containing fungistatic microbes. These behaviors efficiently suppress the weed without affecting the crop. This integration of specific behaviors with termite-derived microbes appears to be the proximate mechanism of how microbes are topically used by termites to confine the weed while keeping the crop unaffected.

Better safe than sorry: leg amputations as a prophylactic wound care behaviour in carpenter ants

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Department of Animal Ecology and Tropical Biology, University of Würzburg

Animals often sustain injuries, which are susceptible to lethal infections. In social insects, wound care behaviours have evolved to reduce these risks. But the limits of wound care behaviours remain unclear. Here we investigated the wound care behaviours of the ant Camponotus maculatus. Our findings show that amputation of legs infected with Pseudomonas aeruginosa significantly reduced mortality. However, nestmates do not differentiate between infected and sterile injuries, providing similar treatments regardless of infection. Even though we show that early amputation correlates with higher survival rates, nestmates amputate indiscriminately on legs with fresh or old wounds. Additionally, cuticular hydrocarbon profiles differed between ants with infected or sterile wounds only 24 hours post-injury, a timepoint when amputations are no longer effective. We propose that C. maculatus workers perform prophylactic amputations regardless of injury state or age. This is in sharp contrast to previous studies that showed clear capabilities to treat infected wounds differently in ants using antimicrobial compounds. This work therefore shows the limits of wound care behaviours in social insects, allowing us to better understand the evolutionary drivers of this unique behaviour.

Gut microbiome–environment interactions in managed honey bees across the island of Ireland

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The gut microbial community in animals is important for a diversity of functions, including health and pathogen susceptibility. Honey bees are known to harbour a simple but distinctive gut bacterial community making them an ideal model for uncovering gut microbiome-environment interactions. Here we first conducted a comprehensive study of 150 apiaries across the island of Ireland and characterised all major pathogens and pesticides present in colonies in all apiaries. Next, using both amplicon and assembly-based whole metagenome sequencing on pooled bees from each of the 150 apiaries, we recover detailed community information on the bee gut bacteria, their differential relative abundance, and significant interactions between major pathogens, pesticides, the environment, and the gut bacteria. We also gain high-resolution lineage and subspecies information on the honey bee hosts. Our results drive forward our understanding of host–gut microbiome interactions and evolutionary processes, and ultimately the future-proofing of these key pollinators.

Metabolic plasticity supports a flexible nutritional symbiosis in Cardiocondyla ants

Jan Oettler
Universität Regensburg

Nutritional symbioses have repeatedly evolved in insects, yet how hosts regulate these partnerships to balance benefits across environments remains unclear. In Cardiocondyla obscurior, which carries and occasionally loses the vertically transmitted symbiont Cand. Westeberhardia cardiocondylae, we reveal the regulatory dynamics and function of this labile association. The symbionts with a drastically reduced genome (~530KB, 372 genes) provide shikimate-derived nutrients that enhance colony resilience under protein limitation, while hosts actively regulate symbiont abundance during protein scarcity and cuticle formation. In the symbiont’s absence, ants can compensate by upregulating genes enabling tyrosine acquisition from external sources. This metabolic flexibility allows C. obscurior colonies to exploit symbiont-derived and environmental nutrients, sustaining both growth and survival across nutritional contexts.

Nematode Infection and Body Condition Across Social Systems in Sweat Bees

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Social organization may influence host-symbiont interactions, yet how the physiological costs of infection vary across social systems remains unclear. Bees exhibit substantial variation in social complexity, from solitary nesting to eusocial colonies, providing a useful comparative framework for examining how infection-associated effects differ with social structure. This experiment investigates potential associations between infection by Acrostichus spp. nematodes and host body condition across solitary, socially flexible, and eusocial sweat bees (Hymenoptera: Halictidae). We also compare reproductive and non-reproductive castes within social species.

Acrostichus are non-feeding nematodes that can occur at high infection intensities in sweat bees. They are often described as commensal, but their effects on the host's energetic condition have not been well characterized. We quantified host body condition using methanol-chloroform lipid extractions to estimate fat body content, a proxy for energetic reserves in insects. This approach enables direct comparison of body condition across species and castes, while accounting for variation in nematode burden.

By integrating physiological measures of condition with comparative analyses across social systems, this work evaluates whether the magnitude of nematode-associated variation in body condition differs between solitary and social hosts, and among castes in social bees. Rather than assuming consistent costs of infection, this study explores how tolerance to infection may vary across levels of social complexity. Overall, this work aims to contribute to a broader understanding of how social structure may shape host-symbiont relationships and the physiological correlates of infection in bees.

Uncovering pathogen pressures in wild Bombus terrestris: A genomic and latitudinal perspective

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Bumblebees are key pollinators that play an important role in maintaining terrestrial ecosystems and supporting global agriculture production. However, their populations are undergoing a marked decline in both abundance and diversity across multiple regions worldwide. The causes of this population decline are multifactorial and often closely interconnected. The present study focuses on two of these potential drivers: pathogen prevalence and its relationship with the introduction of non-native subspecies for commercial purposes.

To this end, a total of 466 wild Bombus terrestris were collected between 2024 and 2025 from 19 sampling sites along a south-north latitudinal gradient across the Iberian Peninsula (365 workers and 101 males). The prevalence of microsporidians (Nosema ceranae, N. apis and N. bombi), and trypanosomatids (Lotmaria passim, Crithidia mellificae and C. bombi) was assessed using previously developed molecular techniques. Subsequently, a genomic approach was used to analyse the potential relationship between the pathogen prevalence and the degree of introgressive hybridization among B. terrestris subspecies in each specimen. The distribution of pathogens in each sex, as well as the possible correlation with the latitude at which they were collected, was also analysed.

Understanding the sanitary status of bumblebee populations and identifying the factors that influence parasite prevalence will contribute to the development of strategies aimed at mitigating the ongoing population decline of these important pollinators.

Keywords: bumblebee, pathogens, Microsporidia, Trypanosomatida, introgression.

Gut microbiome disruption by antibiotics reduces learning in honey bees

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Learning and cognition in honey bees are shaped by both nutrition and the gut microbiome, via microbiome-mediated regulation of biogenic amines that modulate neural function. In apiculture, the antibiotic tetracycline is widely used to control brood diseases, yet it disrupts the gut microbiome and may impair physiological and cognitive functions essential for colony performance. In parallel, dietary omega-6 to omega-3 fatty acid ratios (omega-6:3) influence microbial communities and neural performance, but how antibiotic exposure and dietary lipid composition together affect bee survival and learning remains poorly understood.

Here, we tested the effects of tetracycline exposure and dietary omega-6:3 ratio on honey bee survival and learning. Worker bees were reared on three artificial diets differing in lipid composition: two oil-supplemented diets with balanced or high omega-6:3 ratios, and one diet without added oils, each provided with or without tetracycline. Survival was monitored throughout the rearing period, and learning performance was assessed using proboscis extension response conditioning, alongside measurements of sensory responsiveness.

Tetracycline exposure significantly reduced survival and impaired learning. Dietary lipid composition did not alter the effect of tetracycline on learning. In contrast, under antibiotic exposure, bees fed diets without added oils showed higher survival than bees fed oil-supplemented diets. Dietary omega-6:3 ratio also affected water responsiveness, indicating modulation of sensory and motivational state.

These findings show that antibiotic-driven microbiome disruption impairs honey bee survival and learning, that dietary lipid composition shapes physiological resilience; analyses of the gut microbiome and biogenic amines are currently underway to investigate underlying mechanisms.

