12 AU 14 MAI 2025

LYON

BOOKLET

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Réseau Ecologie des Interactions Durables

&

IMMUNINV

Amphithéatre Laura Bassi

INSA INSTITUT NATIONAL DES SCIENCES APPLIQUÉES LYON

CAMPUS DE LA DOUA
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Programme et informations

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Monday 12th May 2025

12:30	*Accueil*		
13:00	**Conference opening**		
13:15	**Keynote speaker: Silvia De Monte**		Single-cell phenotypes structure the social life of the amoeba *Dictyostelium discoideum*
14:15		**"Sex and CI" session (1/2)**	
	14:15	Jean PECCOUD	A virus feminizes carriers in a pill bug
	14:35	Théo UlvÉ	Coexistence of three sex determinants in a population of the pill bug *Armadillidium arcangelii*
	14:55	Nicolas RODE	Male host genetic background strongly impacts *Wolbachia*-induced cytoplasmic incompatibility in an invasive pest
15:15	**BREAK**		
16:00		**"Sex and CI" session (2/2)**	
	16:00	Julien AMOROS	Evolution of cytoplasmic incompatibility genes among maternally inherited symbionts: *Wolbachia* do not walk alone
	16:20	Richard CORDAUX	Sex ratio distorters and the evolution of sex determination in the isopod *Armadillidium vulgare*
	16:40	Alice NAMIAS	Perte de fonction répétée des protéines de type sexuel chez les champignons *Microbotryum*
17:00	***end of the 1st day***		

Tuesday 13th May 2025

09:00		**"Genome evolution" Session**	
	09:20	Maxime MAHOUT	*Wolbachia* metapangenomics of individual *Culex* mosquitoes reveal shared phage rearrangements across large geographic distances
	09:40	Thibault JOSSE	Discovery of endogenous viral elements in *Campopleginae* wasps suggest widespread nudivirus domestication
	10:00	Jesus MENDEZ LEYVA	Distinct host-endosymbiont co-evolutionary trajectories in cereal weevils
	10:20	Jonathan FILÉE	Genome evolution and between-host transmission of *Spiroplasma* endosymbiont in wild communities of Morpho butterflies
10:45	**BREAK**		
11:15		**"Extended phenotype" Session**	
	11:15	Antoine GUIGUET	Rôle du venin dans l'induction des galles de Cynipidés : une approche omique comparative
	11:35	Justine BOUTRY	First evidence for the evolution of host manipulation by tumors during the long-term vertical transmission of tumor cells in *Hydra oligactis*
11:55		**Presentation of SYMBIOTRON**	
12:15	**LUNCH offered by REID**		
13:15	**POSTER Session**		

14:15		**"One health" session (1/2)**	
	14:15	Axelle GENTIL	Spatiotemporal dynamics of breeding site composition: which impact on the asian tiger mosquito biology and behaviour ?
	14:35	Raphaël JORGE	Functional analyses of interactions between bedbugs and their symbionts *Wolbachia* and *BEV-like*
	14:55	Pierre ANTONELLI	Microbiota influence on mosquito larvae mediate glyphosate toxicity
	15:15	Louise CHEYNEL	Effet de la pollution lumineuse sur l'immunité d'un vertébré nocturne, le crapaud commun.
15:35	**BREAK**		
16:05		**"One health" session (2/2)**	
	16:05	Claire LOISEAU	Effects of microplastics on mosquito development and avian malaria transmission
	16:25	Valentin CHAUVIN	Adaptive Phenotypic Plasticity of *Plasmodium* in Response to Environmental Cues
	16:45	Mélody LEBRUN	Impact des vagues de chaleur sur la Maladie de l'Anneau Brun induite par *Vibrio tapetis* chez la palourde *Ruditapes philippinarum*
	17:05	Justine BOUTRY	Heatwave on 'Off-Host' Parasite Stages: Reduced Infection Risks and Costs in *Pasteuria ramosa*–Daphnia magna system
19:00	**"Conférence Grand public" (Lyon 7ème)** **Fabrice Vavre**		"Je suis un écosystème dans l'écosystème : la santé unique à tous les étages"
20:00	**Lets meet at "La Commune"**		3 rue Pré-Gaudry Lyon 7ème https://lacommune.co/

Wednesday 14th May 2025

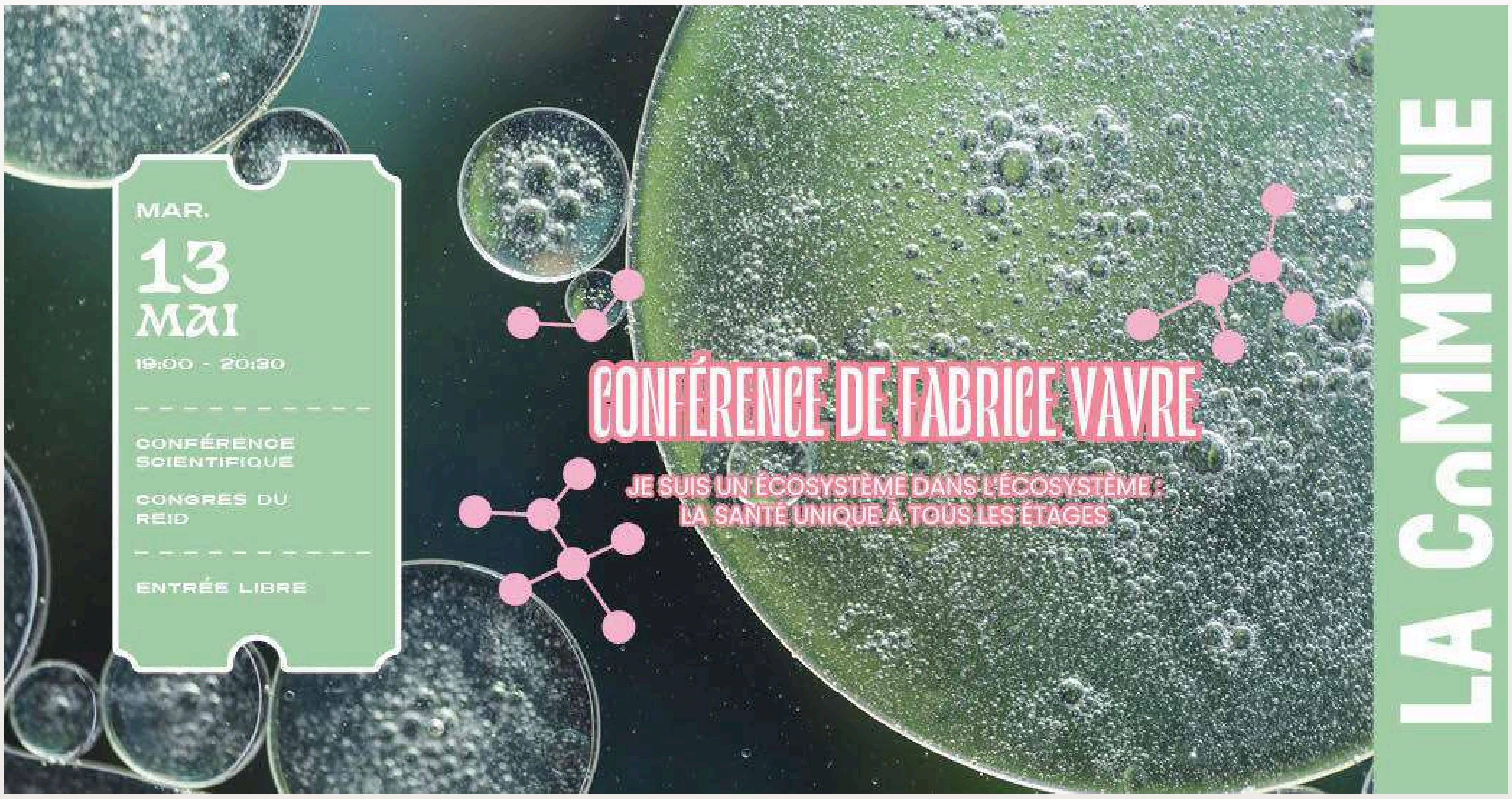
09:00	**Keynote speaker:** **Jens Rolff**		Why did complete metamorphosis of insects evolve?
10:00		**"Microbiome" session**	
	10:00	Joël MEUNIER	Microbiome turnover during offspring development varies with maternal care, but not moult, in a hemimetabolous insect
	10:20	Fanni BORVETÕ	Impact of the Varroa Mite on the Microbiota of *Apis mellifera* and *Bombus terrestris*
10:40	**BREAK**		
11:10		**"Coévolution" session**	
	11:10	Jean-Michel DREZEN	Evolution of bracoviruses, insights from the genome of Toxoneuron nigriceps a parasitoid wasp from Cardiochilinae
	11:30	Églantine MATHIEU-BÉGNÉ	If the door is locked, take another one: Evolution of alternative entrance points for a parasite
	12:10	Giacomo ZILIO	Bridging multiple infections across scales: from co-circulation to co-infection
12:30	***End of REID & conclusion***		
12:40	**LUNCH offered by REID**		

13:40		**"Immuno-ecology" session**	
	13:40	Alexandre GOERLINGER	Inefficiency of immune priming via the oral route and prevalence of injuries in *Tenebrio molitor* reinforce the hypothesis of a wound-driven evolution in adult beetles
	14:00	Louis PAILLER	Reproduction-immunity trade-off in females of the European earwig
	14:20	Simon DE WEVER	Immune cost of maternal care towards eggs and juveniles in the European earwig
	14:40	Vincent DOUBLET	Drivers of sex differences in insect immunity
15:00	**BREAK**		
15:30		**"Effectors of immunity" session**	
	15:30	Auréline LALOUETTE	Investigating the IMD pathway in the bedbug *Cimex lectularius* and its function in the control of infections and mutualistic symbioses
	15:50	Céline ZATYLNY-GAUDIN	Identification of new antimicrobial peptides in *Armadillidium vulgare* using PepTraq
	16:10	Mélanie BRETTON	Immune regulation of the bacterial microbiota of the tiger mosquito in response to interference with de novo production of aromatic amino acids
	16:30	Sarah DAMETTO	Deciphering the molecular dialogue between the trematode parasite *Schistosoma mansoni* and its intermediate host snail *Biomphalaria glabrata*
16:50	***End of IMMUNINV & conclusion***		
17:00	***Closure of the conference***		

POSTER session - Tuesday 13th May 2025 13:15-14:15

1	Amandine AVILES	Impacts of Microplastics on Mosquito Life History Traits and midgut microbiota
2	Christine BRAQUART-VARNIER	Chronic exposure of Cadmium leads to deleterious effects on *Armadillidium vulgare* immune cell's mitochondria
3	Alice BRUNNER	Distinct Dynamics of *Wolbachia* and its pWCP Plasmid During *Culex* Mosquito Development
4	Camille-Sophie COZZAROLO	Size- and sex-biased gene expression in the acanthocephalan parasite *Neoechinorhynchus agilis*
5	Yann DUSSERT	Dumpster diving into sequencing data to uncover unknown microorganisms involved in symbiotic relationships in marine species
6	Bernard DUVIC	Transcriptional response against biocontrol agents in the agricultural pest *Spodoptera frugiperda* (Lepidoptera: Noctuidae)
7	Noor FATTAR	Multi-scale evolutionary convergence of nutritional symbionts in ticks
8	Pierre GREVE	Identification and expression of potential feminizing factors in the three *Wolbachia* strains infecting *Armadillidium vulgare*.
9	Henri Séraphin ESSOMBA	Diversité et dendrologie des cacaoyers d'une agroforêt en zone de forêt dense et humide de l'Est-Cameroun
10	Jordy LARGES	Variation in the duration of the immune protection after priming stimulation among populations of *Tenebrio molitor*
11	Marie PANZA	Invasion-driven changes in Drosophila and their parasitoid communities along a latitudinal gradient in the Rhône valley
12	Romain PIGEAULT	Within-host tissular heterogeneity is associated with phenotypic but not genomic diversity in *Wolbachia* endosymbionts
13	Philippe REMIGI	Plant-mediated selection of nitrogen-fixing symbiotic bacteria
14	Diego SANTOS GARCIA	Symbiotic communities of Planococcus ficus (vine mealybug)
15	Charlotte TANNEAU	Symbiotic control as an alternative of insecticides used to control bedbugs (*Cimex lectularius*) based on a One Health approach

Session Grand Public



Je suis un écosystème dans l'écosystème : la santé unique à tous les étages

Nous ne vivons pas isolés. Entre conflit et coopération, la très grande majorité des organismes, humain compris, interagissent d'abord avec l'ensemble des microorganismes qui constituent leur microbiote. Ces interactions avec notre 'moi microscopique' construisent les individus comme des écosystèmes et nous interrogent sur notre propre individualité.
Mais cet individu écosystème est aussi la cible et l'acteur d'un environnement plus large avec lequel il interagit et qui interroge ses interdépendances et son rapport au monde.
Mais au bout du compte, qui suis-nous, qui-sommes-je ?

Attention, le nombre de places étant limité (et ouvert à l'extérieur (c'est le principe d'une conférence grand public), pensez à vous inscrire ici si vous souhaitez assister à la conférence.

3 rue Pré-Gaudry Lyon 7
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Jean Macé → LA COMMUNE → 10 min
Je viens en tcl !

