



Poitiers
10 – 12 Mai, 2023



Programme & infos

<https://reid-2023.sciencesconf.org/>

Contact

reid.2023.poitiers@gmail.com



Participation gratuite pour les étudiants, doctorants et post-doctorant

Permanents : 55€ TTC

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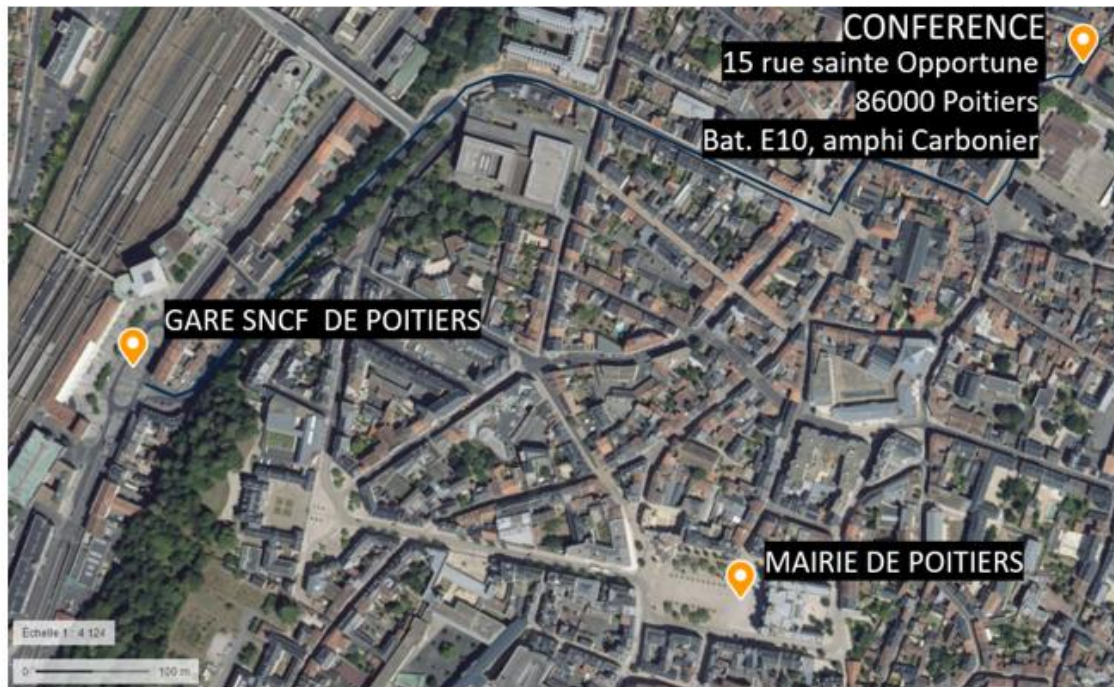
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Programme



Wednesday 10/05/2023		
09:00	Conference opening	
09:15	<u>keynote speaker</u> : Claude Loverdo	Bacteria in the digestive tract : interaction with the immunity system and evolution in a flow.
10:00	Cheutin Marie-Charlotte	The gut microbiota of the European forficula does not promote sociality in its host
10:15	Alizon Samuel	Modelling vaginal microbiota community dynamics
10:30	Coffee break	
11:00	Gomes Elisa	Pesticides impair gut bacterial diversity in honeybee queens (<i>Apis mellifera</i>)
11:15	Huguet Elisabeth	Nudivirus domestication in Campopleginae parasitoid wasps
11:30	Terrasson Hugo	Bacteriocyte-specific Cysteine-Rich (BCR) peptides form a new aphid-specific defensin-like family and are promising regulators of aphid symbiosis
11:45	Drezen Jean-Michel	Peaceful relationships in an old symbiotic couple
12:00	Lunch	
13:45	Ouverture session grand public	
14:00	Alizon Samuel	Réconcilier Pasteur et Darwin
14:45	Laffitte Maud	Transmission de la peste de l'écrevisse dans les populations naturelles en France
14:55	Delavat François	Découverte de nouvelles bactéries bénéfiques dans nos océans
15:05	Destoumieux-Garzon Delphine	La croisière en mer des agents pathogènes
15:50	Coulon Mathias	Tolérance au stress hydrique, fonctionnement racinaire et flux de carbone optimisés, pour une amélioration du rendement chez le pois
16:00	Claveyroles Noémie	<i>Xenorhabdus</i> : bactéries tueuses d'insectes et leurs métabolites
16:10	Morand Serge	Epidémies et l'émergences des maladies infectieuses : liens avec les changements d'usage des terres et la perte de biodiversité.
17:00	Départ balade Street Science	
19:30	Lets meet at "l'îlot Tison"	Apéro, food truck (Chem. de Tison, 86000 Poitiers)