Partner fidelity between Cyphomyrmex ants and their fungal cultivars

Alison Pagalilauan

Yeast agriculture is a puzzling chapter in the evolution of agriculture by fungus-growing (attine) ants. Only a small group of attines practice yeast agriculture, growing their fungal crops as yeast nodules instead of hyphal strands. All other forms of ant agriculture are highly reliant on hyphal growth for nutrition, and the reasons why some ants cultivate the fungus in the yeast form are unknown. I hypothesize that yeast cultivars are less easily acquired by non-coevolved ant hosts due to fitness costs associated with reduced hyphal growth. To test this hypothesis, I will assess partner fidelity and cultivar fitness after replacing the native hyphal cultivars of three lower attine ant species in the genus Cyphomyrmex (C. muelleri, C. longiscapus, and C. costatus) with a novel yeast cultivar grown by the species group C. rimosus. I predict that most colonies will reject yeast cultivars, and that those that accept the yeast cultivar will have lower fitness than colonies that maintain their native fungus. Using garden biomass as a proxy for fitness of the fungi and the ants, I will compare fitness estimates between switched colonies and control colonies. Any outcome in which non-yeast-growing Cyphomyrmex ants reject yeast cultivars would contrast with existing ideas of low partner fidelity between Cyphomyrmex ants and their cultivars. These experiments aim to improve our understanding of partner fidelity and fitness consequences associated with yeast agriculture.

Exploring microbial and functional adaptations in termitophilous beetles within microbe-termite-termitophile tripartite symbiotic system.

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Social insects often acquire gut microbial symbionts from the environment or other species during interspecific interactions. Such horizontal microbial transfer can drive rapid adaptation to new diets or habitats. Termites are among the most remarkable examples of the critical role that insect gut microbiomes have in adaptation of insects to a dietary niche. In addition, a diverse range of arthropods live with termites, forming a range of symbiotic relationships. The obligate inhabitants of termite nests are called termitophiles, among them, rove beetles (Aleocharinae) is the most diverse and abundant group. They have independently transitioned from free-living to a termitophilous lifestyle many times. The cohabitation of termites and termitophilous beetles raises the possibility of gut microbial exchange between them, a question that has never been systematically addressed. For this project, I am exploring microbiome composition across globally sampled Illumina short-read dataset of termitophilous beetle and termite host species. I am using a metagenomics pipeline, which generates bins representing distinct microbial taxa. The preliminary data suggest that except for abundant intracellular bacteria (Wolbachia) the gut of some termitophilous beetles host Enterobacteriaceae or Oxalobacteraceae families. Additionally, I address gut functional adaptations in termitophilous beetles using a comparative morphological approach based on X-ray microtomography. Assuming that termitophilous beetles have similar diet and gut microbiome as their hosts, the termitophilous beetle gut structure might have evolved convergently to resemble those of termites rather than free-living beetles. To test this, I am constructing 3D beetle gut models, to compare termitophilous beetles and their free-living ancestors.

Mapping the Social Microbiome: Microbial Transmission Networks in Bombus terrestris

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Gastrointestinal microbial symbionts share a deep evolutionary relationship with their animals due to the important ecosystem services they provide their hosts (e.g. metabolism, immune support). Emerging research suggests that host-associated microbiomes form socially structured metacommunities, but mechanistic evidence linking social network position to transmission and community stability remains limited in animal systems. Additinoally, similar microbiomes between individuals may reflect direct transmission, shared environment, or parallel exposure. However, evidence that microbes move through social networks remains scarce. Bumblebees (Bombus terrestris) offer a tractable system given eusocial organization and amenability to longitudinal behavioral and microbiota tracking.

We investigate how social network structure influences microbial transmission dynamics in bumblebee colonies. Using controlled microbial depletion and targeted microbial inoculation of workers or queens, we combine longitudinal fecal sampling with behavioral tracking to quantify microbial transmission through social networks. We treat colonies as microbial transmission networks and ask whether microbial dispersal, co-transmission, acquisition, abundance, and persistence are predicted by network proximity, interaction frequency, and centrality.

We predict highly heterogeneous microbial transmission, with central individuals acting as hubs that shape colony-level microbiome structure. We hypothesize that socially transmitted microbes will exhibit greater persistence and stability than environmentally acquired taxa. Integrating network analysis with microbiome dynamics, this work moves beyond descriptive associations to identify social mechanisms governing microbial transmission.

We clarify how social organization structures the bumblebee microbiome and evaluate whether colonies function as integrated entities in microbiome assembly, advancing understanding of the social microbiome as a mediator linking behavior, ecology, and host health.

Gut dysbiosis and epithelial damage in Brazilian stingless bees exposed to mancozeb fungicide

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The widespread use of fungicides in agriculture raises concerns about sublethal effects on pollinators, particularly stingless bees, which are key contributors to tropical agroecosystems. Because bee health is closely linked to the composition of the gut microbiota, this study evaluated the effects of the mancozeb fungicide on gut microbial communities and midgut epithelial integrity in two Brazilian stingless bee species, Scaptotrigona aff. postica and Tetragonisca angustula. Both species exhibited a conserved bacterial core; however, exposure to mancozeb caused species-specific changes in microbial community structure. Scaptotrigona aff. postica showed increased bacterial richness and greater microbiota destabilization, whereas T. angustula maintained relatively stable bacterial diversity but displayed pronounced shifts in fungal communities. Beta-diversity analyses revealed treatment- and host-dependent shifts in community composition. Histopathological analyses demonstrated substantial damage to the midgut epithelium of exposed bees, indicating compromised gut integrity. Overall, the results showed that mancozeb can induce biologically relevant sublethal effects on stingless bees by disrupting gut microbiota and damaging gut epithelium, compromising immunity and bee health.

Keywords: Stingless bees, fungicide, gut microbiota, metabarcoding, morphology.

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SYMPOSIUM 28 · Arthropod inquilines of social insects' colonies
ORAL · Mon 17 Aug · 10:15 · K6 · Session 2 · Abstract ID 149913

Species diversity and evolutionary history of termitophilous rove beetles associated with Hodotermopsis termites

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Seven species in four genera in the subfamily Aleocharinae, Hodotermophilus, Hodotermopsiphila, Termophidoholus, and Yakuus, are known to be associated with a damp wood termite, Hodotermopsis sjostedti in Japan, Taiwan, and Laos. These beetles are closely related, but previous studies have indicated that their phylogenetic position within the subfamily is unclear.

Although H. sjostedti is broadly distributed in eastern Asia, the termite is found only in limited areas of Japan. All Japanese beetles associated with the termites, 4 species in 3 genera, are known only from Yaku-shima Island in Japan. Recently, we discovered three unfamiliar beetle species from nests of Hodotermopsis in western Shikoku, one of main islands of Japan. The three species were subsequently determined as new species of Yakuus and Hodotermopsiphila, as well as new species of new genus. The validities of new taxa were also confirmed genetically, but no consistent tendency was found in genetic distances between the new species and their related known species. Our phylogenetic analysis further confirmed that the beetles are not members of Lomechusini. In additions, as results of comparisons morphology and genetic sequences among the Hodotermopsis termites, we found the termites in Shikoku are also a new species.

These results indicate that the Hodotermopsis termites and the termitophilous beetles were co-speciated in Shikoku, but inconsistency of genetic distances found in the beetles makes it difficult to understand their evolutionary history. In this presentation, we will discuss their complex evolutionary history together with the geological history of Japan.

SYMPOSIUM 28 · Arthropod inquilines of social insects' colonies
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Endless forms most bloated: insights on diversity and evolutionary significance of post-imaginal growth in termitophilous beetles

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Symbiotic associations with social insects have repeatedly driven extreme morphological and life-history innovations. Among the most striking of these is physogastry, a post-imaginal enlargement of the abdomen that characterizes many termitophilous beetles and other termite-associated arthropods. Despite its prominence, the evolutionary origins, proximate causes, and functional significance of post-imaginal growth remain only partially explored. Here, we review and synthesize comparative morphological, behavioral, and natural history data across termitophilous beetles to outline an integrative framework for the evolution of physogastry. We suggest that post-imaginal growth may have originated as a non-adaptive byproduct of feeding within termite societies—most plausibly via trophallaxis or predation involving the ingestion of host-derived hormones—and was subsequently shaped by natural selection into diverse, lineage-specific morphologies. These transformations likely facilitated deep social integration, including enhanced chemical and tactile interactions with hosts, but also imposed substantial costs on mobility and dispersal. We further propose that physogastry is associated with a diphasic life cycle, in which divergent selection favors a mobile, stenogastric extranidal phase and a highly integrated, parasitic physogastric intranidal phase. Finally, we discuss how post-imaginal growth may complicate taxonomy and phylogenetic inference by obscuring species boundaries through ontogenetic transformation. Overall, we highlight post-imaginal growth as a key innovation in the evolution of social parasitism, linking developmental plasticity, life-history evolution, and integration into termite societies.