Je suis un écosystème dans l'écosystème : la santé unique à tous les étages

Fabrice Vavre*[1]

[1]Laboratoire de Biométrie et Biologie Evolutive - UMR 5558 – Université Claude Bernard Lyon 1, VetAgro Sup - Institut national d'enseignement supérieur et de recherche en alimentation, santé animale, sciences agronomiques et de l'environnement, Centre National de la Recherche Scientifique – France

Résumé

Nous ne vivons pas isolés. Entre conflit et coopération, la très grande majorité des organismes, humain compris, interagissent d'abord avec l'ensemble des microorganismes qui constituent leur microbiote. Ces interactions avec notre 'moi microscopique' construisent les individus comme des écosystèmes et nous interrogent sur notre propre individualité.
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Mais au bout du compte, qui suis-nous, qui-sommes-je ?

Mots-Clés: Individu, microbiote, écosystème, environnement, santé unique

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*Intervenant

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Keynote Speakers

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Single-cell phenotypes structure the social life of the amoeba Dictyostelium discoideum

Silvia De Monte*[1]

[1]Institut de biologie de l'ENS Paris – Département de Biologie - ENS-PSL, Institut National de la Santé et de la Recherche Médicale, Centre National de la Recherche Scientifique – France

Résumé

The 'social' amoeba *Dictiostelium discoideum* is a facultatively multicellular organism. Starvation triggers a life cycle where single cells come together to form multicellular fruiting bodies, essential for efficient dispersal and long-term survival. In this process, part of the cells dies while promoting the survival of the spores. The evolution of self-sacrificial behaviour is more easily understood when all cells in the body share the same genome. It is therefore puzzling to observe that in natural conditions multicellular aggregates tend to be genetic chimeras, so that genetic conflicts are unavoidable. Theory predicts that the spread of genotypes that reap more than their fair share of benefits from the group – the so-called cheaters – should prevent cooperative behaviour to be evolutionary stable. We compared the social performance in chimeras composed of isogenic cells harvested at different phases of population growth, and found that social behavior is modulated by phenotipic plasticity as well as genetic background. By tracing the origin of spore biases to the process of aggregation from single cells, we explored the single-cell determinants of differences in social behaviour. Finally, we show that biases due to non-genetic sources of phenotypic variation are comparable to genetic effects, and can dominate over genetic differences, overturning classical definitions of social behaviour. Our observations suggest that inevitable heterogeneity in cell-level physical properties may act – by breaking heritability of social behaviour – as a hindrance to the evolutionary success of cheaters, and this even when social interactions within the multicellular body are neglected. We use mathematical models for heterogenous aggregating agents to explore the possible role of mechanical differences in the evolutionary maintenance and emergence of aggregative multicellular life cycles.

Mots-Clés: Social behavior, aggregation, conflict, Dictyostelium discoideum

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*Intervenant

Why did complete metamorphosis of insects evolve

Jens Rolff*[1]

[1]Freie University Berlin (FU-Berlin) – Königin-Luise-Strasse 1-3 14195 Berlin, Allemagne

Résumé

Today, the vast majority of extant animal species are holometabolous insects. These organisms have three life-stages: larva, pupa, adult. During the pupal phase, the larva undergoes an extreme form of metamorphosis, during which the body is radically reorganized. When the adult emerges, it is morphologically, anatomically and ecologically different from the larva. Little is known about why it is adaptive to rebuild the body.
Here, I will discuss three mutually non-exclusive hypotheses to explain the evolutionary advantages of complete metamorphosis in insects: (1) A pupa permits the decoupling of growth and differentiation enabling fast growth. (2) A decoupling of life stages permits the exploitation of different niches. And (3) the decoupling of larval and adult microbiota, which is facilitated by the renewal of the gut during pupation.

Mots-Clés: complete metamorphosis, fast growth, microbiota, immune genes

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*Intervenant

Abstract

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If the door is locked, take another one: Evolution of alternative entrance points for a parasite

Eglantine Mathieu-Bégné * [1], Sabrina Gattis [2], Dieter Ebert [3]

[1] Department of Environmental Sciences, Zoology, University of Basel – Vesalgasse 1, 4051, Basel, Switzerland
[2] School of Zoology, George S. Wise Faculty of Life Sciences – Tel Aviv University, Tel Aviv, Israel
[3] Department of Environmental Sciences, Zoology, University of Basel – Switzerland

The acquisition of alternative routes of infection by parasites is a way to circumvent host resistance. This strategy only makes sense if host resistance to alternative routes is based on distinct loci. We investigated this hypothesis by examining whether the alternative infection routes of the parasite *Pasteuria ramosa* in its crustacean host, *Daphnia magna*, are associated with different resistance loci. We examined the genomic basis of host resistance to a strain of *P. ramosa*, P15, capable of attaching to and penetrating the host either from the hindgut or the foregut. We used a worldwide panel of 174 *D. magna* genotypes, further refined through breeding experiments. Our findings support our hypothesis: hindgut attachment is determined by the D locus, whereas foregut attachment is governed by a newly identified locus, named the G locus. We established a gene model for the G locus, which predicts Mendelian segregation and epistatic interaction with at least one other *P. ramosa* resistance locus. Through genomic Pool-sequencing data analysis, we localized the G locus within a known *Pasteuria Resistance* gene cluster on chromosome 4, whereas the D locus is located on chromosome 7. Two candidate genes for the G locus, both belonging to the Galactosyltransferase gene family, were identified. Our study sheds new light on how hosts and parasites coevolve and enhances our understanding of how parasites evolve infection strategies.

Keywords: Coevolution, Mendelian locus, Fine mapping, Epistatic interactions, Infection strategies

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*Speaker

Adaptive Phenotypic Plasticity of Plasmodium in Response to Environmental Cues

Valentin Chauvin * [1], Ana Rivero *

2

[1] Evolution of host-microbe communities – CNRS-IRD-Université de Montpellier – France
[2] Evolution of host-microbe communities – CNRS – France

Phenotypic plasticity allows organisms to adapt their traits in response to environmental changes. Plasmodium parasites, which cause malaria, have been shown to adjust their morphology, growth rates, and virulence depending on factors such as host immune responses and ressource availability. This plasticity enables them to adapt to diverse host environments, evade host defenses, and enhance their survival and transmission. The aim of my research is to determine what are the environmental factors that trigger an adaptive change in a phenotypic trait in Plasmodium.

In the vertebrate host, the parasite may be broadly found in three different stages: 1) actively replicating but non-transmissible asexual blood stages, 2) Non-replicating, but transmissible sexual blood stages (gametocytes) and 3) exoerythrocytic stages found in deep tissues, which play a crucial role as reservoirs of infection and which may (or not) be in a state of dormancy. Gametocytes are the only blood stages of the parasite that can be transmitted to mosquitoes.

Using avian malaria (*P. relictum*, lineage pSGS1) as a model, we first investigate the phenotypic plasticity of three key life-history traits of Plasmodium within the vertebrate host: blood asexual parasitaemia, the conversion rate from asexual stages to sexual gametocytes, and the sex allocation of these gametocytes (male or female). We investigate how these parameters respond to different environmental triggers representing various risks and opportunities for the parasite, such as mosquito bites, co-infection with a different parasite lineage, or host stress. Furthermore, we explore the underlying mechanisms by which the parasite detects these environmental cues, either directly or indirectly through the host.

Keywords: Plasmodium, Phenotypic plasticity, Gametocytes, Transmission, Life, history traits, Avian malaria

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*Speaker

Heatwave on 'Off-Host' Parasite Stages: Reduced Infection Risks and Costs in Pasteuria ramosa–Daphnia magna system

Justine Boutry * [1], Noa Levi Shasha [1], Frida Ben-Ami [1]

[1] School of Zoology, Tel Aviv University – Israel

Heatwaves challenge our understanding of how environmental stressors reshape host-parasite interactions, particularly during the critical "off-host" stages of endoparasites. These stages, often dismissed as inert and unaffected by changes in their environment, remain a blackbox in ecological research despite their key role in parasite life cycles. Here, we examine how heatwaves affect the infectivity and life cycle progression of *Pasteuria ramosa*, a bacterial parasite of *Daphnia magna* a the planktonic crustacean abundant in freshwater ecosystems.

In order to measure the respective influences of the bacterial genes and the environmental fluctuations, we exposed the off-host transmission stages (=spores) from using four genetically distinct parasite isolates to three temperature regimes (20○C, 30○C, 40○C) and tested their subsequent performances and consequences on the extended host phenotypes, in a common garden infection experiment.

Heatwaves significantly reduce parasite infectivity, without significant impact of parasite genotypes. Individuals infected after a heatwave also exhibited disruptions at early infection stages (e.g., cauliflowers and grape formations). While late-stage remained unaffected across all thermal treatments, ensuring stable reproductive output. Intriguingly, heat-stressed spores induced genotype-specific shifts in host manipulation: one strain increased castration rates at higher temperatures, while others experienced moderate to dramatic declines. Furthermore, individuals exposed to heat-stressed spores but remaining uninfected, exhibited enhanced survival, suggesting reduced costs of resistance or tolerance against damaged parasites. This study provides novel insights into how environmental fluctuations, endured only by the parasite can modulate various aspects of host-parasite interaction, underlying the importance of considering the parasite's environmental history in host-parasite interactions.

Keywords: 'off, host' stages, heatwave, host, parasite, Daphnia magna, Pasteuria ramosa

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*Speaker

First evidence for the evolution of host manipulation by tumors during the long-term vertical transmission of tumor cells in Hydra oligactis

Justine Boutry * [1,2], Océane Rieu [2], Lena Guimard [2], Jordan Meliani

[1] School of Zoology, Tel Aviv University – Israel
[2] Centre de Recherches Ecologiques et Evolutives sur le Cancer – UMR 224 MIVEGEC (IRD, UM, CNRS), Montpellier – France

While host phenotypic manipulation by parasites is a widespread phenomenon, whether tumors – which can be likened to parasite entities, can also manipulate their hosts is not known. Theory predicts that this should nevertheless be the case, especially when tumors (neoplasms) are transmissible. We explored this hypothesis in a cnidarian *Hydra* model system, in which spontaneous tumors can occur in the lab, and lineages in which such neoplastic cells are vertically transmitted (through host budding) have been maintained for over 15 years. Remarkably, the hydras with long-term transmissible tumors show an unexpected increase in the number of their tentacles, allowing for the possibility that these neoplastic cells can manipulate the host. By experimentally transplanting healthy as well as neoplastic tissues derived from both recent and long-term transmissible tumors, we found that only the long-term transmissible tumors were able to trigger the growth of additional tentacles. Also, supernumerary tentacles, by permitting higher foraging efficiency for the host, were associated with an increased budding rate, thereby favoring the vertical transmission of tumors. To our knowledge, this is the first evidence that, like true parasites, transmissible tumors can evolve strategies to manipulate the phenotype of their host.

Keywords: transmissible cancer, host, tumor interactions, manipulation, hydra oligactis

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*Speaker

Immune regulation of the bacterial microbiota of the tiger mosquito in response to interference with de novo production of aromatic amino acids

Mélanie Bretton * [1], Pierre Antonelli [2], Edwige Martin [2], Laurent Vallon , Catherine Legras-Lachuer [3], Claire Valiente Moro *

[1], Aurélien Vigneron *

1

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[2] UMR Ecologie Microbienne – Univ Lyon, Université Claude Bernard Lyon 1, CNRS, INRAE, VetAgro Sup – F-69622 Villeurbanne, France, France
[3] Laboratoire dÉcologie Microbienne - UMR 5557 (LEM) – Université Claude Bernard Lyon 1, Université de Lyon, Ecole Nationale Vétérinaire de Lyon, VetAgro Sup - Institut national d'enseignement supérieur et de recherche en alimentation, santé animale, sciences agronomiques et de l'environnement, Centre National de la Recherche Scientifique : UMR5557, Institut National de Recherche pour l'Agriculture, l'Alimentation et l'Environnement : UMR1418 – BAT GREGOR MENDEL (ex 741)-4 et 43 Bvd du 11 Novembre 1918 69622 VILLEURBANNE CEDEX, France

In their successful colonization of terrestrial environments, insects have developed the ability to thrive on nutritionally unbalanced food sources. Among insect essential nutrients, aromatic amino acids (AAAs) are crucial for their development, immunity, and motricity while often lacking in their diets. These AAAs can be supplied to insects by their associated microorganisms, which can synthesize them *via* the shikimate pathway. The availability of AAAs fluctuates in the environment, influencing the need for insect to depend to their microbiota. However, it is unclear whether insects can specifically regulate their microbiota for AAAs provisioning. This project used the Asian tiger mosquito *Aedes albopictus* to address this question. This insect undergoes an aquatic and detritivore larval phase with highly variable nutrient availability across habitats. To induce competition between the host and its microbiota, mosquito larvae were exposed to glyphosate, a shikimate pathway inhibitor, making the microbiota auxotrophic for AAAs and competing for their availability in the insect diet. In response to glyphosate exposure, we observed a stage-specific decrease of the bacterial microbiota independent of the inhibitor's action, suggesting activation of local immune processes. RNA-Seq analysis further characterized the insect transcriptional response to glyphosate, revealing the expression of genes encoding Defensins, broad-spectrum antimicrobial peptides. RNAi-mediated silencing of *defensin* partially restored bacterial microbiota density, validating that microbiota elimination due to glyphosate involves local immunity. This project highlights a direct link between nutrient availability and host-microbiota interactions in the Asian tiger mosquito, suggesting mechanisms governing the intricate dialogue between mosquitoes and their associated microorganisms.

