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Insect Behaviour Special Interest Group

Conference 2023

09:30		Arrive	
10:00	Chair	Michelle Fountain	Welcome to NIAB East Malling
10:05	Keynote	Bart Lievens	Potential of insect-microbe chemical communications to improve biological control of insect pests
10:35	Keynote	Noushin Emami	Natural molecular strategies to break disease transmission
11:05		Short break	
11:30	15-min talk	Gareth Thomas	Using the odour of bacteria to tackle Acute Oak Decline
11:45	15-min talk	Lucien Dobel-Ober	Investigating Mosquito Behaviour using novel Gnotobiotic methods
12:00	15-min talk	Durlave Roy	Studies on the use of Plant extracts - importance in sustainable agriculture
12:15	Lunch		
	Poster	Sandra Cortes	Aphid infestation changes metabolic activity and composition of bacterial communities in the wheat rhizosphere
	Poster	Biplove Bala	Microbes could play an important role in insect behaviour
	Poster	Tchoudjin Gertrude Loveline	Effect of habitat on diversity and composition of leaf litter ant species: implications for conservation management.
13:45	Chair	Jozsef Vuts	Welcome to Rothamsted Research
13:55	15-min talk	Daniel Leybourne	Can endosymbionts influence the development, fitness, and behaviour of cereal aphids?
14:30	Keynote	Brendan Daisley	Design and application of a novel spray-based probiotic formula for sustainable microbiome management in honey bees
15:00		Short break	
15:15	Keynote	Kelly A. Hamby	Behavioral responses of spotted-wing drosophila to free-living fungi
15:45	15-min talk	Rudra Gouda	Physiological functioning of gut bacteria characterized in forager and hive bee of Apis mellifera
16:00	15-min talk	Fardiina Rahimi	Genetic basis interspecies impacting the horticultural pest Drosophila Suzukii
16:15	15-min talk	Ana Laura Nussenbaum	Studies on symbiont microorganisms of Anastrepha fraterculus (Diptera: Tephritidae) and their use in sustainable pest management strategies
16:30	Keynote	Boaz Yuval	The microbiome and fruit fly behaviour
16:45		Close of meeting	





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Bart Lievens, KU Leuven, Belgium

Potential of insect-microbe chemical communications to improve biological control of insect pests

Recent studies have shown that microorganisms emit a bouquet of volatile compounds that influence insect behavior. However, it remains largely unclear whether microbial volatile organic compounds (mVOCs) can attract natural enemies of pest species and thus be exploited as attractants to improve biological control of insect pests. Using the aphid parasitoid Aphidius colemani, we performed a number of experiments to investigate the potential of mVOCs to attract parasitoids. First, we tested the behavioral and electrophysiological responses of A. colemani females to the volatile blends of a diverse range of bacterial strains. Next, putatively attractive compounds were selected and tested both individually and in mixtures for their effect on the olfactory responses of A. colemani under laboratory conditions. Finally, synthetic mixtures were created to assess their attractiveness under greenhouse conditions. Results showed that A. colemani exhibits a wide variation in its response to bacterial volatiles, ranging from significant attraction over no response to significant deterrence. Our results further showed that bacterial phylogeny largely determines the outcome of mVOC composition and the associated olfactory response. And finally, we found that synthetic mixtures of mVOCs could be developed that were able to attract the parasitoids in greenhouse experiments over a distance of at least 5 meters. Altogether, these findings open new possibilities for attracting and retaining natural enemies of pests, which may lead to improved biological control and consequently more sustainable agricultural practices.

Other authors: Tim Goelena, Francine A.C. Van Neerbosa, and Hans Jacquemynb

Noushin Emami, NRI, University of Greenwich, UK

Natural molecular strategies to break disease transmission

The most evolved pathogen can overwrite the natural program of the host for its advantage. The vector-pathogen sensing and alteration signals that govern pathogen survival and transmission success are an under-investigated area of vector-borne diseases. Recent findings have revealed that there are information networks among pathogens, hosts, and vectors. However, the molecular mechanisms underpinning the pathogen-vector-host communication remain largely unknown, and we are far from understanding the functional complexity and the ecological, and evolutionary consequences of such communication networks. Deciphering the multiple layers of vector-pathogen-host communication can ultimately lead to new approaches for curtailing the spread of such diseases, thereby impacting the lives of billions of people worldwide at risk of contracting vector-borne diseases. My team is uniquely situated to pioneer this new field of pathogen-vector-host communication.