Post-imaginal growth and convergent abdominal appendages in termitophiles

Jordan Rainey
Biology Centre CAS - Institute of Entomology

Post-imaginal growth refers to the development that occurs after an insect has reached the adult stage. This is a rare phenomenon documented in a limited number of taxa, including Isoptera queens, Ixodida, Siphonaptera, and the termitophilous Corotocini (Coleoptera: Staphylinidae). In Corotocini, post-imaginal growth enables a dramatic transition from a stenogastric to a physogastric body form and permits the development of extreme morphological novelties, such as large abdominal pseudoappendages in the genus Spirachtha Schiødte. Using transmission electron microscopy (TEM), scanning electron microscopy (SEM), and micro-computed tomography (micro-CT), we investigate the mechanisms underlying post-imaginal growth, its effects on cuticular layers, and the functional morphology of associated abdominal outgrowths, with particular attention to their potential glandular activity. Comparisons are made with convergent abdominal appendages found in termitophiles from across insect orders, including Rhyncomya Robineau-Desvoidy (Diptera: Calliphoridae), Acridotarsa divisus (Silvestri) (Lepidoptera: Tineidae), and a new genus and species of Lomechusini (Coleoptera: Staphylinidae). Ultrastructural data are used to assess the presence of glands or secretory structures associated with these appendages and the body surface, providing insights into the role of such convergent structures in facilitating social integration within termite colonies.

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Disentangling the co-phylogenomics of termitophilous rove beetles (subfamily Aleocharinae) and their termite hosts

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Aleocharinae is the largest subfamily of rove beetles (Staphylinidae), comprising more than 16,000 described species and 1318 genera in 62 tribes. Around 700 described Aleocharinae species lives as social symbionts inside termite colonies, representing the most species-rich group of termitophilous insects. Termitophiles exhibit remarkable morphological adaptations i.e., physogastric and limuloid body plans, which enabled the co-evolution with their termite hosts and their tens of convergent incorporations into termite colonies. (Kanao et al., in preparation). Termitophily is thus a very promising model system to study evolutionary convergence of genotypes and phenotypes and also host-symbiont co-evolution. To exploit the potential of this group of organisms, a robust phylogenetic hypothesis of both termitophiles and their termite host is essential. With the aim to elucidate the cophylogeny of termitophiles and termites, here we present a molecular co-phylogeny for 154 species of termitophilous beetles their 110 species f termites host. Phylogenetic reconstructions are based on full mitochondrial genome gene set and ultra conserved nuclear elements (UCEs). The topology comparison of the termitophiles and their termite hosts' maximum-likelihood and Bayesian phylogenies reveals a high degree of congruence on one hand, while events of termite host switching are also detected. The frequency and evolutionary distance at which the phylogenetic incongruence between the termite and termitophile phylogenetic trees occur can uncover the existence of distinct infiltration mechanisms with distinct levels of host specificity in different termitophile groups. We are currently analyzing these patterns and the first results will be shared in this conference presentation.

Exploring the genomic convergence in termite-associated rove beetles (Aleocharinae)

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The ability to live in symbiosis with termites (termitophily) has evolved at least 40 times independently throughout Insecta. It is especially prevalent within rove beetles (Aleocharine) where it has evolved tens of times convergently. The majority of termitophiles have evolved one of two phenotypic adaptations to termitophily: physogastry or limuloidy. This enables termitophiles to evade an aggressive response from their hosts. This project aims to use Aleocharinae as a model system to explore the genetic signatures of the convergent evolution of termitophily by means of comparative genomics. The dataset includes 9 free-living and 26 termitophilous Aleocharinae species covering six independent origins of termitophily. As most Aleocharinae are a few mm in size and thus contain little DNA, PacBio HiFi long-reads have been sequenced from 1-6 individuals per species. The HiFi reads have been assembled for each specimen and scaffolded using OMNI-C chromatin capture sequencing data. The assemblies of all specimens within each species will be combined into one consensus genome assembly per species using a custom pipeline currently in development. Of the 35 species, 18 have an N50 above 10Mbp. Preliminary assemblies suggest that Aleocharinae have relatively small genomes (150-720 Mbp) within Staphylinidae (350-1400Mbp). The genome size does not differ between free-living and termitophilous Aleocharinae ($p=0.973$). The heterozygosity appears to be significantly lower in termitophilous than in free-living Aleocharinae ($p=0.012$). With the annotated chromosome-level assemblies we plan to test hypotheses that e.g. gene family sizes, and transposable element content evolved convergently in termitophilous Aleocharinae.

Drivers of Myrmecophile Diversity and Abundance in Wood Ant Nests (Formica rufa group)

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Mound-building Formica ants of the rufa group, commonly referred to as red wood ants (RWA), are a Holarctic group widespread in temperate and boreal forests. As keystone and umbrella species, RWAs provide numerous ecosystem services, and their large nest mounds form stable microhabitats for diverse assemblages of associated arthropods known as myrmecophiles. Ongoing declines in RWA populations raise increasing conservation concerns for these specialized communities. We investigated the drivers of myrmecophile diversity in RWA nest mounds and assessed whether nest characteristics buffer environmental gradients.

We sampled 313 nest mounds of six RWA species across six regions in Germany using pitfall traps and funnel extraction, combined with morphological identification and metabarcoding. In total, 4,187 arthropods representing 88 facultative and obligate myrmecophile species were identified. Diversity was highest in nests of F. rufa and F. polyctena, intermediate in F. lugubris, Formica aquilonia and F. truncorum, and lowest in F. pratensis; in F. lugubris, diversity also increased with altitude. Polydomous (multi-nest) colonies harboured a higher myrmecophile diversity compared to nests of monodomous (single-nest) colonies, and similarly, larger nest volume was positively associated with increased myrmecophile diversity. Both ant-myrmecophile and region-myrmecophile interaction networks were generalised, except for the Hunsrück region, which showed strong specialisation. Overall, ant species, colony type, and nest size were key drivers, while abiotic factors such as region, climatic conditions, and altitude had only marginal effects. Our study highlights the ability of nest mounds to buffer environmental influences and the importance of protecting large, well-connected, polydomous colonies for myrmecophile conservation.

SYMPOSIUM 28 · Arthropod inquilines of social insects' colonies
ORAL · Mon 17 Aug · 11:45 · K6 · Session 2 · Abstract ID 148566

Abundance and diversity of metazoan microfauna in ant mounds of Formica lugubris Zetterstedt, 1838

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Red wood ant mounds (Formica rufa group) are often considered biodiversity hotspots that host specialised invertebrate communities distinct from those of the rest of the focal habitat, yet their metazoan microfauna remains poorly known. Here, we examined how Formica lugubris mounds shape the abundance, biomass, and community structure of the main groups of microfauna: nematodes, rotifers, and tardigrades, across the Šumava National Park (Czech Republic). We sampled 30 ant mounds, collecting material from the mound surface and mound centre, together with adjacent forest-floor litter as a control. This sampling design, which explicitly matches mound material with an equivalent litter control, refines existing approaches for microfauna sampling in social insect nests and allows a more appropriate comparison with the surrounding habitat. Microfauna groups were separately extracted, identified into trophic or taxonomic groups and quantified. Here we show that abundances and (for nematodes) biomasses of all groups were significantly lower in the mound surface and especially the mound centre than in the control, although the microfauna community structure was nonetheless markedly altered in mounds. Trophic group composition of nematodes, as well as taxonomic composition of tardigrades and rotifers, differed between the mound surface and the control. Our results show that red wood ant mounds act as environmental filters that reduce the abundance of metazoan microfauna, but selectively favour some taxa or trophic groups, thereby potentially modifying soil food-web structure. This study further helps to fill an important knowledge gap about the hyperdiverse microhabitat of the Formica nest mound.