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*Speaker

Keywords: Aedes albopictus, mosquito, microbiota interaction, local immunity, RNA interference, transcriptomics

Genome evolution and between-host transmission of Spiroplasma endosymbiont in wild communities of Morpho butterflies

Jonathan Filée * [1]

[1] Évolution, Génomes, Comportement et Écologie (EGCE) – CNRS, Université Paris-Saclay – France

The evolution of endosymbiont genomes is likely influenced by the ecological interactions with their hosts. Here, we studied the evolution of *Spiroplasma* genomes, as well as their transmission patterns within and between *Morpho* butterflies sampled in the wild. *Spiroplasma* was detected in 4 out of 11 *Morpho* species studied and displayed a 3 times larger genome size as compared to *Spiroplasma* genomes documented in other hosts. This inflation in genome size is caused by massive and recent expansion of various mobile genetic elements and by the acquisition of new genes stemming from prophages. Interestingly, these new Spiroplasma genomes also revealed a peculiar evolution of toxin genes in plasmids that may enhance host resistance to parasites. Phylogenetic comparisons with *Spiroplasma* extracted from other plant and insect host suggest multiple independent colonization of Lepidoptera by *Spiroplasma*, and probable horizontal exchanges among distantly-related butterfly species occurring in South America. In contrast, resequencing data obtained for multiple populations of the two sister-species *M. helenor* and *M. achilles* living in sympatry over the majority of their distribution revealed an opposite prevalence (97% in *M. achilles* and 3% in *M. helenor*), suggesting low levels of transmission between these sympatric host-species. Reconciliation analysis of the phylogenetic relationships of mitochondrial genomes within *M. achilles* and *Spiroplasma* strains furthermore confirms predominant vertical transfers of the endosymbiont within species. Altogether, our results indicate persistent interactions between *Spiroplasma* symbiont and some *Morpho* species, as well as contrasted prevalence among sympatric host-species, consistent with an evolution of ecological interactions between the endosymbiont and its different hosts that may modify their genomic evolution.

Keywords: Lepidoptera, Endosymbiont, Toxin Genes, Speciation, Insertion Sequences

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[*] Speaker

Spatiotemporal dynamics of breeding site composition: what impact on the asian tiger mosquito biology and behaviour ?

Axelle Gentil * [1], Jonathan Gervaix [2], Edwige Martin [3], Laurent Vallon [4], Aurélie Fildier , Laure Wiest [5], Emmanuelle Vulliet [6], Amélie Cantarel [7], Rémy Cazabet [8], Patricia Luis [9], Claire Valiente Moro [10]

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[2] Plateforme Activités Microbiennes dans l'Environnement – niv Lyon, Université Claude Bernard Lyon 1, CNRS, INRAE, VetAgro Sup – France

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The Asian tiger mosquito, *Aedes albopictus*, is considered one of the world's most invasive species and is responsible for the transmission of various viruses to humans, such as dengue and chikungunya viruses. Native to the tropical forests of Southeast Asia, its strong ecological plasticity has allowed it to thrive in contrasted environments, particularly urban areas, where numerous artificial breeding sites (e.g., storm drains, utility boxes) serve as larval habitats. In cities, these breeding sites are exposed to various pollutants resulting from human activities, including micropollutants that alter their physicochemical and microbial characteristics. However, the biotic and abiotic properties of these habitats, as well as their influence on the mosquito's life cycle and oviposition behaviour, remain poorly understood. In this context, we conducted a

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*Speaker

spatiotemporal analysis of microbial diversity and physicochemical properties across six larval habitats colonized by *Ae. albopictus* over a five-month period, with samples collected twice a month. In parallel, monthly laboratory experiments were performed using water collected from three sites to assess their attractiveness for oviposition and their effects on key mosquito life-history traits (i.e., development time, survival, sex ratio, and fecundity). Our results revealed a strong preference of female mosquitoes for artificial breeding sites over controls. On average, females laid 3.3 times more eggs in the water collected from urban breeding sites. Significant variations in life-history traits were also observed, both among different habitats and within the same habitat over time. Ongoing analyses aim to identify the microbial and physicochemical factors-individually or in interaction-that drive these variations, as well as to characterize the specific environmental determinants that promote the urban success of this mosquito species.

Keywords: Aedes albopictus, Urban breeding site, Attractivity, Microbial and physicochemical properties

Microbiota influence on mosquito larvae mediate glyphosate toxicity

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The exposome is the science of the environmental stress exposure of living organisms. If human exposome has been extensively studied, it was largely neglected for other species. Anthropized ecosystems are shifting the exposome of many species, and mostly alter biodiversity while some species seems to be favored. This is the case for the Asian tiger mosquito *Aedes albopictus*, which gradually colonized every inhabited continent over the last decades. This mosquito thrives in urban areas where it is exposed to various human-made xenobiotics at every stage of its life cycle. Like demonstrated in other insect models, microbiota could also contribute to insect xenobiotic's responses. This led us to hypothesize that the mosquito-associated microbiota could play a key role in insect response to highly polluted environments. To that end, we first evaluated the toxicity of seven urban water contaminants on freshly hatched mosquito larvae. The lethal concentration for 50% mortality was then estimated for glyphosate, copper sulfate and fluoxetine, as well as their impact on larval survival in the presence or absence of extracellular microbiota. The microbiota did not impact the larval survival for copper sulfate and fluoxetine contrary to glyphosate where a negative impact was observed. Larvae without microbiota exhibited a 30% reduced mortality compared to their microbiota-associated counterparts. We further explored two hypotheses that could support this observation: (i) glyphosate-induced dysbiosis leads to the selection of harmful pathogens; (ii) microbiota-mosquito interaction interfere with glyphosate metabolism to increase its poisoning effect. Regarding the first hypothesis, bacterial microbiota metabarcoding combined with qPCR analyses and *in situ* epifluorescence microscopy showed that glyphosate ingestion highly disrupts most of the larval bacterial community, hence refuting the hypothesis of a pathogen invading the insect hemocoel. Regarding the second hypothesis, we used stable isotope to track glyphosate assimilation in larvae. We showed

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*Speaker

that axenic larvae (without microbiota) accumulate less glyphosate within their tissues. To dig further this interaction, we showed that glyphosate was catabolized within larvae associated with microbiota. Moreover, glyphosate collateral impact on larvae metabolism was explored and showed different primary metabolism patterns. All together, these results highlight a negative impact of the microbiota in the response to a xenobiotic in an insect model. This emphasizes the importance of studying interactions between microbiota and host-metabolism to assess the toxicological relevance of the bacteria-xenobiotic interplay for the host.

Keywords: Asian tiger mosquito, glyphosate, interactions, metabolism, microbiota

Identification of new antimicrobial peptides in Armadillidium vulgare using PepTraq.

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Several antimicrobial peptides (AMPs) have been discovered in the model organisms, the common woodlouse *Armadillidium vulgare*. More generally, The EBI team has already identified 110 ALFs (anti-lipopolysaccharide factors), 73 crustins and 18 armadillidins in the Armadillidiidae and Porcellionidae(1). Nevertheless, although important, this repertoire is still far from reflecting the diversity and abundance of peptides that can be found in a given species, as shown by the literature on other less conventional Arthropod models such as the tobacco sphinx(2) or the black soldier fly(3). In order to establish a more exhaustive repertoire of the defence molecules present in *A. vulgare*, we have developed two complementary methodologies as part of the PHARMA project. The first is a targeted *in-silico* approach consisting of searching for AMPs in the *A. vulgare* genome using the PepTraq software (4) developed at the University of Caen https://peptraq.greyc.fr/. The second approach consisted in studying the evolution of the proteome of *A. vulgare* hemolymph in the presence of salmonella. In both approaches, precursors ranging from 50 to 200 amino acids in length were targeted, presenting a signal peptide and characteristics common to crustacean PAMs, such as a high proline, glycine or cysteine content. Several promising sequences were identified, including a double β-defensin and a scorpin-related peptide.

Keywords: Antimicrobial peptides, Immunity, Armadillidium, Peptraq, Proteome

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*Speaker

A virus feminizes carriers in a pill bug

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Maternally transmitted endosymbionts can manipulate the reproduction of their hosts in different ways, including cytoplasmic incompatibilities, male killing and feminization of carriers. Feminization is quite astonishing because it makes the symbiont a new sex-determinant that can eliminate feminizing (X or W) sex chromosomes in host populations. This replacement induces strong sex-ratio biases (which correspond to the symbiont's transmission rates). To date, only few feminizing symbionts are known: two bacteria (*Wolbachia*and *Cardinium*) and some microsporids. All infect arthropods, mostly crustaceans. In terrestrial isopods (crustaceans commonly known as pill bugs), feminizing *Wolbachia* strains infect many species and induce excesses of females. Lineages lacking *Wolbachia* have their sex determined by mendelian chromosomes, hence produce even sex-ratios. In the pill bug *Armadillidium arcangelii*, females collected from several populations produce strongly biased sex ratios. Yet, total DNA sequencing of ovaries has not found any microbe that could induce feminization. Through a combination of crosses and RNA sequencing, we found that sex-ratios biases were caused by an RNA virus whose genome comprises four genes. This virus proved specific to females of a unique matriline, indicating a single external acquisition followed by strict maternal transmission of a *de facto* feminizing virus.

Keywords: endosymbiosis, virus, reproduction manipulation, sex determinants, sex ratio distorters, crustaceans

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[*] Speaker

Deciphering the molecular dialogue between the trematode parasite Schistosoma mansoni and its intermediate host snail Biomphalaria glabrata

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MiRNAs are short, single-stranded non-coding sequences that play a crucial role in the regulation of gene transcription in many biological processes such as embryonic development, cell proliferation, apoptosis or immunity. Indeed, miRNAs are known to regulate the host's internal defense system and the immune cell response, which is a crucial process in host-parasite interactions. We have previously described a constitutive set of miRNAs, the so-called miRNome, in Biomphalaria glabrata snails, the primary intermediate host of the trematode parasite Schistosoma mansoni, the causative agent of schistosomiasis. This B. glabrata miRNome is characterized from the hemolymph, known as the main immune-related tissue of the snail, which contains circulating haemocytes, the snail's innate immune cells. Here, we investigate thanks to a massive sequencing approach of small RNAs, if some parasite's miRNAs may be identified in haemocytes or circulating in the snail hemolymph. The present study was done by comparing different strains of parasite originating from different geographical localities and interacting with strains of B. glabrata respectively selected for their high level of compatibility. Our results reveal specific miRNAs that are exclusively expressed in some specific strains of parasites, suggesting a specificity of expression for the miRNAs. In vitro and in vivo approaches revealed the strategy of cell-to-cell communication of S. mansoni using exosome-like vesicles to target specific cells or tissue of his host and deliver his miRNAs. One question remains : does the parasite unify infection strategies in intermediate and final host infections ?

Keywords: miRNAs, Host, pathogen interaction, immunology

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*Speaker

Distinct Dynamics of Wolbachia and its pWCP Plasmid During Culex Mosquito Development

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Mosquitoes are major vectors of pathogens such as arboviruses and parasites, causing significant health impacts each year. *Wolbachia*, an intracellular bacterium widely distributed among arthropods, represents a promising vector control solution. This bacterium can indeed reduce the transmission of arboviruses like dengue, Zika and chikungunya and manipulate the reproduction of its host through its WO phage. Although research on the *Wolbachia* mobilome primarily focuses on WO phage and the phenotypes it induces, the function of *Wolbachia* plasmid pWCP, recently discovered and reported to be strikingly conserved worldwide, remains unknown. In this study, we analyzed the presence and abundance of pWCP as well as *Wolbachia* in two different species of *Culex* mosquitoes, one of the most widespread genera in the world and a vector of numerous diseases. We compared relative densities of the bacterium and its mobile genetic element in *Culex pipiens molestus* and *Culex quinquefasciatus*, a facultatively autogenous and an anautogenous species, respectively, throughout their development from larval stage L1 to adult individual specimen using quantitative PCR. Our results indicate that both *Wolbachia* and pWCP exhibit distinct dynamics throughout the mosquito's life cycle in each species, with each element showing increased levels at specific development stage. Nonetheless, data revealed an overall correlation between pWCP and bacterial density within individual mosquitoes. Interestingly, we observed an unexpected pattern of non-correlation at a stage larval 2 in *Culex pipiens molestus*. These findings suggest potentially distinct roles and behaviors of the plasmid in the bacterium's biology in different mosquito species as well as complex interaction dynamics between *Wolbachia*and its host during its life cycle.

Keywords: Wolbachia, life cycle, plasmid

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*Speaker

Plant-mediated selection of nitrogen-fixing symbiotic bacteria

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Rhizobia are soil bacteria that can form mutualistic relationships with legume plants. During this symbiosis, bacteria are hosted into dedicated root organs, called nodules, where they provide organic nitrogen to their host plant in exchange for carbon compounds derived from photosynthesis. As horizontally-transmitted symbionts, rhizobia experience diverse selective pressures throughout their life cycle, including host-imposed control mechanisms and interactions with other members of the microbiome. However, the relative contributions of these selective pressures to the micro-evolutionary dynamics of rhizobial populations is poorly known. Our recent work aimed at quantifying some of the selective pressures acting on rhizobial populations. Using the tropical legume plant Mimosa pudica and its bacterial symbionts as a model system, we examined how inter-bacterial interactions affect rhizobial fitness at different stages of the life cycle. By comparing bacterial fitness in single- versus co-inoculation experiments, we showed that interactions between rhizobial strains are pervasive, and that they mostly occur at the nodulation step, during which bacteria enter in their host plant. We also identified one case where the proliferation of a rhizobial strain within nodules depends on the identity of the strains having colonized other nodules of the same host plant, representing a potentially novel mechanism by which two rhizobial strains may interact indirectly (e.g. when the interaction is mediated by the plant) during the later stages of symbiosis. We are now testing whether the interactions identified in co-inoculation experiments are conserved in more complex communities, comprising between 6 to 8 strains, or if higher-order interaction effects occur in these contexts. Overall, this work provides a more detailed understanding of the multiple factors shaping rhizobial fitness and evolution.