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Gareth Thomas, Protecting Crops and the Environment, Rothamsted Research

Using the odour of bacteria to tackle Acute Oak Decline

Acute Oak Decline (AOD) poses a threat to native oak trees in the United Kingdom. Three bacterial pathogens, Brenneria goodwinii, Rahnella victoriana and Gibbsiella quercinecans, are frequently isolated from necrotic stem lesions characterising AOD, showing necrogenesis to live bark in lesion formation. Larval galleries of the two-spotted oak buprestid beetle, Agrilus biguttatus (Coleoptera: Buprestidae), commonly co-occur with these lesions, indicating beetles may be involved in vectoring AOD bacteria by bringing them to trees, and/or introducing bacteria to live phloem through larval ingress/feeding. Post-emergence, beetles fly to the tree crown, feed on leaves, and mate upon maturation. Gravid (mated) females then oviposit on bark cracks on the outside of the stem. Semiochemical cues from healthy trees show a role for beetles in host location, although changes to the composition of cues following AOD infection are unknown. Our hypotheses are therefore as follows: 1) AOD infection causes changes to Volatile Organic Compound (VOC) production from tree foliage, which attract beetles more so than healthy tree VOCs, and 2) AOD bacteria produce VOCs which attract gravid female beetles to bark lesions, as sites for oviposition.

To test hypothesis I, VOC collections from healthy vs. AOD infected trees were performed and analysed using gas chromatography (GC)/GC-coupled mass spectrometry (GC-MS), showing unique VOC production in infected vs. healthy trees. The role of these VOCs on beetle behaviour, using four arm olfactometer tests, will be discussed. To test hypothesis 2, VOC collections from AOD bacteria were performed and analysed by GC-MS. AOD bacteria produce unique VOC profiles, including two B. goodwinii specific VOCs which elicit strong antennal responses by A. biguttatus in coupled GC-electroantennography (GC-EAG). Four-arm olfactometry using extracts from the bacterial headspace collections showed greater attraction of gravid female beetles to a combination of a synthetic bark blend + headspace extract from mixed colonies of AOD bacteria, compared to the bark blend alone, suggesting bacteria infected bark is more attractive than non-infected bark.

This work will reveal the role of VOCs in the host-pathogen-herbivore ecological system and may clarify the role of A. biguttatus in bacterial transmission. Identified attractant VOCs can aid the development of semiochemicals-based lures to improve the detection and control of A. biguttatus, and the spread of AOD.

Other authors: Dr John Caulfield (Protecting Crops and the Environment, Rothamsted Research), Dr Sandra Denman (Forest Research, Centre for Forestry and Climate Change), and Dr József Vuts (Protecting Crops and the Environment, Rothamsted Research)





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Lucien Dobel-Ober, Liverpool School of Tropical Medicine (LSTM)

Investigating Mosquito Behaviour using novel Gnotobiotic methods

The mosquito microbiome is of great interest to those seeking to design novel vector control methods. Using symbiotic bacteria such as Wolbachia we are already capable of reducing pathogen transmission by exploiting the interactions between with arboviruses in the mosquito vector. While much attention is being paid to the tripartite interactions between pathogens, vectors, and environments, less is known about the ways these interactions affect mosquito behaviour, a component of life history crucial in assessing vector capacity. The role that behaviour plays in vector biology is often difficult to interrogate, and must account for diverse complex interactions between insect, bacteria, and environments. The role that mosquito behaviour plays in human and animal disease systems is often overlooked, and there exist many ways in which an improved understanding could lead to new ways to protect communities.

Gnotobiotic methods represent a fresh way to investigate these interactions, by allowing us to control the contents of the mosquito microbiome, and observe the effects of infection with a pre-selected community of microbes. I will present my work on exploring this field, with a particular focus on mosquito reproductive behaviour. I aim to explain and explore how I intend to apply new gnotobiotic methods as a unique new way to interrogate the effect of the microbiome on adult Aedes aegypti mosquitoes, outlining my initial work on combining gnotobiotic and behavioural research methods, and how these methods could represent an important step forward in understanding mosquito behaviour.