SYMPOSIUM 28 · Arthropod inquilines of social insects' colonies
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The uninvited guest ant - population genetics of the wood ant commensal Formicoxenus nitidulus

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Habitat specialists, particularly those that are poor dispersers, are highly susceptible to population isolation as a result of habitat fragmentation. Population isolation can lead to inbreeding, resulting in reduced genetic diversity and an increased risk of local extinction. The shining guest ant, Formicoxenus nitidulus, lives only within the nests of its wood ant (Formica rufa group) hosts. It is thus an extreme habitat specialist, dependent on patchy nesting sites within an already fragmented woodland habitat. We present the first data on the population genetics of this species, characterising its genetic diversity and degree of population isolation.

We developed eight novel nuclear microsatellite markers and generated mitochondrial DNA sequence data of the COI region to characterise samples from seven UK F. nitidulus populations collected from nests of three wood ant hosts: Formica aquilonia, Formica lugubris and Formica rufa. We found clear differentiation between populations correlating with spatial separation. The six largest study populations were genetically diverse and showed signs of effective within-site dispersal. Our data show that wood ant nests often host multiple genetically distinct F. nitidulus colonies, providing new insights into the mode of colony foundation in this elusive species.

We conclude that despite the risk of population isolation in this extreme habitat specialist species, genetic diversity has been maintained in multiple populations. Our results also indicate that a single wood ant host nest can have high conservation importance for the multiple F. nitidulus colonies it supports.

SYMPOSIUM 28 · Arthropod inquilines of social insects' colonies
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What limits myrmecophile abundance in ant nests?

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Despite being well-tolerated by their hosts and having unlimited access to host colony resources, many kleptoparasitic myrmecophiles occur in low numbers inside ant nests and produce fewer eggs than free-living relatives. This could be because myrmecophiles have difficulty finding mates, or because they must produce energetically expensive secretions or movements to appease their hosts. Alternatively, host colonies may die or abandon their nests if myrmecophiles become too numerous. Here, we report the effects of two different kinds of myrmecophiles on host colony survival, nest abandonment, and brood production across colony ontogeny. We calculated the minimum number of workers needed to support one myrmecophile, then measured colony responses to incremental increases in myrmecophile load. Crematogaster ashmeadi and C. pinicola colonies are parasitized by several myrmecophile species: The beetle Gnostus floridanus is a host-specialist that solicits trophallaxis from ant hosts, while the Eastern ant cricket, Myrmecophilous pergandei, is a host generalist that eats host brood and resources. While individual beetles could not survive in founding nests, individual crickets ultimately killed their host queen or colony by reducing host productivity 5 - fold . Mature host colonies could support more myrmecophiles, but their responses to increased parasite load suggest that there is a size-specific carrying capacity. The costs imposed by internal parasites can differ depending on host size, age, and body condition. Our findings suggest that a minimum number of workers is needed per kleptoparasite, which may select for certain myrmecophile life history traits, like small clutch size.

SYMPOSIUM 28 · Arthropod inquilines of social insects' colonies
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Spies inside army ant raids: Eavesdropping on the help pheromone of injured ants

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Army ants stand out for their ability to conduct large-scale battles with their prey, even when they suffer open wounds. Deadly infections are the leading cause of death among injured ants unless nestmates treat the wounds. However, field observations of injured ants receiving first aid showed that they were occasionally attacked by the myrmecophile rove beetle Tetradonia marginalis. Despite decades of observations of this beetle following raids, killing, and feeding on workers, no detailed study has addressed the nature of this interaction with injured army ant workers. Our study found that the myrmecophile T. marginalis preferentially hunts injured over healthy ants. Behavioural and chemical experiments confirmed that the help pheromone originates in the mandibular gland. A combination of the most abundant mandibular gland compounds, 4-methyl-3-heptanone and 4-methyl-3-heptanol, elicited the fastest attraction to beetles. We confirmed that the attraction occurred preferentially to injured workers by presenting groups of injured and non-injured workers in falcon tubes to the foraging column. Rove beetles were attracted 1.5 times more to open falcons containing injured workers than to closed falcons, which prevented pheromone spread. This study sheds light on the relationship between the myrmecophile T. marignalis and army ants. Because injured workers die from infections without help, the exploitation of help-calling pheromones in injured ants may introduce a third party into consideration when studying the evolution of social immunity strategies. The conflict between calling for help and being preyed upon can shape the coevolution of signalling and detection between injured ants and their myrmecophile predator.

Host-side optimization promotes acceptance of social parasites: Insights from signal detection theory

Tomohiro Nakazono; Kiyotaka Yabe; Kenji Matsuura
Kyoto University

Nestmate recognition systems in social insects restrict altruistic interactions to nestmates and thereby sustain social cohesion. Nevertheless, some social insect colonies can host social parasites that evade exclusion by host recognition processes and exploit colony resources while living among host individuals. Previous studies have primarily emphasized parasite traits underlying their acceptance, including morphological or chemical mimicry and defensive behaviors against host aggression. However, parasite acceptance is not determined solely by parasite traits but is also shaped by the host's optimization of discrimination decisions based on its own cost–benefit balance. Here, using a signal detection theory framework, we model the optimization of host discrimination thresholds and examine how colony-level and behavioral factors influence the tendency to accept social parasites. Signal detection theory predicts that parasite acceptance increases when parasites constitute only a small fraction of the individuals encountered by hosts. Simulations of individual movement show that the parasite encounter probability inferred by hosts declines in larger host colonies and when host walking speed is higher. We further show that variation in host recognition signals can alter the range of parameter values over which acceptance is favored in the model. These results suggest that social structure and behavioral dynamics of hosts influence parasite acceptance through their effects on the location of optimal recognition thresholds. This framework offers a theoretical basis for understanding how differences in colony organization and behavior contribute to patterns of parasite acceptance across social insects.

Interaction dynamics among social parasites sharing a common host ant

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Social insect activity structured by complex social systems represents a major evolutionary driving force shaping surrounding organisms. Symbionts inhabiting social insect nests maintain exceptionally close associations with host societies and thus provide powerful model systems for understanding how non-social organisms adapt to highly organized social systems. Previous studies have primarily focused on pairwise host–guest interactions, revealing sophisticated host-use strategies of individual inquilines. In natural systems, however, multiple guest species frequently co-occur within the same host colony, and host responses experienced by inquilines may therefore differ fundamentally from those under single-species occupancy. Here, we show that a social parasitic silverfish excludes a competing species by elevating host aggression. Focusing on three social parasites associated with the ant Tetramorium tsushimae—two ant crickets (Myrmecophilus tetramorii and M. affinis) and one silverfish (Nipponatelurina kurosai)—field surveys revealed that co-occurrence between M. tetramorii and N. kurosai was significantly rarer than expected by chance. In contrast to M. affinis, which frequently

contacted hosts and received oral feeding, both M. tetramorii and N. kurosai were consistently treated as non- nestmates, suggesting overlap in their use of nest-associated resources. Under co-occurrence conditions, N. kurosai exhibited a distinctive abdominal tapping behavior directed toward M. tetramorii, coinciding with a marked increase in host aggression toward M. tetramorii. These results demonstrate that interference among parasites can strongly modify host–parasite interactions and shape parasitism patterns at the habitat scale, highlighting the importance of guest–guest interactions for understanding the adaptive strategies of inquilines within host societies.

Evolution of Social Parasitism in a hyperdiverse clade: An integrative study of Camponotus carpenter ants

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Social parasitism is a widespread life-history strategy in ants, in which a parasite species exploits the social behavior of a closely related host for survival and reproduction. Camponotus carpenter ants form a hyperdiverse, cosmopolitan clade with several proposed centers of diversity including the Eastern Mediterranean and Anatolia. From these regions, two socially parasitic Camponotus species are known, yet their evolution remains unstudied.