Keywords: nitrogen fixation, legume rhizobium symbiosis, life cycle, selective pressures, bacteria bacteria interactions

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*Speaker

Inefficiency of immune priming via the oral route and prevalence of injuries in Tenebrio molitor reinforce the hypothesis of a wound-driven evolution in adult beetles

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Immune priming is a phenomenon observed in many invertebrates, characterised by an enhancement of an individual's immunocompetence after a non-lethal exposition to a pathogen, which confers a protection against a subsequent infection by the same pathogen. Given that immune stimulation on the long term should be costly, immune priming should have primarily evolved in response to the most dangerous pathogenic threats. However, the infection route might have partly driven the evolution of immune priming, and while studies on septic immune priming are abundant, fewer studies have considered the oral route. In addition, individuals present different energetic demands according to their development stage. While juveniles invest mainly on their growth, adults must allocate an important part of their energetic resources to reproduction. Since juveniles might be exposed to a strong selection pressure in order to reach the reproductive stage, it could be expected that they invest more than adults in their immune responses when they are exposed to repeated infection risks. However, very few studies have conducted a direct comparison of immune priming expression in both development stages. In this study, we have designed an oral immune priming protocol using the mealworm beetle, *Tenebrio molitor*, as an insect model. Larvae and adults were fed with inactivated *Bacillus cereus*, then they were later subjected to a septic infection with the same living bacterium. No survival benefit compared to the control group was observed over the monitoring period, suggesting that the oral exposition to *B. cereus* did not induce any priming. This sharply contrasts with the result of another experience where individuals were primed by pricking them with a needle dipped in a pellet of inactivated *B. cereus*, which conferred long-term protection to a second infection, although only in adults. The analysis of some immune effectors (haemocytes count, phenoloxydase pathway and antimicrobial activities) only partly explains the survival results, suggesting that further effectors should be investigated for a complete understanding of priming in the larval stage.

The difference in the efficiency of the two priming routes might indicate that the infection risk driving the evolution of priming in *T. molitor* is more pronounced via septic injuries rather than oral contaminations. The high proportion of injured adults in our different stock populations is in line with this hypothesis, and may also explain why septic immune priming was efficient in adults and not in larvae. All in all, our results provide new insights into the ecological relevance of immune priming throughout the life of *T. molitor*.

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*Speaker

Keywords: development stage, immune effector, immune priming, injury, oral infection, septic wounding, Tenebrio molitor

Sex ratio distorters and the evolution of sex determination in the isopod Armadillidium vulgare

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In the common pillbug *Armadillidium vulgare* (Crustacea, Isopoda), chromosomal sex determination follows female heterogamety (ZZ males and ZW females). In addition, many *A. vulgare* populations harbor maternally-inherited *Wolbachia* bacterial endosymbionts which can convert genetic males into phenotypic females, leading to populations with female-biased sex ratios. This bias selects against the W sex chromosome in lines infected by *Wolbachia*, such that all individuals are ZZ genetic males. Therefore, sex is only determined by the inheritance of *Wolbachia* by the *A. vulgare* individual, thereby leading to a shift from chromosomal to cytoplasmic sex determination. Surprisingly, some *A. vulgare* lines exhibit biased sex ratios despite the lack of *Wolbachia*. This bias is induced by the f-element, which we previously identified as a large piece of the *Wolbachia* genome recently transferred to the *A. vulgare* nuclear genome. The f-element is another sex-determining locus in pillbugs and the chromosome carrying the insert is a new feminizing chromosome. The f-element biases sex ratios because it is transmitted to significantly more or significantly less descendants than a mendelian element. Its transmission rate appears to be idiosyncratic as it differs between related females. We found that f-element copy number per cell varied erratically between individuals and between tissues within individuals. Interestingly, the average number of f-element copies per gonadic cell correlated with its transmission rate to offspring. Furthermore, f-element contigs could not be anchored in any of the chromosome-scale scaffolds of a genome assembly of *A. vulgare*. Taken together, our results suggest that the f-element is located on a supernumerary B chromosome, which would explain its non-Mendelian transmission. Overall, our results indicate that *Wolbachia* bacteria can drive shifts in sex determination mechanisms in *A. vulgare*. More generally, they emphasize that bacterial endosymbionts can be powerful sources of evolutionary novelty for fundamental biological processes in animals, such as sex determination.

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[*] Speaker

Keywords: Wolbachia, endosymbiont, terrestrial isopod, reproductive manipulation

Size- and sex-biased gene expression in the acanthocephalan parasite Neoechinorhynchus agilis

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Acanthocephalans are endoparasites that use mandibulate arthropods as intermediate hosts and gnathostome vertebrates as final hosts. Despite the peculiar role they play in aquatic ecosystems - not only as an economic burden for pisciculture but also as bioaccumulators of heavy metals - and their great interest in evolutionary ecology - in particular for the behavioral alterations that some of them induce in their intermediate host - molecular data is scarce, with only one published genome to date. The present study is a contribution to filling this gap. We generated a whole-body transcriptome assembly of 63 Neoechinorhynchus agilis specimens of various sizes, sampled from thin-lipped mullet digestive tracts. We conducted differential expression analyses to investigate sex-biased gene expression and to unravel the molecular bases of their sexual maturation. Gene ontology enrichment of sex-biased genes suggests that male worms are more strongly exposed to competition for reproductive success while female worms are streamlined for high fecundity. In addition, we discuss 15 genes as particularly promising candidate targets of acanthocephalan control due to their apparent role in worm growth in both males and females N. agilis.

Keywords: helminths, sex, biased gene expression, growth, Acanthocephala

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*Speaker

Within-host tissular heterogeneity is associated with phenotypic but not genomic diversity in Wolbachia endosymbionts

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The mechanisms underlying within-host diversification in parasite populations are still poorly understood. Yet, phenotypic and genotypic variation in parasites can shape their evolutionary trajectories and have important epidemiological consequences. Our aim was to determine whether the constraints associated with infecting different host tissues lead to the emergence and coexistence of multiple parasite sub-populations with distinct phenotypes. We tested this hypothesis using the most widespread bacterial endosymbiont, *Wolbachia.* We injected *Wolbachia* bacteria isolated from three tissues of the common pill-bug (*Armadillidium vulgare*) into uninfected individuals and monitored the growth rate and virulence of each bacterial sub-population in the new hosts. Our results highlight that within-host tissue heterogeneity leads to diverse *Wolbachia* phenotypes. High-depth genome re-resequencing of *Wolbachia* sub-populations revealed that this polymorphism was not due to genomic variation but was more likely a result of phenotypic plasticity. Indeed, we found no recurrent tissue-specific genomic variation among infected individuals. The single nucleotide polymorphism (SNP) filtration pipeline, developed to ensure SNP validity, detected only a single substitution. This *Wolbachia* variant, observed in only one female, was present in all three bacterial sub-populations, with frequencies ranging from 24% to 58% depending on the tissue. Overall, our results support the stability of the *Wolbachia* genome with respect to the rarity of point mutations, in agreement with reports from other symbiotic systems. Finally, from a methodological perspective, our study highlights the need for considerable caution when detecting variants in endosymbiont populations, as our conservative approach led us to exclude more than 99% of the initially called variants.

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*Speaker

Keywords: endosymbiont, infection dynamics, polymorphism, within host evolution

Characterization of a Symbiopectobacterium infecting bedbugs.

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Some B vitamins, necessary for insect growth and fertility, are scarce or absent in the blood. As other obligate blood feeding arthropods, bedbugs are thus associated with nutritional bacterial symbionts that supplement their diet in B vitamins. In bedbugs (*Cimex lectularius*), the intracellular, vertically transmitted, bacterium *Wolbachia (w*Cle) has been shown to produce two B vitamins: riboflavin (B2) and biotin (B8), both required for the fitness of bedbugs.

However, bedbugs can also be infected by another symbiont, a gamma-proteobacterium called BEV-like, closely related to a *Symbiopectobacterium* (BEV) that can be pathogenic in leafhoppers. In bedbugs, BEV-like is localized in specialized symbiotic structures called bacteriomes, in ovaries, and in the Malpighian tubules. As the impact of BEV-like on bedbug fitness has not been described yet, we sequenced and studied its genome to determine whether some genomic signatures could be indicative of its evolution (*i.e.*, pathogenic or mutualistic properties; lifestyle). Because of its large gene content, we are currently testing its cultivability. We also studied the dynamics of BEV-like during larval development and in response to blood feeding, and focused on the correlation of its density with that of *Wolbachia*, which could reveal common control mechanisms.

These results will enable us to gain a better understanding of the impact of BEV-like on bedbugs, and its potential interactions with *Wolbachia* and bedbugs. From a societal point of view, bedbug infestations strongly increase in developed countries, mainly due to the evolution of insecticide resistance and globalization, and require the development of alternative strategies to control bed bug populations. Ultimately, our results could thus pave the way to disrupt the obligate nutritional interaction between bed bugs and their endosymbionts.

Keywords: Bedbug, BEV, like, Wolbachia, nutritional symbiosis, endosymbiosis, hematophagy

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*Speaker

Effects of microplastics on mosquito development and avian malaria transmission

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Plastics are among the most widely used materials, with global production doubling from 234 to 460 million tons between 2000 and 2019. This surge has led to massive waste accumulation, posing severe environmental and biological threats. As plastics degrade, microplastics ($<$ 5 mm) and nanoplastics ($<$ 100 nm) seep into ecosystems and food chains, impacting organisms from zooplankton to humans. In wildlife, ingestion can cause reproductive harm, metabolic disorders, and microbiome imbalances (i.e. dysbiosis). Microplastics also carry chemicals and pathogens, including antibiotic-resistant bacteria. Although research has explored their environmental and biological impacts, significant gaps remain - particularly regarding their effects on complex host-vector-parasite systems. For example, mosquitoes do not avoid microplastic-contaminated water and ingest particles during their larval stage. However, the consequences for pathogen transmission are still unknown.

In our study, we exposed *Culex quinquefasciatus* larvae to one of four treatments: (i) a microplastic-free control, (ii) clean virgin polyethylene (PE), or environmental PE microplastics that had aged two months either (iii) in a city storm drain, or (iv) in an urban river running through a park. We then exposed adult females overnight to infected birds carrying avian malaria, *Plasmodium relictum*, and tested their salivary glands for sporozoites (the transmissible stage of avian malaria) via qPCR 14 days post-blood meal. We also analyzed the diversity and composition of their midgut microbiota* using metabarcoding sequencing, as well as the microbiota present on the microplastics themselves and in field-sampled free water.

Our results showed that females exposed to virgin PE experienced higher pupal mortality and emerged later than those exposed to PE that had aged in the environment. In addition, these females had significantly higher sporozoite concentrations than control females. These results suggest that bacteria from the microplastics may have a priming effect or mask the effects of virgin microplastics. These findings highlight the importance of using environmentally relevant microplastics in experimental work.

**Microbiota data are still being processed and may provide further insights into the observed results. By May, the data will be analyzed and presented.*

Keywords: avian malaria, Culex quinquefasciatus, microbiota, plastic pollution, vectorial capacity

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*Speaker

Drivers of sex differences in insect immunity

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Sex differences in immunity are considered common across animal taxa with males typically showing lower immune responses. However, recent studies in diverse taxa seem to challenge this notion of a general female bias in immunity. We performed a meta-analysis of sexual dimorphism in immunity in insects, and examined several mechanistic and evolutionary factors that may shape sex-biased immune competence. With this, we wanted to examine whether sex dimorphisms are related to variables such as immune parameters considered in studies (i.e. type of assay), insect taxa or species-specific characteristics such as sex determination system and invasiveness status to identify potential fitness-related traits that may influence sex-specific investment in immunity across insects. We collected 1212 published experimental data sets from 156 species, investigating sex differences in at least one standard measure of immunity. Additionally, we collected 127 published datasets on sex-specific survival following pathogen infection from 10 species. Generally, we found that insect females are significantly more immunocompetent than males. However, this sex bias is not consistent across insect orders, and the magnitude of sex-difference depends on how immunity is assayed. In particular, we found no significant difference between males and females for survival and pathogen load. Interestingly, we found that haplodiploidy and X0/XX karyotypes are associated with female biased immune responses. This could indicate a major role played by sex chromosomes in shaping immune response, as observed in mammals. Additionally, species listed as invasive show a female biased immune response, as opposed to non-invasive species, hinting at potential ecological consequences of sex-differences in immunity.