Other authors: Grant Hughes, Phillip McCall, Luca Facchinelli (all LSTM)

Durlave Roy, Masters Student, Bangladesh, Open University

Studies on the use of Plant extracts - importance in sustainable agriculture

Different field study was conducted to evaluate the neem products work by intervening at several stages of the insect's life. The action of neem products fulfills all priorities among environmental objectives. This unique tree is perhaps the most significant example of how nature can combine diverse functions i.e., the action of de-oiled neem cake as a pesticide . neem cake @ 200kg/acre to the fields when maize is grown with zero tillage. Deep plowing before every crop season to open up the soil to expose FAW pupae to sunlight and predators.Recently, plant protection strategy has recommended, minimizing the use of chemical pesticides. Therefore, studying the side effect of insecticides on the natural enemies is highly required to exclude the detrimental effects on the natural enemies. Every crop is infested by various pests; some but not all of





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them may be controlled by biological means using pathogens, predators, parasitoids and spiders. But to achieve a satisfactory control of complexes of pests, selective pesticides are also indispensable. In fact, they are a prerequisite of Integrated Pest Management.

Daniel Leybourne, The University of Liverpool, UK

Can endosymbionts influence the development, fitness, and behaviour of cereal aphids?

Aphids can form facultative (non-essential) relationships with a diverse range of endosymbiotic bacteria. Some of these endosymbionts confer beneficial phenotypes to the aphid host, with a key example being protection against parasitism, a trait that is often associated with the endo-symbiont Hamiltonella defensa. However, despite the clear ecological and evolutionary benefit of this protective phenotype, the frequency of endosymbiont infection in aphid populations is highly variable, indicating that a fitness cost might be associated with harbouring endosymbionts.

Cereal aphids are an important group of herbivorous insects. Cereal aphids can cause significant damage to cereal crops through feeding and the transmission of plant viruses, including barley yellow dwarf virus. As observed in other aphid species, the frequency of endosymbionts in cereal aphids is highly variable. In order to determine how endosymbiont prevalence might influence the agricultural importance of cereal aphids, it is important to identify fitness benefits or costs associated with endosymbiont presence in cereal aphids. Including any influence endosymbionts have on aphid behaviour, fitness, or interactions with aphid-vectored viruses. Here, three important cereal aphid species were sampled and lab populations were established. In total, eight bird cherry-oat aphid (Rhopalosiphum padi), 25 grain aphid (Sitobion avenae), and four rose-grain aphid (Metapolophium dirhodum) populations were established in the lab and the endosymbiont profile of each population was characterised. For R. padi and S. avenae, each population was also genotyped using a sequencing approach, providing an additional level of intra-species characterisation.

In the R. padi populations only two endosymbionts were detected, H. defensa and Fukatsia symbiotica; for S. avenae endosymbiotic relationships with Regiella. insecticola, F. symbiotica, and H. defensa were detected, including an R. insecticola + F. symbiotica co-infection; for M. dirhodum R. insecticola was detected, alongside a R. insecticola + H. defensa co-infection. Endosymbiont prevalence was variable between the aphid species. All M. dirhodum populations harboured at least one endosymbiont. For S. avenae, 92% of aphid populations harboured at least one endosymbiont, with R. insecticola the most prevalent endosymbiont (present in 72% of the aphids). For R. padi, 28% of the populations harboured H. defensa and 28% of the populations were infected with F. symbiotica.

A range of lab experiments were conducted to determine whether these endosymbionts influence aphid phenotype, with a focus on phenotypes of agricultural importance, including susceptibility to insecticides, aphid development time, aphid reproductive success, and virus transmission efficiency. Findings indicate that natural endosymbiont infection does not influence aphid





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susceptibility to insecticides in any of the cereal aphid species examined. However, initial analysis indicates that endosymbionts can alter aphid fitness, including a modulation of nymph development time in R. padi populations that form associations with F. symbiotica. Current research is focussed on further examining the behavioural and wider ecological impacts endosymbiont infection has on aphid behaviour, including interactions with important plant viruses.