To test competing hypotheses about the evolution of social parasitism, we present the first population-level phylogenomic reconstruction of Camponotus from the Mediterranean using ultra-conserved elements (UCEs) as genetic markers. We integrate phylogenomic results with population-genetic, morphological, and biogeographical data to investigate the origin of social parasitism, host specificity, and diversification processes in this group.

Our analyses support a single origin of social parasitism in Camponotus, but reveal contrasting host-use strategies. Camponotus ruseni is strictly associated with its single host, C. oertzeni, whereas C. universitatis exploits three host species: C. aethiops, C. oertzeni, and C. pilicornis. The former two are close relatives of the parasites and show signatures of recent divergence or reticulation, suggesting complex host-parasite co-evolution. In contrast, C. pilicornis is phylogenetically distant, highlighting pronounced behavioral plasticity. We also identify several closely related, previously undescribed non-host taxa from the Eastern Mediterranean and Anatolia, underscoring the taxonomic complexity of the clade.

Overall, our findings indicate that social parasitism in Camponotus carpenter ants originated once and involved secondary parasite speciation and host shifts. Our study also provides a phylogenomic framework for resolving species boundaries in Eurasian carpenter ants.

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An ant social parasite helps its fungus-growing ant host with nest hygiene

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Parasites are seen as harmful, but sometimes their interactions with hosts lead to unexpected benefits. While still a parasite, some of their actions and traits may have positive effects on the host. Known as conditionally helpful parasitism, this phenomenon remains largely unexplored in social insects. To investigate such conditions, we examined the relationship between the fungus-growing ant Sericomyrmex amabilis and its cohabiting guest ant social parasite, Megalomyrmex symmetochus. We hypothesize that the parasite shares an interest with its host in maintaining a healthy nest and fungus garden, thus reducing disease pressure. We first assessed the antifungal capacity of M. symmetochus alkaloid venom against fungal pathogens of Attine ants (Beauveria, Escovopsis, Trichoderma, etc.) using in-vitro assays and determined the minimum inhibitory concentration. In another experiment, we observed the parasite's interactions with the fungus garden for five days following exposure to Escovopsis weberi. After removing the ants, we monitored cultivar survival for seven days and compared it with a control group lacking parasite intervention. The alkaloid venom inhibited all pathogens, showing fungistatic effects at 0.83 µg and fungicidal effects between 1.66 and 6.64 µg. Unexpectedly, the social parasite has similar cleaning behaviors previously reported only in fungus-growing ants and applied low venom doses prophylactically (0.10 µg). Although pathogen removal was incomplete, infected cultivar exhibited higher survival when cared for by M. symmetochus. These results suggest that under high pathogen pressure the benefits provided by this social parasite may outweigh their costs, revealing a novel case of context-dependent mutualism in social insects.

Understanding the behavioural integration of a paper wasp social parasite into the dominance network of the host colony

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Social integration, i.e. the incorporation of newcomers into the social structure of a group, is a key process to understand how animal groups form and change. Among insects, obligate social parasites must enter a host colony and exploit brood care to reproduce, representing an outstanding example of social integration. To achieve this, parasites employ communicative strategies, but their ability to behaviourally integrate within the host society and the effects at the group level have been overlooked. We propose a framework to assess behavioural integration of a social parasite using a paper wasp model: Polistes sulcifer–Polistes dominula. Polistes dominula colonies show behavioural castes determined by a linear dominance hierarchy among foundresses and workers. Only the alpha retains the reproductive role while the others participate in nest maintenance and brood care. Polistes sulcifer enters the colony and assumes the reproductive role by eliminating the alpha. In this scenario, the parasite should integrate into the social network of the host colony and match the alpha's behavioural repertoire. To test this hypothesis, we generated usurped and control colonies and followed inter-individual dominance interactions. We tested whether usurpation influenced social network metrics at global, motif and individual scale. We found an overall success in the integration of the social parasite within the host social network at the levels investigated. Beyond offering insights into strategies adopted by inquiline social parasites, our conceptual and analytical framework can be used to understand social integration across animal societies.

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The dynamic associations between social insects and their arthropod guests during introductions and invasions

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Invasions and managed introductions of social insects are transforming ecosystems worldwide. An understudied aspect is that these events create new opportunities for the spread and exchange of nest-associated guests, a diverse group of symbiotic arthropods, such as beetles, mites and flies, that live exclusively within and around social insect nests. Based on an extensive literature review, I provide a comparative and quantitative overview of interactions between social insects and their guests during invasion and introduction. I first discuss the diversity of these guests in the native ranges of social insect species that are invasive or introduced elsewhere, to establish a comparative baseline. I then examine five key processes shaping host–guest dynamics during invasions: (1) guest release, the loss of guests during social insect invasion (2) co-invasion, the joint spread of host colonies and hitchhiking guests (3) guest spillover, when invasive guests colonize native host colonies (4) guest spillback, when native guests infiltrate invasive host colonies; (5) intentional introductions of parasitic guests to control social insect invasions. Finally, special attention is given to managed bees (honey and bumble bees), whose global translocation, introduction and feral escape have amplified opportunities for guest exchange. Together, these processes reveal the complex, yet often overlooked, interplay between invasive and managed social insects and arthropod guests.

Obligate commensalism between the cleptobiotic ant Strumigenys incerta and its host Cryptopone sauteri

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Cleptobiosis in ants is a form of compound nesting in which one species obtains food by stealing it from another. Here, we investigated host dependence, cleptobiotic behavioral traits, and host impacts in the attine ant Strumigenys incerta, a species previously suggested to exhibit cleptobiosis toward the ponerine ant Cryptopone sauteri. Field surveys revealed that colonies of S. incerta were found exclusively within nests of C. sauteri, and laboratory rearing experiments further showed that substantial colony growth of S. incerta occurred only under host-cohabitation conditions. Behavioral observations demonstrated that S. incerta primarily relied on specialized cleptobiotic foraging, stealing prey items temporarily stored by the host, and rarely showed independent hunting in the presence of the host. In contrast, under host-removal conditions, S. incerta workers engaged in hunting behavior; however, their hunting success was markedly lower than that of other Strumigenys species, indicating that cleptobiosis constitutes the primary foraging strategy of S. incerta. Aggression by host workers toward S. incerta was extremely rare. When encountering host workers, S. incerta workers frequently remained immobile with their antennae and legs folded. This behavioral adaptation, together with environmental camouflage and small body size, likely facilitates a peaceful coexistence without attacks within host nests. Importantly, the presence of S. incerta did not significantly affect the colony growth of C. sauteri. Together, these results suggest that the cleptobiotic association between S. incerta and C. sauteri represents a relationship close to commensalism, imposing no detectable costs on the host colony.

The transition to a social parasitic lifestyle influences maintenance and expression of essential immune defence traits

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Social parasites and their equally social hosts offer interesting systems to understand gains and losses in evolution. Yet, they have so far rarely been used to study the evolution of immune defence traits. To gain a better understanding of the evolutionary consequences of a transition to a social parasitic lifestyle on immune defence traits, here we investigated the facultative social parasitic ant Formica sanguinea, the obligate social parasitic ant Polyergus rufescens and their common social host ant species Formica fusca in mixed as well as single species experimental setups. We found that during sanitary care of fungal entomopathogen exposed pupae, F. fusca performs not only most of the sanitary behaviour of brood grooming but performs brood grooming also according to the degree of social parasite specialization, engaging in four and ten times more brood grooming in mixed setups involving F. sanguinea and P. rufescens, respectively. We also found that F. sanguinea engages in brood grooming and worker allo-grooming irrespective of F. fusca presence, while P. rufescens never expressed these sanitary behaviours. Consequently, the presence of F. fusca delayed fungal outgrowth on brood of P. rufescence and diminished its worker mortality risk, while F. fusca presence was not similarly beneficial to F. sanguinea. Finally, we found that in the absence of F. fusca, F. sanguinea upregulates the use of venom for sanitary purposes. We conclude that social parasites are interesting systems to study the maintenance and expression of immune defence traits and the evolutionary pressures that shape investment in these traits.