Keywords: Insect, Immunity, Meta, analysis

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[*] Speaker

Wolbachia metapangenomics of individual Culex mosquitoes reveal shared phage rearrangements across large geographic distances

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Wolbachia is an endosymbiotic bacterium of the order *Rickettsiales* living inside the cells of around 50% of all arthropods, of particular interest for mosquito vector control strategies. *Wolbachia* can influence pathogen transmission and confer mosquitoes manipulative reproduction phenotypes including cytoplasmic incompatibility through key genes of its prophage WO. In addition to phage WO, the *Wolbachia* mobilome of *Culex* species comprises a highly conserved and likely beneficial plasmid pWCP. However, despite its importance, little is known about the dynamics of the mobilome in *Wolbachia* of *Culex* populations across large geographic distances. Here, we used state-of-the-art assembly, binning and metapangenomic approaches to study the ecology and genetic diversity of *Wolbachia* from 36 *Culex quinquefasciatus* mosquitoes collected in Mexico, New Caledonia and La Reunion. Metapangenomics, hereby defined as the conjoint study of the pangenomic information and the genomic environmental information, enabled a well-curated and refined analysis of the bioinformatics assembly results in comparison to reference genomes. This coupled analysis of the functional genome and the raw read data confirmed the widespread presence of pWCP plasmid worldwide including in Indian and Pacific Ocean islands. In addition, groups of contiguous genes belonging to specific WO prophage regions were found to be differentially present among sampled localities, with genomic regions shared by all samples in some localities but only by few specimens in other localities. Further bioinformatics and modelling analyses will be performed to confirm the nature of these phage rearrangements at large scale.

Keywords: phage rearrangements, metagenomics, pangenomics, mosquito ecology

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*Speaker

Microbiome turnover during offspring development varies with maternal care, but not moult, in a hemimetabolous insect

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The ecological success of insects often depends on their association with beneficial microbes. However, insect development involves repeated moults, which can have dramatic effects on their microbial communities. Here, we investigated whether and how moulting affects the microbiome of a hemimetabolous insect, and whether maternal care can modulate these effects. We reared European earwig juveniles with or without mothers and used 16S rRNA metabarcoding to analyse the prokaryotic fraction of the core microbiome of eggs, recently and old moulted individuals at four developmental stages and the resulting adults. The 218 samples obtained showed that the microbiome diversity changed non-linearly during development and that these changes were associated with bacterial biomarkers. Surprisingly, these changes did not occur during moulting, but rather between the beginning and end of certain developmental stages. We also found that access to maternal care affected the microbiome of both juveniles and adults, even when the last contact with mothers was two months before adulthood. Overall, these results provide new insights into our understanding of the (in)stability of the prokaryotic microbiome in hemimetabolous insects and its independence from moult. More generally, they question the role of microbiome acquisition through maternal care in maintaining family life in species where this behaviour is facultative.

Keywords: Insect, Microbiota, Transmission, Moult, Parental care

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*Speaker

Investigating the IMD pathway in the bedbug Cimex lectularius and its function in the control of infections and mutualistic symbioses

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In insects, the innate immune system is based on two main responses: the humoral and cellular responses. The humoral immune response involves the production of antimicrobial peptides (AMPs) that protect insects against bacteria, fungi or viruses. The production of AMPs in response to Gram-negative bacteria infections is mainly mediated by the Immune Deficiency (IMD) transduction pathway. In *Drosophila melanogaster*, the IMD pathway is triggered upon recognition of bacterial peptidoglycan by the PGRP-LC receptor, which activates a downstream signalling cascade involving Imd and resulting in the activation of the transcription factor Relish, which in turn activates the expression of effector genes, including AMP-encoding genes. However, some IMD signalling components, which are highly conserved across insect orders, appear to be absent in hemipteran species. For example, in the bedbug *Cimex lectularius*, previous studies have shown that two genes encoding key components of the pathway (the IMD and Kenny proteins) are absent from the genome. In contrast, the genes encoding the NF-B transcription factor Relish and some AMPs are conserved. The aim of this study was thus to investigate whether the transcription factor Relish is involved in the regulation of AMPs in this species, despite the apparent lack of Imd. To this end, we used RNA interference (RNAi) to silence *relish*, and challenged bedbugs with Gram-negative bacteria. Gene silencing efficiency and the induction of a humoral immune response were assessed by RT-qPCR, by following the expression of *relish* and three AMP-encoding genes, respectively. The results show an extinction of the immune response when *relish* is silenced, with a significantly reduced expression of the three studied AMPs, as compared to control conditions (*gfp* RNAi). This result raises the question of whether the IMD pathway remains functional in the bed bug, contrary to what had been speculated. To further investigate this possibility, we identified a gene encoding a PGRP-LC receptor in the bedbug genome, and silenced *pgrp-lc* before challenging the insect with Gram-negative bacteria. As previously, we found that the induction of AMP-encoding genes was significantly decreased in the *pgrp-lc* RNAi context, as compared to control RNAi, confirming that the IMD pathway is still functional. Taken together, these results raise the

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[*] Speaker

question of whether the IMD protein is really absent from the bed bug genome, and if it is, of the alternative mechanisms that could allow both PGRP-LC and Relish to regulate the AMP expression independently of Imd. Last, because the bed bug is a strict hematophagous insect that lives in association with an obligate nutritional endosymbiont, *Wolbachia*, the existence of a functional IMD pathway would open the possibility that this immune response plays a role in the control of the endosymbiont, as demonstrated in other insect species, such as the cereal weevils *Sitophilus zeamais* and *S. oryzae.*

Keywords: IMD pathway, immune response, symbiosis, bedbug

Distinct host-endosymbiont co-evolutionary trajectories in cereal weevils

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Most insects thriving on unbalanced diets have evolved obligate associations with intracellular symbionts (endosymbionts) that complement their diet with nutrients lacking in their habitat. Endosymbiosis is a fundamental driver of evolutionary success, enabling hosts to adapt to diverse environments while facilitating niche expansion and phenotypic diversification. However, these obligate associations are not permanent, endosymbionts have been lost or replaced during insects' evolutionary history. Phylogenetic studies on weevils from the *Sitophilus* genus showed a recent symbiont replacement (≈30 KYA) by a Gram-negative bacterium of the *Sodalis*-allied clade, constituting an ideal model to study the evolutionary processes of endosymbiogenesis. The *Sitophilus* genus, consisting of 14 described species, shows a variety of host-bacteria interactions and ecological niches. The notorious pests, *S. oryzae* and *S. zeamais* infest both cereal fields and cereal-containing silos, while *S. granarius* is restricted to silos. Other species dwell in trees, such as *S. rugicollis*, which infects the seeds of the *Myrtaceae* family. This study investigates the host and endosymbiont genetic hallmarks underlying the rapid and contrasted phenotypic diversification observed. We revealed differences in endosymbiont genome size and contents, showing distinct levels of genome degradation. Notably, we uncover the loss of the type III secretion system in two of the *Sodalis* genomes, which was previously shown to be key for host cell re-infection. Following a metagenomic assembly approach we discovered the co-occurrence of multiple symbionts previously unknown in *Sitophilus* weevils. We reconstructed a pangenome of the five *Sodalis* endosymbionts, showing a core genome composed of around 400 genes and accessory genes ranging from 4 to 352 depending on the *Sodalis* studied. These findings provide insights into the molecular bases of endosymbiogenesis and the varied trajectories of host-symbiont co-evolutionary routes.

Keywords: comparative genomics, coevolution, insects, endosymbiosis

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*Speaker

Impacts of Microplastics on Mosquito Life History Traits and midgut microbiota

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Microplastics represent a major source of pollution worlwide, as they are ubiquitous in the environment, including in waters where mosquito larvae develop. While more and more studies investigate the impact of microplastics on mosquitoes, which are the main vectors of diseases worldwide, most of these studies use exposure conditions that are not representative of what happens in the field. Designing environmentally relevant set-ups of exposure to microplastics is critical to better understand the consequences of microplastic pollution on mosquito populations and how it may affect disease transmission.

In this study, we investigated the effects of microplastic exposure on the life history traits and midgut microbiota of *Culex quinquefasciatus* (slab strain), using two set-ups: one with laboratory rearing conditions (constant temperature of 27○C) and the other with environmentally relevant temperature variations (mimicking external temperature variations late spring in the south of France). First instar larvae were exposed to two types of plastic polymers: polyethylene (PE) and polystyrene (PS), alone or in a mixture of both, at four concentrations (0, 60, 200 and 600 microplastic particles MP/mL), until adult emergence. We collected data on life history traits (i.e. survival, time to pupation, emergence rates), wing size (a proxy for adult size), and female midgut microbiota composition.

We found that at constant temperature, PE and PS did not affect mortality and life history traits. When using environmental temperatures, the mosquito life cycle was extended, with a time to emergence of around 16 days, instead of 8 days at constant temperature. Wing length was also higher at environmental temperatures, and larval mortality was high for all treatments (around 65%), but was reduced for mosquitoes exposed to the highest concentration of PE (mortality rate of around 52%). Microbiota data are still being processed, and may provide insights into the observed results.

Keywords: Culex quinquefasciatus, microplastics, microbiota

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[*] Speaker

Impact of the Varroa Mite on the Microbiota of Apis mellifera and Bombus terrestris

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Corbiculate bees such as Honey bees (*Apis mellifera*) and the Buff-tailed bumblebees (Bombus terrestris) harbor a consistent microbiome composed of relatively few species that are host specific. It has been shown that they play an important role in bee health not only in nutrition but also in the immune functions.
A. mellifera hives in Europe are commonly infested by the *Varroa destructor* mite, vector of several bee pathogens such as Deformed wing virus (DWV). The association of these two can lead to an increased viral load in foraging bees which are in regular contact with wild bumblebees.
In this study, we aim to explore the interactions between the honey bee specific parasite Varroa, viral prevalence and the microbiome of managed and wild bee populations. Our dataset consists of *A. mellifera* and *B. terrestris* samples from varroa infested and varroa free sites. Results from 16s rRNA sequencing reveal correlations between changes in the microbiome and the presence of pathogens in honey bees, namely Pseudomonas, Wolbachia and SBPV. While in bumblebees, we observe a strong effect of the presence of Varroa at the sampling site, and prevalence of DWV-B, despite the fact that Varroa is a honey bee specific parasite.

Keywords: microbiome, bee, parasite, Varroa, virome

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*Speaker

Chronic exposure of Cadmium leads to deleterious effects on Armadillidium vulgare immune cell's mitochondria

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Heavy metals have adverse effects on ecosystems. Due to anthropogenic activities, cadmium is one of the most abundant in soil, and has significant impact on the physiology of exposed organisms. Many ecotoxicological studies have demonstrated its effects on reproduction and growth. However, the effects on the immune system of soil organisms are poorly explored. We address this knowledge gap using the common woodlouse *Armadillidium vulgare*. In this species, symbiosis with *Wolbachia* is known to confer protection against pathogens. Here, we investigated the effect of cadmium on immune cells in symbiotic and asymbiotic females. Individuals were exposed during 28 days, at concentrations similar to those found in fields. We measure the hemocytes concentration, phenoloxydase activity, and developed new methods to measure immune cell health, such as calcium movement in the different cell compartments, reactive oxygen species production and mitochondrial membrane potential. Overall, this study demonstrates the deleterious effect of cadmium on immune cells, specifically affecting the mitochondria of hemocytes. This highlights the importance of investigating physiological parameters, which are still under-studied in arthropods, in the context of soil pollution.

Keywords: Armadillidium vulgare, Hemocytes, Mitochondria, Soil pollution

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[*] Speaker

Impact des vagues de chaleur sur la Maladie de l'Anneau Brun induite par Vibrio tapetis chez la palourde Ruditapes philippinarum

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Le changement climatique, y compris l'augmentation des vagues de chaleur, perturbe l'environnement côtier et altère les interactions hôte-pathogènes chez les espèces marines (Olivier et al., 2021 ; Simon et al., 2023). Nous nous intéressons au modèle hôte-pathogène impliquant les palourdes *Ruditapes philippinarum* et la bactérie *Vibrio tapetis*. Cette bactérie est responsable de la Maladie de l'Anneau Brun (MAB) et affecte de nombreuses écloseries de palourdes le long des côtes européennes. La MAB est fortement influencée par l'environnement, elle est exacerbée par une température de 14○C et une faible salinité (20 ppm). À l'inverse, une température de 21○C et une salinité élevée (35 ppm) sont associées à une stimulation du système immunitaire de la palourde et à une guérison de la maladie (Paillard et al., 2025 ; Reid et al., 2003). Notre hypothèse est que les conditions estivales futures caractérisées par des vagues de chaleur, pourraient améliorer la résistance à la MAB et la guérison, en modulant la composition du microbiote et son activité anti-*V. tapetis*.

Dans notre expérimentation, les palourdes ont été acclimatées aux conditions estivales, et quatre vagues de chaleur (VC) ont été simulées selon le scénario climatique SSP5-8.5 (Kwiatkowski et al., 2020 ; Simon et al., 2023). Tout au long de l'expérience, la croissance et la nutrition des palourdes ont été suivies. Des prélèvements réguliers d'hémolymphe ont été effectués avant et pendant chaque VC, permettant de suivre l'évolution des paramètres des cellules immunitaires et pour tester si la cytotoxicité est encore induite par *V. tapetis*. Après la première et la dernière VC, un challenge bactérien a été effectué pour évaluer si la susceptibilité des palourdes à *V. tapetis* est modifiée par les VCs. À la fin de l'expérience, le microbiote " estival " a été collecté dans les palourdes ayant subi les 4 VCs et sera testé *in-vivo* par transplantation pour tester son effet potentiellement protecteur contre la MAB. Toutes les coquilles ont été précieusement gardées pour les analyser et suivre l'évolution de la prévalence de la maladie.