Brendan Daisley, University of Guelph, Canada

Design and application of a novel spray-based probiotic formula for sustainable microbiome management in honey bees

Managed honey bee (Apis mellifera) populations play a crucial role in supporting adequate pollination of food crops but are facing unsustainable colony loss as the result of rampant disease spread within agricultural environments. Antibiotics have failed to resolve the issue so far, whereas mounting evidence from in vitro experiments suggest that select lactobacilli strains (some of which are symbionts in honey bees) can inhibit a broad range of important pathogens via multifaceted mechanisms. Importantly, there has been very little validation at the field-level potentially due to the fact that delivery methods for applying viable lactobacilli to the hive are lacking. Here, we compare how different delivery systems (standard pollen patty and a novel spray-based formula) influence the efficacy of a three-strain lactobacilli consortium (LX3) in reducing overall bacterial and fungal disease burden within a pathogen-dense region of California post-almond harvest. Hives were supplemented for 4-weeks, followed by a 20-week monitoring period. Results reveal long-lasting beneficial effects of LX3 in delivery-dependent and -independent manners. The most striking finding was that spray-based LX3 supplementation led to >100-fold reduction in Ascosphaera apis (deadly fungal agent of Chalkbrood disease), whereas patty-based LX3 showed unique nutritional benefits. In addition, spray-based LX3 was also highly active against many well-known opportunistic plant pathogens in the hive suggesting this method may be especially useful for reducing honey bee vectoring of plant diseases. The collective scope of this work is expansive and broadly relevant to microbial disease management in terrestrial ecosystems.

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Kelly A. Hamby, Department of Entomology, University of Maryland College Park

Behavioral responses of spotted-wing drosophila to free-living fungi

Although spotted-wing drosophila (Drosophila suzukii) attack ripe, unspoiled fruit, their interactions with free-living fungi are consistent with other Drosophila species that rely upon microbe rich fermenting substrates. Adults and larvae feed on and are attracted to yeasts, which are critical for larval survival. Both life stages can discriminate between and exhibit preferences for specific yeasts. Beyond yeasts, D. suzukii encounters and feeds on other free-living fungi that occur within their habitat, such as fruit rot fungi. Drosophila suzukii carries an inconsistent fungal community on the exterior of their body with higher richness, frequency of detection, and propagule density than their interior community. This community includes fruit rot causal agents which primarily are found on their exteriors. Cladosporium occurs most frequently and was detected on the exterior of 35 out of 71 adults sampled across two sites and three years. They may also be able to vector fungi. In a worst-case scenario Petri dish laboratory vectoring assay, adult flies could transfer Botrytis cinerea and Cladosporium cladosporioides to sterile media 0, 24, 48, and 72 hours after exposure to densely sporulating cultures. D. suzukii and free-living fungi reciprocally impact each other's life histories, with D. suzukii exhibiting a range of behavioral responses from attraction to repulsion.

Other authors: Margaret T. Lewis

Rudra Gouda, Indian Agricultural Research Institute, Pusa Campus, New Delhi

Physiological functioning of gut bacteria characterized in forager and hive bee of Apis mellifera

Apis mellifera, a superorganism with a high degree of sociality has been recognized as a prominent bee product producer in apiculture. In this study, the differential role of gut microbes in forager and hive bee is recorded. Initially generic characterization is carried out by 16S ribosomal RNA probes and metagenomics analysis by next generation sequencing on Illumina MiSeq platform. In the present study 51 aerobic gut bacteria species in forager bee gut region and 32 species in hive bee gut region were recorded. The bacterial isolates from forager bee belonged to three Phyla out of which 59 % of isolates belong to Firmicutes (Aneurinibacillus, Bacillus, Clostridium, Lysinibacillus, Paenibacillus), 37 % of them to Proteobacteria (Cedecea, Enterobacter, Klebsiella, Ochrobactrum, Pantoea, Salmonella, Serratia, Stenotrophomonas, Xanthomonas). Whereas, in the hive bees the Firmicutes (Bacillus, Clostridium, Enterococcus, Lactobacillus, Lysinibacillus) accounting for majority of the isolates (65 %) followed by Proteobacteria including Enterobacter, Klebsiella, Pseudomonas, Serratia constituted 26 % of the isolates and Actinobacteria (Microbacterium, Streptomyces) accounted for the rest. Two species of Lactobacillus have also been identified from the foregut of hive bees of A. mellifera. Over all, greater bacterial diversity was observed in forager bees than hive bees.