Behavior, diet, and phylogeny as drivers of chemical strategies in ant–myrmecophile interactions: a systematic review

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Ants utilize cuticular hydrocarbons (CHCs) for nestmate and species recognition, creating a chemical barrier that organisms that interact with ants (myrmecophiles) must navigate to coexist within ant territories. While various chemical strategies such as mimicry, camouflage, and insignificance are well-documented, the factors determining which strategy a myrmecophile employs remain poorly understood. We aimed to offer a comprehensive understanding of chemical strategies, enhancing our predictive capabilities regarding the forces influencing these strategies in various ant-myrmecophile systems. We conducted a systematic review of 153 studies, identifying 456 unique descriptions of chemical strategies across 44 years of research. Using multinomial models, we tested the influence of behavior, diet, interaction type, and phylogeny on these chemical strategies. Our results demonstrate that all four factors significantly shape chemical strategies. Specialized parasitic interactions predominantly utilize chemical mimicry, particularly when the myrmecophile resides inside the nest. In contrast, mutualistic and commensal partners typically show an absence of chemical convergence with their hosts. Furthermore, behavioral acts (e.g., rubbing or clinging) and dietary sources are essential for the active acquisition of CHCs. Finally, phylogeny exerts a strong influence, with certain taxa specializing in specific strategies while others exhibit high plasticity. These findings highlight a predictable continuum of chemical specialization driven by ecological and evolutionary pressures. We suggest that future research adopt a multitrophic and behavioral approach to further refine these chemical ecology models in ant-myrmecophile interactions.

Collective behaviour and emergent sociality in Ephydridae (Diptera) inhabiting extreme environments

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Research on social insects has traditionally focused on eusocial systems; however, collective behaviours are also widespread among non-eusocial insects and offer valuable perspectives on the ecological and evolutionary drivers of sociality. Species of the dipteran family Ephydridae frequently inhabit extreme or highly constrained environments, such as hypersaline, alkaline, or polluted habitats, where suitable resources and microhabitats are limited in space and time.

Under these conditions, adult Ephydridae often exhibit pronounced aggregative behaviours, particularly around feeding, mating, or oviposition sites. Such aggregations may confer indirect adaptive benefits, including increased mate encounter rates, more efficient exploitation of ephemeral resources, or enhanced tolerance to environmental stress. Although Ephydridae lack reproductive division of labour and stable social organization, their collective responses to ecological constraints show functional analogies with group-level processes observed in eusocial insects.

This contribution is based on field observations and analyses of the spatial distribution and behaviour of adult Ephydridae in extreme habitats, aiming to identify ecological factors associated with the emergence of collective behaviour. By adopting a comparative framework, this study highlights the relevance of non-eusocial insects for understanding the continuum of sociality and the ecological mechanisms that may promote collective organization in insects.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
ORAL · Thu 20 Aug · 10:15 · K6 · Session 50 · Abstract ID 146365

Effects of vector-borne transmission on viral ecology and evolution in bees

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Honey bees are arguably one of the most intensively managed insect species, nevertheless, they often interact with wild pollinators through shared floral resources whereby they can share pathogens. The epidemiology of host-parasite interactions in this system has been drastically altered by the ectoparasitic mite and viral vector Varroa destructor. This vector can directly transmit pathogens to the honey bee's hemolymph, circumventing many of its anti-viral defence mechanisms. Deformed wing virus, a formerly benign virus that has long been associated with honey bees, has re-emerged with Varroa and is now causing high over-winter mortality in hives around the globe. Using a 'natural experiment' of island populations with and without Varroa, we study how this novel vector-borne viral transmission route affects the viral landscape of honey bees and bumble bees. We find that varroa reduces viral diversity in honey bees and promotes the dominance of deformed wing virus (DWV), although it is not linked to the emergence of DWV recombinants. Modelling supports that vector-mediated transmission turns honeybees into virus super-spreaders in these communities. We explore the parameter space for transmission, to test how mitigation measures such as vector control can affect viral prevalence.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
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Viruses in ants: current knowledge and future directions

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Ants are among the most abundant and ecologically important insects, yet they remain an understudied group in insect virology. Compared to well-characterized systems such as honeybees, relatively little is known about the diversity, prevalence, and ecological significance of viruses in ants. In this presentation, I will first provide an overview of current knowledge on viruses in ants. I will then present results from my own research on viral diversity, host specificity, and infection activity across multiple ant species, and how colony social organization influences viral prevalence and abundance. I will conclude by highlighting major open questions in the field, including the effects of viral infections on host fitness, mechanisms of transmission within and between colonies, and the evolutionary dynamics of ant–virus associations. Addressing these questions will be essential for understanding the role of viruses in ant biology and social evolution.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
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Honeybee viral and gut microbial associations in Varroa free vs impacted landscapes

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The western honeybee (Apis mellifera) is a globally significant pollinator whose health is tightly linked to its associated microbial communities. A. mellifera, native to the UK, was introduced to the island state of Tasmania in Australia in the 1830s. A major threat to A. mellifera is Varroa destructor, an invasive, parasitic mite first detected in the UK in 1992, and on Australia's east coast in 2022, but remains absent from Tasmania. Varroa not only harms bees directly but is also a vector of pathogenic bee viruses, which may form a bidirectional relationship wherein viral infection disrupts gut microbial communities, and in turn microbial imbalance influences viral dynamics. Using meta-transcriptomics, 16S rRNA sequencing, phylogenetic, and co-occurrence analyses, we compare honeybee viromes and gut microbiomes across Varroa-impacted and Varroa-free regions, incorporating environmental data to assess how climate and landscape context shape the diversity, composition, and relative abundance of these communities. We test three hypotheses: (i) honeybee virome community and genomic profiles will be more similar within regions than between regions, with greater homogeneity in the UK consistent with a "Varroa effect"; (ii) gut microbial diversity metrics will differ between regions, particularly among facultative and environmentally associated genera; and (iii) virus–microbe associations will vary across Varroa-free and Varroa-impacted landscapes. This research highlights the complex interplay between viruses, gut microbes, and environmental pressures in shaping pollinator health.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
ORAL · Thu 20 Aug · 11:00 · K6 · Session 50 · Abstract ID 146450

Bumble bee viral communities: Are they shared across species, locations, or both?

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The United States Midwest has been identified as being in critical need of bumble bee conservation and is home to the endangered Bombus affinis and other imperiled species such as Bombus pensylvanicus. Declines within the genus are driven by multiple complex stressors rather than a single factor. Bumble bees naturally suffer from a variety of parasites, parasitoids, and pathogens; however, transmission may have increased due to the importation of non-native species, such as the European honey bee (Apis mellifera), and industrial-scale use of commercial bumble bees (Bombus impatiens).