Nos résultats montrent que les VCs futures n'ont pas impacté la survie des palourdes, elles ont même stimulé leur indice de condition ($>$ 5) ainsi que leur croissance. Au niveau cellu-

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*Speaker

laire, la variabilité du nombre d'hémocytes (THC) semble augmenter à chaque succession de VC, en parallèle d'une diminution de leur viabilité. Chaque VC semble impacter directement les hémocytes, car leur adhérence est modifiée. Nos tests de cytotoxicité montrent également qu'après la première VC, les hémocytes sont plus susceptibles à *Vibrio tapetis*, et cet effet semble s'atténuer avec les VC suivantes. A l'inverse, l'analyse des coquilles semble présenter une prévalence et une intensité de la MAB en augmentation avec les VCs actuelles.

Pour mieux comprendre les mécanismes sous-jacents, des analyses du microbiote, et des analyses protéomiques, transcriptomiques et épigénétiques seront réalisées prochainement. Actuellement, nous conditionnons des palourdes dans des conditions pré-printanières associées à des dessalures importantes. Ces palourdes recevront le microbiote ” estival ” afin de quantifier l'impact du microbiote ” estival ” sur l'interaction hôte-pathogène, afin de valider notre hypothèse.

Keywords: Changement climatique, Palourde, Maladie de l'Anneau Brun, Hémocyte, Vague de chaleur, Microbiote

Diversité et dendrologie des cacaoyers d'une agroforêt en zone de forêt dense et humide de l'Est-Cameroun

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Le défi actuel des acteurs de la filière cacao au Cameroun est de trouver des stratégies pour augmenter la production en cabosses matures et mûres des systèmes agroforestiers à base de cacaoyers (SAFc) camerounais afin de mieux répondre à la forte demande mondiale en fève de cacao. L'objectif de cette étude était de caractériser la diversité des cacaoyers et évaluer la dendrologie de variantes de cacaoyers identifiées dans un SAFc en zone de forêt dense et humide camerounaise. Un inventaire d'aménagement forestier a été fait du 02 septembre au 25 octobre 2020 afin de collecter les informations sur les cacaoyers de l'Exploitation Agricole BETTI (EAB). 3597 tiges de cacaoyers ont été dénombrées, représentant une densité moyenne de 309,11 tiges/ha et une surface terrière moyenne de 6,81 m2/ha. La caractérisation floristique des cacaoyers faite suivant des critères morphologiques des cabosses a permis d'identifier 18 variantes différentes de cacaoyers dont cinq : BoLiAl, BoPrOv, VePrOv, VbPrAl, BoPrAl ont des indices d'efficacités plus élevées dans un environnement complexe et très contraignant, c'est-à-dire qu'elles ont une production élevée en termes du nombre de cabossese t une bonne résistance de ces cabosses aux maladies et ravageurs. Le suivi de chacune de ces cinq variantes dans des parcelles sous traitements d'ombrage différent serait intéressant pour définir des modèles de SAFc qui combinent les ambitions de production du cacao de qualité et en quantité et de conservation d'un niveau élevé de la biodiversité en milieu forestiers.

Keywords: Mots clés : Systèmes Agroforestiers à base cacaoyers (SAFc), variantes de cacaoyers, production des variantes de cacaoyers, indices d'efficacités des variantes, modèles de SAFc.

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*Speaker

Evolution of cytoplasmic incompatibility genes among maternally inherited symbionts: Wolbachia do not walk alone

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Cytoplasmic incompatibily (CI) is a powerful evolutionary phenomenon shaping arthropod population dynamics, induced by specialized, maternally inherited bacterial symbionts. This selective pressure favors the reproduction of infected female arthropods (the transmitting sex), promoting the rapid spread of CI symbionts within the population. This phenotype is driven by the presence of the cif operon, which, when expressed, provides a significant selective advantage to maternally transmitted bacteria.
Wolbachia is the most extensively studied CI symbiont, possessing a high prevalence of the cif operon (detected in approximately 75% of known strains). Phylogenetic analyses of its key components, cifA and cifB, indicate that the operon primarily disseminates via horizontal gene transfer, occurring both between closely related and more distantly related Wolbachia strains. This extensive mobility is thought to be facilitated by its association with mobile genetic elements, including WO prophages, transposons, and retrotransposons. Given its remarkable mobility, the cif operon has been likened to a selfish genetic element subject to dynamic gain and loss, capable of crossing genus barriers, as it has been sporadically identified in at least eight other bacterial genera. In some of these, such as Rickettsia and Mesenet, CI is also expressed, meaning that these bacteria can mimic Wolbachia through the cif operon. However, the full extent of the cif operon's distribution and evolution beyond Wolbachia remains largely uncharacterized, as does the potential for other symbiotic genera to induce CI using this operon.

In this study, we carried out an extensive analysis of non-Wolbachia cif operons by examining a broad genomic dataset of over 700 maternally inherited symbionts and their close relatives, all distinct from members of the Wolbachia genus (including newly sequenced and publicly available genomes). Our analyses reveal that cif operons are more widespread outside the Wolbachia genus than previously recognized, particularly within the Rickettsiaceae family. We found that cif operons are restricted to a specific ecological subset of maternally inherited bacteria mirroring the lifestyle of Wolbachia.

By comparing the protein domain composition and pseudogenization patterns of cif genes between maternally inherited bacteria, we provide novel insights into the evolution of CI, the origins of the cif operon, and its functional implications. Furthermore, we investigated the genomic context of cif loci in non-Wolbachia symbionts, identifying their close association with a diverse array of mobile genetic elements. Surprisingly, we identified new redundant genomic regions for cif operons outside WO prophages, revealing previously unrecognized mobile elements associated with Rickettsiaceae. This association may drive recent, and potentially ongoing, horizontal transfers of cif operons over long phylogenetic distances between symbionts commonly co-occurring within arthropod cells through multiple and distinct rearrangement and transfer mechanisms, all possibly taking place in the cytoplasmic arena.

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*Speaker

Finally, we identified novel bacterial candidates that may be capable of inducing CI, hijacking their hosts' reproduction, particularly in ticks, which serve as vectors for numerous and previously unrecognized pathogenic agents.

Keywords: Wolbachia, cif genes, mobile elements, horizontal transferts, genomic comparative, reproductive manipulation, cytoplasmic incompatibility, evolution of interaction, arthropod symbiosis

Reproduction-immunity trade-off in females of the European earwig

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Reproduction and immunity are two fundamental biological processes that are crucial for the fitness and survival of organisms. In insects, accumulating evidence indicates that pre-oviposition trade-offs between immunity and reproduction often favour the latter, with mating typically leading to reduced investment in immune functions. However, post-oviposition trade-offs - such as those involving egg-laying and parental care - remain largely unexplored in this taxon. In this study, we addressed this knowledge gap in the European earwig, an insect with extensive maternal care. We selected 75 ovipositing and 75 non-ovipositing females, injected them with either a solution of heat-killed *Serratia marcescens* bacteria or a control solution, and then measured their humoral (phenoloxidase activity) or cellular (hemocyte) immune responses. To conduct these tests, we identified and classified three types of hemocytes based on their morphological features, marking the first such classification in Dermaptera. Our results show that the presence of eggs reduced the proportion of Type 3 hemocytes, while increasing the proportion of Type 2 hemocytes and the total hemocyte count. However, it had no effect on phenoloxydase activity or the proportion of Type 1 hemocytes. Similarly, either the type of immune challenge nor female size had a direct or interactive effect with egg presence on any of the measured immune traits. Overall, these findings indicate that maternal investment in reproduction after oviposition induces some changes in cellular immunity but not in humoral immunity. This highlights the importance of post-oviposition maternal investment in reproduction in shaping immune function and call for future research into the dynamics of these trade-offs and the specific role of hemocyte types in Dermaptera.

Keywords: Life history traits, Trade offs, Oviposition, Earwig

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*Speaker

Why did complete metamorphosis of insects evolve

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Today, the vast majority of extant animal species are holometabolous insects. These organisms have three life-stages: larva, pupa, adult. During the pupal phase, the larva undergoes an extreme form of metamorphosis, during which the body is radically reorganized. When the adult emerges, it is morphologically, anatomically and ecologically different from the larva. Little is known about why it is adaptive to rebuild the body.

Here, I will discuss three mutually non-exclusive hypotheses to explain the evolutionary advantages of complete metamorphosis in insects: (1) A pupa permits the decoupling of growth and differentiation enabling fast growth. (2) A decoupling of life stages permits the exploitation of different niches. And (3) the decoupling of larval and adult microbiota, which is facilitated by the renewal of the gut during pupation.

Keywords: complete metamorphosis, fast growth, microbiota, immune genes

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*Speaker

Bridging multiple infections across scales: from co-circulation to co-infection

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Most species can be attacked by multiple parasites, often co-circulating simultaneously in the same host population or even co-infecting the same host individuals. Each process – co-infection and co-circulation, respectively – can lead to interactions between parasites. For example, parasite can interfere with each other directly within the same host individual, or indirectly by removing susceptible hosts from the population. However, co-infection and co-circulation are often investigated by different fields (e.g., immunology versus epidemiology). This has resulted in a fundamental gap in our understanding of how parasite interactions at these two levels affect each other, and the implications thereof for infection severity, host health, disease spread, and long-term evolutionary trajectories.

I will present a framework aimed at bridging between individual- and population-level perspectives of interactions among parasites, developed by a consortium of ecologists and evolutionary biologists investigating the topic from theoretical, experimental and field perspectives. First, we employed the Susceptible-Infected framework to characterise the potential range of individual- and population-level host interactions that may occur among co-circulating parasites. Second, we mapped empirical examples from the literature onto this framework, to illustrate the mechanisms driving both types of interactions across diverse host-parasite systems and the evolutionary implications. I will also briefly present results from an ongoing project, combining experimental investigations of co-infection and co-circulation dynamics in an aquatic model system with mathematical modelling.

Careful modelling and experiments can help disentangling when interactions at one scale affect those at another, and how ascribing a pattern to a within-host mechanism that is in fact driven by a between-host process (or vice versa) can be misleading. Given the steady rise of emerging and re-emerging infectious diseases, novel parasite combinations are increasingly likely to be brought together, resulting in new and more frequent interactions and opportunities for selection and evolutionary changes to occur. Thus, better understanding of general rules for interactions between parasites, and key sources of variation in outcomes, will provide insight for public health, conservation and agriculture.

Keywords: Host, parasite interactions, multiple infections, disease spread, epidemiology, priority effects, eco, evolutionary dynamics

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*Speaker

Coexistence of three sex determinants in a population of the pill bug Armadillidium arcangelii

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Coexistence of three sex determinants in a population of the pill bug *Armadillidium arcangelii*
Théo Ulvé, Yann Dussert, Baptiste Lhéraud, Alexandra Lafitte, Romain Pigeault, Jean Peccoud

The sex of individuals in gonochoric species can be determined genetically or environmentally. Genetic determinism implies sex chromosomes carrying a locus whose genotype controls sex determination and it results in a balanced sex-ratio in brood. However, certain maternally transmitted endosymbionts can increase their transmission by distorting sex-ratio towards females in different ways: induction of parthenogenesis, male-killing or feminization. Feminizing endosymbionts can be bacteria like *Cardinium* or *Wolbachia* and microsporids. The spread of a feminizing endosymbiont in a population can lead to the loss of the feminizing sex chromosome (X or W). Hence, the sex of an individual is determined by the infection of the feminizing symbiont.
In a small population of the terrestrial isopod *Armadillidium arcangelii*, we found three different sex determinants: a feminizing *Wolbachia* strain, a feminizing virus and sex chromosomes. The two endosymbionts and the sex chromosomes compete for transmission, and the winner of the competition largely depends on transmission rates. To determine possible outcomes, the type of sex chromosomes (i.e., XY or ZW), the prevalence of the two endosymbionts in the population and their transmission rates were estimated, and the future dynamics of the different sex determinants were investigated by modeling.

Keywords: endosymbiosis, sex, ratio distorters, feminization, Wolbachia, virus, sex chromosomes, pill bugs, crustaceans.

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*Speaker

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

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Parental care is widespread in nature and typically benefits offspring by protecting them from environmental hazards such as pathogens, predators, and starvation. On the other hand, providing care is expected to come at a cost to parents, as the energy and resources invested in caregiving may trade off with other physiological functions. Despite this expectation, the costs of parental care - particularly in terms of immune function - remain poorly studied, especially in insects. In this study, we investigated the immunological costs of maternal care in the European earwig (*Forficula auricularia*), focusing on care directed toward both eggs and juveniles. In this insect species, mothers lay eggs in early winter and cease foraging to provide continuous care until hatching in early spring. They then continue to tend their newly hatched juveniles for an additional two weeks before family dispersal. During this period, mothers engage in various forms of care, including nest protection, egg cleaning, chemical deposition to prevent desiccation, temperature regulation, and food regurgitation for juveniles. However, whether this investment in care comes at a cost to maternal immunity remains unknown. To address this question, we experimentally manipulated maternal investment in care by varying the number of eggs (0, 55, or 110) and juveniles (0, 40, or 80) present in the nests of a total of 1040 earwig mothers. We performed immune measurements on mothers at four different times: before oviposition, right after oviposition, 35 days post-oviposition (approximately one week before hatching) and 15 days post-hatching (at the end of the family phase). The measured immune parameters included lytic activity, phenoloxidase activity, encapsulation rate, assessed both under basal conditions and after immune activation via injection of heat-killed *Serratia marcescens.* Finally, to evaluate the immune competence of the tested females, we also measured their survival rate following an injection of *S. marcescens* at each of the four time points. While data collection is ongoing, we expect that the increase in maternal investment in care will reduce maternal investment in immune function, revealing a trade-off between parental care and self-maintenance in this species. Elucidating the nature and magnitude of these costs will provide valuable insights into the evolutionary constraints that shape parental care strategies and the physiological limits of family life in insects.