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Metagenomics analysis revealed that a complex community of bacteria, comprising Proteobacteria, Firmicutes, Actinobacteria, Bacteriodetes, and Cyanobacteria are associated with the hive bees. Burkholderiales, Enterobacteriales, Pseudomonadales, Lactobacilliales, Neisseriales, Bifidiobacteriales, Rhizobiales Rhodospirillales, and Pasteurellales are the major bacterial orders common to both stages. Streptophyta, Xanthomonadales, and Caulobacterales are unique to hive bees, while Flavobacterales are unique to foragers.

Further, the physiological functioning of gut bacteria was biochemically characterized, where a total of 22 and 11 isolates from forager and hive bees, respectively, possessed cellulolytic ability with a specific activity of cellulase ranging between 0.388 U/mg and 1.493 U/mg in forager bees and 0.47 U/mg and 1.38 U/mg in hive bees. Isolates like Bacillus altitudinis HAmf05 (MW742339), Enterobacter asburiae- HAmf25 (MW742357), and Serratia entomophila HAmf37 (MW742369) showed high cellulolytic activity. Some of the gut bacterial isolates, like Bacillus altitudinis HAmf05 (MW742339), Serratia entomophila HAmf37 (MW742369), and Bacillus mojavensis HAmh03 (MW742379), were found to show significantly higher hemicellulase activities, with the specific activities of the enzyme being in the range of 0.541–3.119 U/mg. All 81 gut bacterial isolates from A. mellifera showed lipolytic activity in the range of 0.166 U/mg to 2.509 U/mg. The pectinolytic activity of the gut bacterial isolates was estimated to be in the range of 0.012 U/mg to 3.693 U/mg in foragers and hive bees, with isolates like Bacillus altitudinis HAmf05 (MW742339), Serratia ureilytica HAmf42 (MW742374), and Bacillus paranthracis HAmh06 (MW742382) showing high pectinase activity. Fifty-one gut bacterial isolates showed invertase activity (0.010 U/mg to 6.062 U/mg), with Bacillus subtilis subsp. stercoris HAmf13 (MW742347), Lysinibacillus macroides HAmh16 (MW742391), and Pseudomonas aeruginosa HAmh21 (MW742396) being the isolates showing high invertase activity. These gut bacterial isolates may probably aid in the digestion of pollen and the processing of nectar in A. mellifera bees. The fundamental understanding of bacterial diversity and function serves as the foundation for developing methods for increasing the abundance of gut microbial diversity and improving A. mellifera longevity. Thus, improving the productivity of bees for the sake of mankind.

Fardiina Rahimi, School of Biological Sciences and Institute of Life Sciences, University of Southampton, NIAB East Malling

Genetic basis interspecies impacting the horticultural pest Drosophila Suzukii

Drosophila suzukii (Matsumura) or Spotted Wing Drosophila (SWD) is a fruit fly species native to Southeast Asia, that acts as an invasive pest in other parts of the world. SWD integrated pest management research has focused on finding biological controls against infestation of soft and stone fruit cultures. In this study we examined the deterrence of SWD egg laying by pre-exposure of egg laying substrates to the sister species Drosophila melanogaster, first noted by Shaw et al., (2017) and further characterized by Tsungadi et al., (2022). Experiments using D. melanogaster cultures raised in the presence of antibiotics or following dechorionation at the embryonic stage demonstrated that this interspecies deterrent signal was elicited by the bacterial microbiome of





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D. melanogaster. Notably, we identified an alternative lab D. melanogaster culture that possessed a bacterial microbiome that attracted rather than repelled subsequent SWD oviposition. Genetic crosses indicated that both the microbiome and the D. melanogaster genotype played a role in determining the valence of the interspecies signal. We will present metagenomics sequencing analyses of repellent and attractive D. melanogaster microbiomes and explain how this information may inform integrated pest management of SWD.

Other authors: Bethan Shaw, Michelle Fountain and Herman Wijnen

Ana Laura Nussenbaum, Institue of Agriculture, Argentina - National Council of Science) Argentina

Studies on symbiont microorganisms of Anastrepha fraterculus (Diptera: Tephritidae) and their use in sustainable pest management strategies

Insects establish symbiotic relationships with bacteria inhabiting their digestive tract. In this association bacteria contribute with metabolites that enable the insect host to utilize nutrient-poor or unbalanced diets and perform degradation of natural or chemical toxins, among other benefits. Anastrepha fraterculus is one of the most important fruit fly pests in South America. Understanding the role of bacteria on insect nutrition and metabolism as well as evaluating the use of gut bacteria as probiotics became an emerging field of research, particularly due to its potential use within the sterile insect technique (SIT).