The goal of this research is to characterize known and potentially novel/emerging viral pathogens in bumble bee populations within an area of documented population decline in the Midwestern United States. We surveyed viral communities across species and sites for five North American bumble bee species, including the imperiled B. pensylvanicus. Approximately 1,200 bees were collected over two years, and a subset of samples was analyzed using high-throughput RNA sequencing to identify and quantify known and potentially novel viruses present across multiple species in Iowa. We address (1) viral diversity and abundance across bumble bee species, including one of significant conservation concern; (2) whether known honey bee or other bee-associated viruses dominate bumble bee viral communities; (3) whether viral communities differ across species; and (4) whether there are significant site-level effects, with viral communities shared across species within a site. These results improve our understanding of bee virus transmission across species, and provide insights to improve management of managed, native, and declining species.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
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Survey of pathogen prevalence in commercial beekeeping operations across Southwest Saudi Arabia: Implications for management and selective breeding

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The native honey bee of the Arabian Peninsula, Apis mellifera jemenitica, is well adapted to arid environments but remains vulnerable to pathogens. We conducted the first molecular survey of Nosema spp. and seven honey bee viruses in A. m. jemenitica colonies from eleven commercial apiaries in southwestern Saudi Arabia. Microscopy and molecular analyses showed that all Nosema-positive samples contained Nosema ceranae, with no detection of N. apis. Infection levels varied among locations. Spore counts averaged 3.43×10^7 spores per bee across sites, with a maximum of 3.39×10^8, while three locations had no detectable spores. Quantitative PCR revealed a mean of 1.86 ± 0.18 $\log_{10}$ DNA copies, with a maximum of 3.24 ± 0.90 $\log_{10}$ copies, and detected infections in some spore-negative samples, indicating greater sensitivity than microscopy. Of the seven viruses tested, Black Queen Cell Virus was detected at low levels in six locations, with one colony showing moderate infection (2.44 ± 0.06 $\log_{10}$ copies per bee). Deformed Wing Virus was present at low levels in two colonies, and Chronic Bee Paralysis Virus was detected at trace levels in three. The remaining four viruses were not detected. Although most colonies were infested with Varroa destructor, levels remained below three mites per 100 adult bees. Overall, the low pathogen and parasite burdens suggest that A. m. jemenitica colonies exhibit a possible natural disease tolerance. These results provide a baseline for disease monitoring and selective breeding programs to improve honey bee resilience in the region

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
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Sub-lethal effects of DWV infection on bumble bee learning behaviour

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In a rapidly globalized world, emerging infectious diseases (EIDs) pose a growing risk to social insect colonies and the ecosystem services they provide. Virus-spillovers frequently occur, especially in insect pollinators, facilitated through shared floral resources. Currently, little is known about the sub-lethal effects of these viruses on colony fitness. One such example is the highly prevalent and globally distributed Deformed Wing Virus (DWV). DWV is a known cause of colony losses in honeybees and has been detected in habitat-sharing bumblebees. Although recent studies have not found a lethal effect, it is still unclear whether DWV infections might have an indirect effect on bumblebee health and colony fitness. Here, we present novel data concerning the effect of DWV infections on foraging and learning behaviour in Bombus terrestris workers using a free-flying cognition assay. Our findings provide a first insight into the sub-lethal effects of DWV infection on B. terrestris cognition, which can directly impact their foraging efficiency and is therefore important for colony fitness.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
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Virus-virus interactions between the Deformed wing virus and Varroa destructor virus-2 in varroa mites

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The varroa mite poses the greatest threat to honey bees by vectoring the Deformed wing virus (DWV), which is associated with colony collapse. Varroa mites also harbour the recently discovered Varroa destructor virus 2 (VDV-2) which selectively replicates in the mite and has been shown to be negatively correlated with DWV in field samples. First, through a large-scale field survey of paired varroa and bee pupae samples in three regions of Aotearoa/New Zealand, we observed a negative association between the DWV-A and VDV-2. Second, we used viral inoculation, DWV-targeting antibodies and DWV-targeting dsRNA to manipulate DWV loads in Varroa. While our functional data suggests that there is no interaction between the two viruses, consistently low VDV-2 levels in our samples underscore the need for further investigation of how virus-virus interactions within a parasite can affect viral loads in its host.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
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Influence of host and viral characteristics on Black queen cell virus virulence

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Black queen cell virus (BQCV) is primarily known for causing the death and discoloration of developing Apis mellifera queens. Characteristics of both the honey bee host and virus itself likely contribute to the apparently conditional, exceptional virulence pattern of this virus. However, little research has explained BQCV virulence from either perspective. Our work thus seeks to explore how BQCV virulence is determined by developing honey bee host and BQCV viral characteristics. We first explored how BQCV virulence may be influenced by BQCV strain variability with a combination of experimental and bioinformatic approaches. To begin understanding host characteristics that determine BQCV virulence, we compare the temporal dynamics of BQCV in workers and queens and link those observations to putative molecular differences between honey bee queens and workers at the critical developmental stages. The broader implications for bee health and understanding an exceptional virus in social insects will be discussed.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
ORAL · Thu 20 Aug · 14:30 · K6 · Session 56 · Abstract ID 149285

Timing of viral infection shapes disease outcome in Bombus terrestris, with modifying effects of the gut microbiome

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The timing of viral infection is thought to be a critical determinant of disease outcome in insects, yet it remains poorly understood in social bees. In bumble bees, preliminary work suggests that survival following viral exposure depends not only on host condition but also on timing of infection during development. Here we investigate effects of early (at adult eclosion) versus delayed (> 8 days as an adult) viral exposure in a controlled laboratory experiment using Bombus terrestris while accounting for differences in gut microbiota establishment, given that the microbiome can provide protection against viruses. As a virus, we used deformed wing virus B (DWV-B), a honeybee-associated virus known to spill over to wild bees. We found that DWV-B infection negatively impacted survival directly after hatching, i.e. early viral exposure, and when the normal gut microbiome was depleted, indicating both a strong effect of infection timing and the potential of the microbiome to mitigate negative effects of early infection. Viral exposure later in adult life and microbiome disturbance did not impact bee survival. However, we found that late viral exposure reduced offspring production, indicating a potential long-term consequence for colony fitness. Overall, these results show that the timing of viral exposure is a key determinant of infection outcome in social bees, linked to gut microbiome establishment, with early infection coupled with a depleted microbiome posing the greatest risk.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
ORAL · Thu 20 Aug · 14:45 · K6 · Session 56 · Abstract ID 149398

Structural and molecular implications of infections by deformed wing virus in the honeybee brain

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Deformed wing virus (DWV) is well known for its most visible effects on honeybees like deformities and early mortality. Less understood are the consequences of chronic infections, when DWV is present at lower levels with often invisible effects. During these infections DWV is detectable in different regions of the honeybee brain, possibly explaining the effects at the cognitive and behavioural levels that have been reported in previous research.

In this study we explored the interplay between DWV infections and the honeybee brain in naturally infected individuals. We performed the transcriptomic profiling (RNAseq) of the mushroom bodies in two groups of bees that presented varying levels of viral infection: experienced foragers and young bees (newly emerged and 3-day old). We identified a clear molecular signature in experienced foragers that separates bees with high vs. low DWV levels, encompassing genes linked to neuropeptide signalling, odorant binding and immunity; this signature however was less evident in 3-day old bees and absent in newly emerged bees. Furthermore we followed the development of the mushroom bodies in the same groups of young bees through a micro-CT scanning approach: this brain region was significantly larger in 3-day old bees with high DWV levels compared to the low-DWV counterpart, while no difference was detected in newly emerged bees.

Our results stress the importance of investigating more subtle effects of viruses on hosts' phenotype and also highlight the power of focusing on specific tissues and age groups to better identify the mechanisms of action of these important pathogens.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
ORAL · Thu 20 Aug · 15:00 · K6 · Session 56 · Abstract ID 149650

Insipient co-evolution: Varroa destructor infestation and DWV infections cause major but non-overlapping shifts in gene expression in Apis mellifera populations

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Pollinators worldwide are under threat of several anthropogenic as well as natural challenges. Particularly the European honeybee, Apis mellifera is currently under threat of the ectoparasitic mite Varroa destructor since its spread from the Asian honeybee (A. cerana). This relationship has only had a short history of co-evolution, which is further complicated by a three-way interaction where V. destructor serves as a viral vector, particularly for Deformed Wing Virus (DWV). Despite variants of DWV being common and horizontally transmitted in bees, the transmission through V. destructor significantly increases the virulence, with negative effects on both individuals and colonies. In this study, we compared the gene expression of V. destructor infested bee populations to uninfested populations on several islands in the North Sea, in order to gain a better understanding of this three-way host-parasite interaction. We found a total of 1,142 Differentially Expressed Genes (DEGs), the majority of which (750) being downregulated upon Varroa infection. Upon exploring functions of these DEGs, we encountered several GO terms associated with perception and development. Upon exploratory analysis of DWV relative abundance, however, despite having a high number of DEGs (548), we find very few DEGs to be overlapping between the two (77; ~7% of the Varroa DEGs, ~14% of the DWV DEGs). This sheds light on the incipient co-evolution of A. mellifera and its recently emerged ectoparasite.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
ORAL · Thu 20 Aug · 15:15 · K6 · Session 56 · Abstract ID 150144