Keywords: immunity, earwig, maternal care, costs

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*Speaker

Rôle du venin dans l'induction des galles de Cynipidés : une approche omique comparative

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De nombreux insectes herbivores manipulent le développement des plantes pour induire des galles, mais les mécanismes moléculaires impliqués restent mal compris. Nous étudions le rôle du venin dans l'induction des galles chez les Cynipidae, un clade majeur d'insectes gallicoles (_˜1400 spp). Notre analyse anatomique comparative révèle une expansion importante de l'appareil à venin chez ces espèces, suggérant son implication dans la manipulation des plantes lors de l'oviposition. Nous avons réalisé une analyse transcriptomique et protéomique comparative des glandes à venin de 12 espèces de cynipidés, ainsi que des deux générations de l'espèce *Disholcaspis quercusmamma.* Nos résultats révèlent une forte diversité de composition du venin entre espèces et générations, suggérant une grande diversité de mécanismes d'interactions avec la plante hôte. L'*Apolipoprotéine D* (ApoD), un transporteur lipidique, apparaît comme un constituant majeur du venin des Cynipini, le clade des guêpes à galle du chêne. Nous avons également détecté des taux élevés de protéines à hème (peroxydases) chez certaines espèces, pouvant expliquer la coloration observée dans certaines glandes à venin. Par ailleurs, l'analyse chimique de quatre espèces confirme la présence de phytohormones dans le venin des cynipidés, suggérant une possible contribution directe à l'induction des galles. Nos résultats mettent en évidence la diversité et les éléments conservés du venin chez les cynipidés et ouvrent de nouvelles perspectives pour comprendre les bases moléculaires de l'induction des galles.

Keywords: galles, venin, parasite, transcriptome, protéome

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*Speaker

Dumpster diving into sequencing data to uncover unknown microorganisms involved in symbiotic relationships in marine species

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Symbiotic interactions, from mutualism to parasitism, play a very important role in the ecology and evolution of marine organisms. A few systems, such as in polychaete worms or in a few coral species, have been extensively studied. Nevertheless, this likely only represents a limited view of the diversity of symbiotic interactions found in marine environments, and a large proportion of microorganisms involved in these interactions remains unknown or poorly described. Large genome sequencing projects, such as the European European Reference Genome Atlas (ERGA) initiative or the Darwin Tree of Life project, aiming to produce chromosome-scale reference genomes, have recently multiplied. These projects represent a great opportunity to discover new prokaryotic and eukaryotic symbionts sequenced along the targeted species, and to obtain high-quality genome sequences for these symbionts. It is notably the only way to sequence microbial organisms that cannot be cultured, such as endosymbionts or obligatory parasites. Our work focused on data from the recently started French Atlas of Marine Genomes (ATLASea) project, whose goal is to assemble the complete genomes of around 4500 eukaryotic marine species from the French coasts with long reads sequencing and genome conformation mapping (e.g., Hi-C). Sequencing data has already been released for a few dozens of species belonging to a wide range of phyla (e.g. Mollusca, Chordata, Cnidaria or Porifera). Using metagenome assembly approaches, we obtained the genome sequences (complete and circularized when possible) of microbial organisms co-occurring with the targeted species. They represented a large diversity of bacterial and archaeal species, with sea sponge hosts harboring the highest numbers of different prokaryotic species. These new genomes, and those that will be produced with future sequencing data from the ATLASea project, will allow the characterization of microorganisms involved in symbiosis in marine species, and will allow a better understanding of the genetic basis of symbiotic interactions through genomic comparative studies.

Keywords: metagenomic, marine species, genome sequencing, host, associated microbiome

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[*] Speaker

Evolution of bracoviruses, insights from the genome of Toxoneuron nigriceps a parasitoid wasp from Cardiochilinae

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Endogenization of viral sequences is common in vertebrate genomes but also in insects. However, in most cases integration ensured by cellular DNA repair mechanisms has no benefit for the virus, which is thought to slowly decay under neutral selection.

In the case of virus "domestication" the whole endogenized virus is conserved and used to confer new abilities to the host. Domestications to date have only been reported in the suborder Apocrita of Hymenoptera but have occurred several times during the evolution of these parasitic wasps. This results in the production of particles that are used to alter the immune response of another insect, parasitized by the wasp. The particles allow the successful development of wasp progeny, that develop within the body of the parasitized insect. Otherwise, wasp larvae would be killed by immune defenses of the insect. Domestications to date have only been reported in the suborder Apocrita of Hymenoptera but have occurred several times during the evolution of these parasitic wasps. Two families of "domesticated viruses" originating from endogenizations of unrelated viruses have been described, collectively known as polydnaviruses (PDVs) because their particles contain dozens of double stranded DNA circular molecules. Among PDVs, Bracoviruses (BVs) are associated with an estimated 50 000 species of braconid wasps forming a monophyletic group. They are thought to derive from a single integration event of a nudivirus -nudiviruses constitute a sister group of baculoviruses- into the genome of a common ancestor of this group. Bracovirus genes are now widely dispersed in the chromosomes but they act coordinately to produce their particles in specialized cells of wasp ovaries, which morphogenesis resembles that of nudiviruses replicating in the nucleus. Functionally PDV genomes are made of two parts: the genes involved in the production of the particles permanently residing in the wasp genome and those encoding the virulence genes involved in parasitism success, which are present in the genome as proviral segments i.e.: the linear forms of the molecule packaged in the particles and injected to the parasitized caterpillar. High quality genomes have been previously obtained from wasps belonging to two subfamilies of braconid wasps, Microgastrinae and Cheloninae, allowing by comparative genomics to study how a virus evolve in a genome when it confers a benefit to its host. Here we provide the analysis of the bracovirus associated with *Toxoneuron nigriceps* a wasp from a third braconid subfamily, Cardiochilinae. These new data significantly modify the current picture of bracovirus evolution and question whether one or two endogenization events occurred during the evolution of braconid wasps.

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*Speaker

Keywords: polydnavirus, parasitoid wasp, comparative genomics

Identification and expression of potential feminizing factors in the three Wolbachia strains infecting Armadillidium vulgare.

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In several isopod species, *Wolbachia* mainly induce feminization of genetic male embryos, which subsequently differentiate into functional females. In *Armadillidium vulgare*, three feminizing strains, *w*VulC, *w*VulM and *w*VulP, have been identified to date, each in distinct host populations. We recently sequenced the complete genomes of these three strains and, using a comparative genomics approach, identified three putative feminization factors: one ankyrin repeat domain containing protein, one helix-turn-helix transcriptional regulator and one hypothetical protein. These proteins encoded by prophage-associated genes are likely secreted by the Type IV Secretion System. Additionally, all three genomes share a latrotoxin-related protein associated with phage relic genes. We also found that these genes are present in the *f* element, another feminizing factor corresponding to large insertions of *Wolbachia* sequences into the genome of an *A. vulgare* lineage. We analyzed the expression of these potential feminizing candidates, along with other genes thought to be involved in regulatory processes, in the various tissues of *A. vulgare* females infected with either *w*VulC, *w*VulM or *w*VulP. Furthermore, we examined their expression during embryonic development, particularly at the stage when *Wolbachia* load increases dramatically.

Keywords: Isopod crustacean, Armadillidium vulgare, Wolbachia, feminizing factors, embryonic development

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*Speaker

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

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With more than 1,500 species spread across the globe, *Drosophila* is a widespread group that can be found in every continent. Although *Drosophila* usually feed on decaying fruit, the arrival of *Drosophila suzukii* in Europe and America over the last decade - a crop-pest originating from East-Asia capable of feeding on ripening fruits - has led to significant losses in berry production. We suspect that the invasion of *D. suzukii* has profoundly transformed *Drosophila* community in France, which could have cascading effects on their natural enemies. Among these natural enemies, parasitoid wasps are the most common. They can be classified into two main groups based on their host stage preference: pupal parasitoids, which lay their eggs inside *Drosophila* pupae, and larval parasitoids, which target *Drosophila* larvae. However, in Europe, only pupal parasitoids can develop on *D. suzukii*, as larval parasitoids succumb to a strong immune response. In its native range, several larval parasitoid species, such as *Leptopilina japonica*, can parasitize *D. suzukii*. *L. japonica* was first observed in Europe in 2019 and detected in France in 2023 in various locations. We therefore hypothesize that its arrival has also affected *Drosophila* and their parasitoid communities. Thanks to a long-term sampling effort, conducted from 2009 and still ongoing along the Rhône valley, we have identified *Drosophila* and their sympatric parasitoid communities at different points in time and locations to answer two main questions: (1) How does latitude impact community composition, and how has it evolved over time? (2) How have the arrivals of *D. suzukii* and *L. japonica* affected the composition and distribution of those communities?

Keywords: Drosophila suzukii, Leptopilina japonica, Parasitoid wasps, Host, parasitoid interactions, Biological invasions, Community dynamics

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*Speaker

Perte de fonction répétée des protéines de type sexuel chez les champignons Microbotryum

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Chez de nombreuses lignées d'eucaryotes, les protéines impliquées dans la compatibilité sexuelle sont connues pour évoluer plus rapidement que les autres protéines. Chez les champignons, la compatibilité sexuelle est contrôlée par les loci de type sexuel (*MAT*). Chez les basidiomycètes, il existe le plus souvent deux loci *MAT* : le locus *P/R* codant pour des précurseurs de phéromones et des récepteurs de phéromones, et le locus *HD* pour des protéines à homéodomaines, qui s'hétérodimérisent (HD1/HD2). Les combinaisons des différents allèles de ces gènes peuvent générer un très grand nombre de types sexuels chez certaines espèces. Chez la majorité des basidiomycètes, ces deux locus sont trouvés sur des chromosomes différents, et le locus *P/R* est biallélique, avec un polymorphisme trans-spécifique très ancien. Le locus *HD* semble avoir un mode d'évolution plus complexe et variable : il est parfois biallélique, le plus souvent multi-allélique, et il n'y a pas de polymorphisme trans-spécifique à large échelle, mais parfois entre certaines espèces proches.

Les champignons basidiomycètes *Microbotryum* infectent et castrent une grande variété de plantes de la famille des Caryophyllacées. Les génomes de plus de 30 espèces différentes de *Microbotryum* sont disponibles, avec des temps de divergence allant de 0,4 à 11 millions d'années. Chez les *Microbotryum*, s'il existe des espèces ayant les loci *HD* et *PR* sur des chromosomes distincts, de nombreux événements indépendants de liaison entre ces loci ont été décrits. Une telle liaison est avantageuse chez les espèces autofécondantes comme ces pathogènes.

Nous avons étudié l'évolution des gènes *HD* chez *Microbotryum*, révélant l'existence d'allèles partagés par des espèces très distantes. On observe également une influence forte de la liaison entre les loci *HD* et *P/R* sur l'évolution des gènes *HD* : chez les espèces ayant ces deux loci liés, il existe une forte diminution du polymorphisme des gènes *HD*, ainsi qu'une perte de fonction convergente de certaines protéines *HD* dans plusieurs lignées. Ceci démontre une influence claire du système de reproduction sur l'évolution des protéines de compatibilité sexuelle.

Keywords: évolution du sexe, incompatibilité reproductive, microbotryum, type sexuel

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[*] Speaker

Symbiotic control as an alternative of insecticides used to control bedbugs (Cimex lectularius) based on a One Health approach

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Even if bedbugs (*Cimex lectularius*) are currently recognized as non-vector of diseases, their presence in human populations is a major issue in public health. Indeed, bedbug infestations can be associated with chronic anxiety, shame, stigmatization and exclusion that could lead to mental diseases like depression.
To limit the resurgence and spread of *C. lectularius* in France, management methods are mostly focused on the use of insecticides that are not specific, and against which many resistance mechanisms have been selected in bedbugs. In addition, the (mis)use of these chemical products can lead to cancer development of the users and increases environmental pollution. Therefore, costs associated with treatments against *C. lectularius* create social inequalities and participate to the resistance of these insects, environmental pollution and human exposition, leading in fine to a huge economical cost for the public health services. A more sustainable and efficient alternative is thus needed to regulate *C. lectularius.*

As many strict hematophagous insects, bedbugs depend on a nutritional symbiont (here the *Wolbachia* strain wCle) for the provision of a few B vitamins, scarce in the blood but essential to bedbug development and reproduction. *Wolbachia* (strain wBm) is also obligate for the survival of nematodes responsible of filarioses. Inhibiting the multiplication and spread of *Wolbachia* bacteria in its host could thus be an alternative specific method of control.