In this work we aimed at assessing the role of gut bacteria on A. fraterculus behavior and physiology, with the aim to select bacterial isolates with a probiotic function. We first studied the effect of removing gut bacterial with antibiotics (ABs) on the nutritional status and reproductive parameters of A. fraterculus males and females. ABs affect the bacterial community of the digestive tract, particularly Enterobacteria. In males, behavioural parameters like mating success, pheromone production, and calling behaviour, as well as protein reserves and survival were negatively affected by ABs. In females, the removal of culturable Enterobacteria from the gut of females was associated to a reduction in fecundity and protein and lipid reserves.

With the aim to evaluate the potential of bacteria as probiotics in the mass rearing of A. fraterculus, we isolated male gut bacteria from wild and laboratory flies. We cultured and identified 180 isolates, principally Enterobacteriacea family. Among these, 23 isolated were potentially diazotrophic and considered as the most promising candidates for probiotic tests. Initial assessment of some of these strains included feeding experiments where bacteria were added to the adult diet. Members from Enterobacter, Klebsiella and Pantoea genera were tested separately. Males were tested in terms of nutritional reserves (total protein content) and sexual pheromone calling behaviour. Results showed that for the 3 isolates, viable bacteria seem to be detrimental (in comparison with unviable, autoclaved bacteria used as control). Not all bacteria affected insects





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in the same way, and Enterobacter and Pantoea showed higher protein contain than Klebsiella. However, the treatment that induced the highest protein content was not higher than the control. The Enterobacter isolate was then tested in terms of male pheromone calling behaviour. In this case, male flies were fed continuously from emergence to day 10 and on day 11 the courtship behavior of the males was measured four times. We found no effects of diet treatments on male calling index.

In sum, Enterobacteria reduction correlates with negative effects on reproductive traits and nutritional reserves in A. fraterculus males and females. Isolates obtained from male guts are possible diazotrophic bacteria, which could constitute a source of nitrogen for the insect. Attempts to positively affect flies' fitness adding some of these isolated to the flies' food were unsuccessful.

Other authors: 1Salgueiro, Julieta, 2Goane, Lucía, 1Belliard, Silvina Anahí, 2Vera, María Teresa, 3Marchesini, María Ines, 1Lanzavecchia, Silvia Beatriz, 1Segura, Diego Fernando

Boaz Yuval, Hebrew University, Israel

The microbiome and fruit fly behaviour

Multicellular organisms maintain intimate relationships with diverse communities of micro-organisms. These interactions have been studied in depth in many insect species, revealing significant and intricate effects of the microbiome on its host. Most famous are nutritional effects, whereby a primary symbiont provides the host with vital nutrients, such as amino acids or vitamins. In addition, we are aware of systems where the symbionts affect host reproduction, immune response, niche breadth, and environmental resilience.

In my talk, focusing on tephritid fruit flies, I will examine the effects of gut symbionts on host behavior. Specifically, I will show how the microbiome affects foraging behavior in larval medflies, oviposition behavior in olive fly females, and copulatory success in medflies.



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Posters:

Sandra Cortes, Rothamsted Research

Aphid infestation changes metabolic activity and composition of bacterial communities in the wheat rhizosphere

Plant-microbe interactions are fundamental to plant defence against herbivores, which cause significant losses in food production worldwide. This project aimed to study the effect of aphid feeding on wheat plants and in the bacterial communities in the wheat rhizosphere.

We designed a microcosm experiment consisting of two treatments (with and without aphid infestation). Rhizosphere samples were taken (i) before infestation, (ii) two weeks post-infestation and (iii) four weeks post-infestation. We analysed bacterial community profiles at taxonomical (16S rRNA gene sequencing) and physiological levels (Ecoplates, Biolog). Moreover, aboveground volatiles and root exudates were collected to characterise their chemical composition. After two weeks of infestation, bacterial diversity was reduced in the rhizosphere of aphid-infested plants in comparison with the non-infested, but a higher abundance of Actinobacteria and Firmicutes was observed. The physiological profiling showed an increase in microbial metabolic activity in the rhizosphere of aphid-infested plants, particularly in response to D-Xylose, N-acetyl D-glucosamine, and some amino acids (p < 0.05).