Primary and secondary antiviral RNAi responses throughout Varroa destructor life stages reveal the vertical transmission of viruses

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One of the most devastating threats to honey bee health is the ectoparasitic mite and viral vector Varroa destructor, yet transmission dynamics of the viruses it carries remain poorly understood. RNA interference (RNAi) is a major antiviral mechanism in invertebrates including Varroa, where replicating viruses are degraded into virus-derived small interfering RNAs (vsiRNAs). Insects typically produce 21–23 nt sense and antisense vsiRNAs, however established viral infections in V. destructor lead to production of 24-nt antisense vsiRNA fragments, like secondary vsiRNA production in nematodes. To understand viral infection and transmission dynamics, we performed small RNA sequencing on mites throughout development to characterise changes in the RNAi response. Five viruses were consistently degraded into antisense 24-nt vsiRNAs across all developmental stages, suggesting these viruses are vertically transmitted. In contrast, bidirectional 23-nt vsiRNA fragments are generated in response to the pathogenic bee virus, Deformed wing virus A in eggs, but the vsiRNA profile transitions to antisense 24-nt vsiRNA at later life stages. Our results suggest that a primary 23-nt bidirectional antiviral response precedes the production of secondary 24-nt antisense vsiRNAs as the infection becomes established. To confirm the presence of primary siRNA synthesis, we treated mites with exogenous dsRNA targeting a non-expressed reporter gene (GFP), which was processed into bidirectional 23-nt siRNAs. Our results show that RNA interference in V. destructor includes primary and secondary processing, and that vsiRNA profiles can demonstrate underlying virus transmission dynamics, which is critical for understanding the persistence and dissemination of pathogenic viruses within honey bee populations.

Gene by environment interactions impact virus infection in mite resistant honey bees

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A principle threat to honey bee health continues to be viral infections, which often compound with other abiotic and biotic stressors to impact individual bee health and colony productivity and survival. Colonies vary in their susceptibility to virus based on genetic and environmental factors, including their ability to resist parasites that vector viruses, like the mite Varroa destructor. A series of studies will be presented that investigate the interaction between honey bee genotype and environment to evaluate specifically how viral infections influence mite resistant populations in the US, like the Pol-line stock bred for Varroa Sensitive Hygiene. Results of one longitudinal study, examined viral strain diversity over time in mite-resistant and mite-susceptible colonies across five commercial beekeeping operations in the US over time. Environment played a large role in the overall viral communities across the populations, but there were interesting dynamics between viruses that arose comparing the mite-susceptible and mite-resistant colonies. Additional work assessing the expression of the “suppressed in ovo virus infection” (SOV) trait in two different US mite resistant populations and the potential for breeding for multiple mechanisms of virus resistance will also be discussed. Overall, information will provide insight into viral infection dynamics of mite resistant populations in the US that are applicable globally.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
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Juvenile Hormone Enhances Viral Activity in Bumble Bees

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Bees are susceptible to viral infections that can compromise individual and colony health. As viruses depend on host cellular resources for replication, we investigated the influence of a key insect regulator, Juvenile hormone (JH), which enhance reproduction and metabolic rate on viral activity. We hypothesized that elevated JH levels would promote viral replication in a tissue-specific manner. To test this hypothesis, we used the bumble bee, Bombus terrestris, and the Israeli acute paralysis virus (IAPV). In our first experiment, we compared IAPV replication in pre- and post-diapause queens, which naturally have low and high JH levels, respectively. Post-diapause queens showed significantly increased viral loads in the fat body and ovaries, but not the brain, supporting our initial hypothesis. To establish causality, we then treated pre-diapause queens with JH before infection. Queens that received JH exhibited substantially higher viral transcript levels in the fat body and ovaries compared to controls, confirming that JH enhances IAPV replication in these tissues. A final experiment examined whether supplemental JH could further boost viral replication in post-diapause queens already possessing high endogenous JH levels. No additional increase in viral titers was observed, indicating a "ceiling effect." Our findings demonstrate that IAPV replication is enhanced by JH, particularly in metabolically active tissues such as the fat body and ovaries. This research uncovers a critical link between host hormones and viral pathogenesis, offering new insights into disease progression in bees.

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Experimental evolution of IAPV pathogenesis and antiviral immune response in Apis mellifera

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The evolution of virus virulence and its influence on host immune systems is the key to understanding disease dynamics and host-pathogen interactions. Using the Israeli acute paralysis virus (IAPV) as a model, we predicted that serial passaging through honey bee workers under bi-directional artificial selection for opposing virulence would yield two divergent IAPV strains - one virulent and the other benign - with accompanying genetic differences from the original strain. We further predicted that this variation in IAPV virulence would differentially shape the antiviral immune response of worker honey bees. A selection experiment with 11 parallel lines for each direction was performed for ten generations. In each generation, newly emerged bees were inoculated and monitored for mortality, and early or late dying bees were collected and frozen in the virulent and benign lines, respectively. Survival analysis indicated substantial heterogeneity among lines, with a significantly higher survival rate of bees subjected to “benign” lines relative to the “virulent” lines or the original IAPV strain overall. Total RNA was extracted from live bees exposed to selected IAPV lines for sequencing library preparation. The underlying changes in virus composition and genome, together with transcriptomes of inoculated workers, will be presented and discussed to explain the IAPV differentiation in our selection experiment and further our understanding of virulence evolution of RNA viruses in the insect host and its consequences for honey bee antiviral immune response.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
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Collective antiviral defense through social transfer in ants?

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Social immunity is very effective in preventing disease spread through insect colonies by removing sources of infection. It is, for example, well established that both bees and ants remove late-stage infected brood by hygienic behavior from the colony. At an earlier stage of infection, allogrooming can remove pathogen from exposed individuals, strongly reducing their risk of developing disease, which does not only protect the colony, but also rescues the exposed individual. While grooming is highly powerful against externally infecting parasites and pathogens, like Varroa mites or fungal spores, the ways how nestmates can contribute to the health of colony members suffering from oral or wound-derived infections, like viral diseases, is only little understood. Studying Lasius niger garden ants infected with Cricket Paralysis virus, we study how nestmate presence affects disease progression of the infected individual, and, vice versa, how social contact to an infected individual affects individual immunity of the nestmates. We particularly test for a possible protective effect of social fluid transfer via trophallactic exchange – forming the colony's circulatory system – both by feeding experiments and by analysis of the fluid itself. Our work shows how variable social immunity can be in response to the highly diverse infection modes and trajectories of different pathogens, and evaluates the understudied role of social transfer in mediating colony health.

SYMPOSIUM 29 · Tiny but mighty: viruses in social insects
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Multiple key hosts and network structure shape viral prevalence across multispecies communities of bees

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Survival of wild bees is threatened by many factors, of which diseases have received increasing attention. Many pathogens are shared between managed and wild bee species, with flowers as the most likely route of interspecific transmission. An increased density in the landscape of managed honeybees, the assumed reservoir hosts of many viruses, may therefore aggravate pathogen spillover among bee communities. To explore this possibility, we manipulated the density of honeybee colonies across 32 agricultural landscapes differing in floral abundance, recorded plant-pollinator interactions, screened managed and wild bee species for common pollinator viruses and estimated the contribution of each bee species to viral R0. We found that the density of virus-positive honeybees, network connectance and network niche overlap were important predictors of viral presence in wild bees. Our study provides insights into the viral transmission dynamics in bee communities which can inform management decisions to reduce disease threat to wild bees.