Recently, Hoffmann et al. developed a molecule (boron-based named Cmpd9) targeting the inhibition of the *Wolbachia* strain wBm, by blocking its aminoacyl-tRNA synthetase activity. This molecule has been tested with success *in vitro* against a LeuRS-tRNA synthetase from the *Wolbachia* strain infecting nematodes (wBm), and in *Aedes albopictus* cells infected by the *Wolbachia* strain wAlb (Hoffmann et al., Sciences advances, 2024). The aim of our study is now to test the inhibition capacity of this compound in different insect species, in particular *C. lectularius.* However, as this insect has a long-life cycle, we will also test the inhibitory capacity of Cmdp9 on fruit flies, which have a shorter life cycle and are easier to rear and handle. The study of the impact of Cmpd9 on other *Wolbachia* strains present in different clades will also allow to test the specificity of its action spectrum.

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[*] Speaker

In conclusion, the findings will emphasize the potential of this new molecule for symbiotic control, offering an alternative to the current use of insecticides for managing *C. lectularius* populations, within the framework of a One Health approach.

Guillaume Hoffmann et al. , (2024) Targeting a microbiota Wolbachian aminoacyl-tRNA synthetase to block its pathogenic host.Sci. Adv.10,eado1453.DOI:10.1126/sciadv.ado1453

Keywords: Cimex lectularius, Symbiotic control, Wolbachia, One Health

Effet de la pollution lumineuse sur l'immunité d'un vertébré nocturne, le crapaud commun.

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Depuis le 19ème siècle, l'urbanisation croissante et l'augmentation des activités humaines se sont accompagnées d'une explosion de l'utilisation de lumières artificielles nocturnes, maintenant considérées comme une source de pollution anthropique majeure. Sur le territoire européen, cette pollution lumineuse affecte désormais la quasi totalité des organismes vivants, à des degrés variables. Bien que les effets de la pollution lumineuse sur la santé de la faune sauvage - et notamment sur l'immunité - sont souvent été suggérés, il existe en réalité très peu d'études sur ces relations en milieu naturel, avec des expositions non expérimentales. L'immunité est une fonction cruciale pour la survie des individus en milieu naturel, où les parasites et pathogènes sont ubiquistes. Une meilleure compréhension des effets de la pollution lumineuse sur l'immunité est donc particulièrement importante, et notamment chez un taxon comme les amphibiens, chez qui les maladies virales et fongiques émergentes sont une source de mortalité massive dans les populations naturelles. Dans cette étude, nous avons caractérisé la condition physique et un large éventail de traits immunitaires chez un amphibien emblématique des zones humides, le crapaud commun, issu de populations naturelles situées sur un gradient d'exposition à la pollution lumineuse. Nous avons trouvé une forte association entre l'exposition à la pollution lumineuse et la masse corporelle ainsi qu'avec certains traits immunitaires. Ces résultats seront discutés en lien avec la caractérisation des communautés bactériennes cutanées et intestinales des mêmes individus.

Keywords: écoimmunologie, pollution lumineuse, pollution anthropique, One Health, microbiote

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*Speaker

Male host genetic background strongly impacts Wolbachia-induced cytoplasmic incompatibility in an invasive pest

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Cytoplasmic incompatibility (CI) is one of the most common reproductive manipulation phenotypes induced in insects by vertically transmitted endosymbiotic bacteria Wolbachia. In recent years, CI has been used to develop environmental-friendly methods for suppressing (incompatible insect technique) or replacing (population replacement strategy) populations of insect vectors. Although crucial to develop effective pest control strategies, we currently lack a comprehensive understanding of the relative impact of Wolbachia and host genotypes in driving the strength of Wolbachia-induced CI. Previous work on whether Wolbachia can induce CI in the invasive agricultural pest Drosophila suzukii has been equivocal. Here, we investigated intraspecific variation in Wolbachia-induced CI in this pest, using crossing assays with D. suzukii strains from both the native (Asia) and invasive area (America and Europe). Overall, we found that CI strength varied between 0% and 70% among D. suzukii strains. Surprisingly, CI strength did not correlate with Wolbachia titers in testes and was neither associated with polymorphism in cif genes known to be generally involved in CI, nor with polymorphism along the entire Wolbachia genome. However, CI strength varied strongly depending on the male host, but not female host genetic background. Our findings suggest that artificial selection of a suitable male host genetic background could represent a promising avenue for the devleopment of incompatible insect technique in species where no strong CI-inducing Wolbachia strain is available.

Keywords: reproductive manipulation, Drosophila suzukii, Whole, Genome Sequencing, introgression, qPCR

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*Speaker

Single-cell phenotypes structure the social life of the amoeba Dictyostelium discoideum

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The 'social' amoeba *Dictiostelium discoideum* is a facultatively multicellular organism. Starvation triggers a life cycle where single cells come together to form multicellular fruiting bodies, essential for efficient dispersal and long-term survival. In this process, part of the cells dies while promoting the survival of the spores. The evolution of self-sacrificial behaviour is more easily understood when all cells in the body share the same genome. It is therefore puzzling to observe that in natural conditions multicellular aggregates tend to be genetic chimeras, so that genetic conflicts are unavoidable. Theory predicts that the spread of genotypes that reap more than their fair share of benefits from the group – the so-called cheaters – should prevent cooperative behaviour to be evolutionary stable. We compared the social performance in chimeras composed of isogenic cells harvested at different phases of population growth, and found that social behavior is modulated by phenotipic plasticity as well as genetic background. By tracing the origin of spore biases to the process of aggregation from single cells, we explored the single-cell determinants of differences in social behaviour. Finally, we show that biases due to non-genetic sources of phenotypic variation are comparable to genetic effects, and can dominate over genetic differences, overturning classical definitions of social behaviour. Our observations suggest that inevitable heterogeneity in cell-level physical properties may act – by breaking heritability of social behaviour – as a hindrance to the evolutionary success of cheaters, and this even when social interactions within the multicellular body are neglected. We use mathematical models for heterogenous aggregating agents to explore the possible role of mechanical differences in the evolutionary maintenance and emergence of aggregative multicellular life cycles.

Keywords: Social behavior, aggregation, conflict, Dictyostelium discoideum

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*Speaker

Discovery of endogenous viral elements in Campopleginae wasps suggest widespread nudivirus domestication

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Nudiviruses, large dsDNA viruses related to baculoviruses, can be endogenized in the genomes of certain parasitoid wasp species, allowing the production of viral particles essential for parasitism success. Alphanudivirus genes, within the genome of *Venturia canescens*, an ichneumonid wasp of the Campopleginae subfamily, allow the production of Virus-Like Particles (VLPs) containing virulence factors. The description of many species phylogenetically related to *V. canescens*, in particular from the *Campoplex* genus, offers the opportunity to describe evolutionary processes involved in viral domestication. The sequencing of the two Campoplex species *C. capitator* and *C. nolae*, allowed the identification of an endogenized nudivirus corresponding to the same endogenization event as the one described in *V. canescens*. Our results show that endogenization of nudiviruses in these parasitoid wasps has repeatedly led to the conservation of the viral RNA polymerase function, allowing the production of functional VLPs. Furthermore, electron microscopy and proteomic approaches revealed that the particles produced by Venturia and Campoplex parasitoid wasps are very similar in morphology and composition. However, interestingly, the virulence proteins contained within the particles were shown not to be the same. This is possibly due to the different host ranges of these wasps, which may have exercised different evolutionary pressures leading to the recruitment of different virulence proteins.

Keywords: parasitoid wasp, nudivirus, campopleginae, Venturia canescens, Campoplex

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*Speaker

Variation in the duration of the immune protection after priming stimulation among populations of Tenebrio molitor

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Immune priming refers to an invertebrate individual's ability to improve its immune response following an initial, non-lethal exposure to a pathogen. This form of innate "immune memory" has likely evolved as a result of repetitive challenges by the same pathogens throughout the invertebrate's lifetime. Adults of the mealworm beetle, *Tenebrio molitor*, exhibit interindividual variation in the duration of the immune protection conferred by the priming response to a standard pathogenic challenge. Immune priming incurs fitness costs, which generate trade-offs with other life-history traits and may, therefore, contribute to variation in its expression. Allocating resources to immune priming should depend on the likelihood of future survival and reproduction, which is a function of mortality risks caused by re-infection exposure. Consequently, short-lived individuals may have a low probability of being exposed to repeated infections by the same pathogen, whereas individuals with extended longevity should benefit from investing in immune priming because they are more likely to face re-infection.

This study investigated whether investment in immune priming, estimated as the duration of the immune protection after priming stimulation, is associated with adult longevity among three genetically distinct populations of *T. molitor* that exhibit contrasted life histories. To this end, age-controlled adults from each population were immune-primed 14 days post-eclosion with a standard dose of inactivated *Bacillus cereus* and then subsequently infected with the live bacterium at different time intervals post-priming stimulation (i.e., 30, 45, 60, 75, and 90 days post-injection). Survival was monitored for 15 days following infection to assess the persistence of the protective effect induced by priming. Long-lived insect populations are expected to exhibit sustained late-life protection than short-lived ones.

Keywords: Immune priming, Tenebrio molitor, duration, survival

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[*] Speaker

Transcriptional response against biocontrol agents in the agricultural pest Spodoptera frugiperda (Lepidoptera: Noctuidae)

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Spodoptera frugiperda (Lepidoptera: Noctuidae) is a major pest of cereal cultures and has become a severe threat in the last few years due to its fast world-wide invasion from its natural range in the Americas. Since then, a major effort is made to control this pest infestation in corn fields, preferably by limiting the usage of chemical pesticides that can promote the emergence of resistant strains. Biological control could be a more sustainable solution, by the use of entomopathogenic agents such as insect specific viruses, parasitoids or entomopathogenic nematodes. However, the targeted caterpillars can mount a powerful and specific immune response against these agents. Understanding the mechanistic details of the insect immune system can provide insight into the ecological parameters of its success. To this effect, we assembled a reference genome for this pest and thoroughly annotated the immunome of *S. frugiperda.* This allowed us to investigate the transcriptional response, at different time-points and immune tissues of *S. frugiperda* caterpillars infested with different biological agents. We described that, in the case of the nemato-bacterial complex *Steinernema carpocapsae/Xenorhabdus nematophila*, the caterpillar can mount a rapid response against each member of the complex, even though ultimately succumbing to the pathogen. In the process, we identified new actors of immunity that are specific of Noctuidae and have been acquired by horizontal gene transfer from bacteria and are investigating whether they are new antimicrobial effectors or if they participate in the specificity of the response. Finally, we are also investigating the molecular basis of immune priming against nematodes bacterial symbionts.

Keywords: Spodoptera frugiperda, Pest, Entomopathogenic nematodes, Interaction, Immune response

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[*] Speaker

Je suis un écosystème dans l'écosystème : la santé unique à tous les étages

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Nous ne vivons pas isolés. Entre conflit et coopération, la très grande majorité des organismes, humain compris, interagissent d'abord avec l'ensemble des microorganismes qui constituent leur microbiote. Ces interactions avec notre 'moi microscopique' construisent les individus comme des écosystèmes et nous interrogent sur notre propre individualité.
Mais cet individu écosystème est aussi la cible et l'acteur d'un environnement plus large avec lequel il interagit et qui interroge ses interdépendances et son rapport au monde.
Mais au bout du compte, qui suis-nous, qui-sommes-je ?

Keywords: Individu, microbiote, écosystème, environnement, santé unique

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[*] Speaker

Symbiotic communities of Planococcus ficus (vine mealybug)

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The vine mealybug (*Planococcus ficus*) is a major pest of grapevines and the principal vector of Grapevine leafroll-associated virus 3 (GLRaV-3), the most widespread virus affecting vineyards. Recent findings suggest that gut-associated bacterial symbionts in hemipterans may influence their vectoring capabilities. This project investigates the composition and dynamics of the gut microbiota of *P. ficus* populations collected from vineyards symptomatic for GLRaV-3 using metagenomic and classical microbiology methods. As preliminary results, we have successfully isolated a *Serratia symbiotica* strain and identified what is likely a new genus within *Acetobacteraceae*, clustering with known gut symbionts of hymenopterans.

Keywords: mealybug, gut microbiota, obligatory symbiosis, metagenomics

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[*] Speaker

Multi-scale evolutionary convergence of nutritional symbionts in ticks

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Context : Nutritional symbiosis is crucial for tick growth, with many tick species associating with intracellular bacteria providing them B vitamins, such as Coxiella-like endosymbionts (CLE) or Francisella-like endosymbionts (FLE). Understanding the tissue tropism of these endosymbionts is vital for unraveling the complex relationships between ticks and their microbial partners.

Objective : This study examines tissue tropism convergence among CLE and FLE endosymbionts across various soft and hard tick species: Ornithodoros moubata, Ornithodoros maritimus, Dermacentor marginatus, and Dermacentor reticulatus. Material and Methods : Both male and female specimens of these tick species were dissected to analyze their Malpighian tubes, testes or ovaries, salivary glands, midgut, and body. Subsequently, qPCR was used to assess CLE and

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*Speaker

FLE distribution in organs, Results : Preliminary findings reveal a convergence in tissue tropism, particularly notable in the Malpighian tubes and ovaries, where CLE and FLE endosymbionts were consistently abundant regardless of the tick species.

Discussion : Ovarian infection indicates maternal transmission of endosymbionts to developing oocytes, leading to a typically higher quantity of CLE or FLE in females compared to males. The high density in Malpighian tubules supports their nutritional role, potentially in B vitamins biosynthesis.

Conclusion : Further research is required to elucidate the significance of these organs in nutritional symbiosis.

Keywords: nutritional symbiosis

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