We detected aboveground volatiles involved in herbivory response (e.g., limonene, α -cubebene, β -Ocimene) in aphid-infested plants. The effects of aphid infestation in both metabolic activity and bacterial communities after four weeks of infestation were less strong than in week two, suggesting a time-dependent effect of aphid feeding. Results from root exudate analysis will provide more information about the chemicals that play a crucial role in plant-microbe interactions under aphid feeding.

Other authors: Adriana Torres-Ballesteros (Rothamsted Research); Vanessa Nessner-Kavamura (Rothamsted Research); Amanda Rasmussen (The University of Nottingham); John Caulfield (Rothamsted Research)

Biplove Bala, Department of Entomology, School of Agricultural Sciences & Rural Development (SASRD), Nagaland University (NU), Medziphema-797106, Nagaland, India

MICROBES COULD PLAY AN IMPORTANT ROLE IN INSECT BEHAVIOUR

Microbes are critical components of insect biology that can significantly impact insect behavior. The microbiome, which includes bacteria, viruses, fungi, and other microorganisms, coevolves



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with insects and can shape a wide range of behaviors, including feeding, reproduction, hostfinding, and social behavior.

Microbes can influence insect behavior through direct signals, such as the production of hormones or other signaling molecules, or by altering gene expression patterns in their hosts. In some cases, microbes have been shown to have a profound impact on insect behavior, leading to the evolution of novel strategies for survival and reproduction. For example, gut microbes can alter insect feeding behavior by affecting the metabolism of food and the regulation of hunger and satiety. Certain gut bacteria can also stimulate the growth and development of their hosts, while others can influence reproductive success by regulating the production of hormones involved in mating and oviposition. In social insects, such as ants, bees, and termites, microbes can also play a role in shaping complex social structures and behaviors, including the regulation of colony size, division of labor, and host-pathogen interactions.

The study of the role of microbes in insect behavior has significant implications for both basic and applied science. Understanding the relationship between insects and their associated microbes can provide new insights into the evolution of insect behavior and the mechanisms underlying the formation of symbiotic relationships. Furthermore, the manipulation of insect-microbe interactions has the potential to provide new strategies for controlling insect-borne diseases and pests, including the development of new biopesticides and the use of probiotics to enhance insect health and productivity.

In conclusion, the study of the relationship between microbes and insects is an exciting and rapidly developing field that holds great promise for advancing our understanding of both insect biology and the role of microbes in shaping behavior and ecology.

Tchoudjin Gertrude Loveline, University of Yaounde

Effect of habitat on diversity and composition of leaf litter ant species: implications for conservation management.

The future of tropical rain forests has never been more uncertain, as many of these forests are being rapidly destroyed and degraded through various forms of human impact, such as infrastructure development, agricultural expansion, and timber extraction.

Ant species were sampled at five habitat types to determine the effect of land-use on their diversity and composition. Four methods were used to sample ant specimens bi-monthly from November 2018 to June 2020. A total of 306 ant species, belonging to 57 genera and 11 subfamilies were recorded. Shannon-Wiener's index indicated that the highest diversity occurred in the forest habitat 209 (H'= 4.4). Significant differences (P<0.05) were observed between the banana farm and old cocoa farm, forest and young cocoa farm but not between the banana farm and palm grove; suggesting that ant diversity varied distinctly with land. Forty-nine ant species (16.01%)





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were common to all five habitats while 19, 12, 8, 4 and 10 species were restricted to the Forest, Banana farm, Old cocoa farm, Young cocoa farm and Palm grove habitats respectively, and showed sensitivity to environmental gradients. These attributes make them potentially useful as subjects or tools for assessing the conservation value of habitats studied. Habitat patch level management for conservation action in the study area should aim at preserving sufficient vegetation that varies in diversity, physiognomy and complexity, as well as a herbaceous layer that encourages the accumulation of leaf litter at habitat sites.

Since the forest habitat in this study may not be well insulated from anthropogenic pressures to guarantee the survival and establishment of resident species without intensive management, ant richness within the forest habitat can be encouraged by using vegetation linkages and corridors between the forest and its surrounding agrarian-transformed landscapes as a matrix.

Key words: ants, species, diversity, land use, habitats, anthropogenic disturbances

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View the Behaviour SIG 23 posters here:



https://www.royensoc.co.uk/behaviour-sig-2023-posters/