Thursday 11/05/2023

09:00	<u>keynote speaker:</u> Louis Lambrechts	Larval ecology, bacterial microbiota and mosquito vectorial capacity
09:45	Santillán Guayasamín Soledad	Impact of larval density and nutritional stress on mosquito life history traits and vectorial capacity
10:00	Isaïa Julie	Impact of within-vertebrate host parasitaemia on the temporal dynamics of Plasmodium in mosquitoes
10:15	Cozzarolo Camille-Sophie	Infection with an acanthocephalan helminth reduces anxiety-like behaviour in crustacean host
10:30	Coffee break	
11:00	Joly Cloé	One parasite can hide another!
11:15	Souq Léa	Delineating species in a group of freshwater snails that transmit fasciolosis to humans, livestock and wildlife in the Americas
11:30	Travers Agnès	Emergence et expansion clonale de <i>Vibrio aestuarianus</i> , pathogène d'huître
11:45	Morot Amandine	Type III secretion system: another role than virulence? The abalone- <i>Vibrio harveyi</i> pair as a model.
12:00	Jacquot Maude	Genetic diversity of the Ostreid Herpesvirus type 1
12:15	Lunch : Buffet offered by REID	
14:00	<u>keynote speaker:</u> Clara Torres-Barcelo	Phages of plant pathogenic bacteria: ecology, evolution and biocontrol
14:45	Billard Estelle	Testing for an effect of multiple infections on the evolution of the rice yellow mottle virus (RYMV) in Burkina Faso
15:00	Leclerc Laétitia	Early modulation of the jasmonate pathway in rice (<i>Oryza sativa</i>) by the oral microbiota of <i>Spodoptera frugiperda</i> larvae
15:01	Delavat François	Genetic and physiological insights into the diazotrophic activity of a non-cyanobacterial marine diazotroph
15:30	Charriere Guillaume	Ecology of free-living amoebae and varying predation capacity against pathogenic vibrios in Mediterranean coastal environments.
15:45	Samba Louaka Ascel Regis	Molecular atlas of <i>Acanthamoeba castellanii</i> remodeling during cyst formation
16:00	NEB	new england biolabs
16:15	Coffee break	



16:45	De La Forest Divonne Sébastien	Characterization of the cytological, transcriptomic and functional diversity of <i>Crassostrea gigas</i> hemocytes
17:00	Crosland Agathe	Immune senescence as a function of environmental-mediated changes in growth duration
17:15	Goerlinger Alexandre	Efficiency of immune priming by oral route or septic wounding in <i>Tenebrio molitor</i>
17:30	Meunier Joël	Trans-generational immune priming occurs after oviposition in the European earwig
17:45	Photo of REID Participants	
18:00	Poster session & Cocktail	
Friday 12/05/2023		
09:00	<u>keynote speaker</u> : Chloé Delmas	Impact of drought on biotic interactions in grapevines: a pathophysiological approach
09:45	Monnereau Benoit	Sugar transport and resistance to <i>B. cinerea</i> in grapevine
10:00	Clavé Corentin	Plant-mediated effects of the entomopathogenic fungus <i>Beauveria bassiana</i> on <i>Spodoptera littoralis</i>
10:15	Cambon Marine	Chemical cues from bark boring beetle larvae trigger the proliferation of <i>Brenneria goodwinii</i> , the main bacterial pathogen in Acute Oak Decline
10:30	Coffee break	
11:00	Poulain Marius	Feeding, sex, and development shape the relative quantity of <i>Wolbachia</i> , the nutritional obligatory symbiont of bed bugs
11:15	Deconninck Gwenaëlle	Invasive success of <i>Drosophila suzukii</i> : Is <i>Wolbachia</i> playing a role?
11:30	Conclusion & closure of the conference	
12:00	END	



Poster session

Nom	Titre
Vazquez Antonio	Alien introductions and the increase of snail-borne diseases in Europe: the case of trematode spill-back by lymnaeid snails
Cassese Ilona	Coffee trees, floral scents and wild entomofauna or how to successfully pollinate in a new agricultural landscape?
Gouthier Laurine	Effects of metal contamination on fish-pathogen interactions
Jorge Raphael	Functional analysis of interactions between bed bugs and their nutritional symbiont <i>Wolbachia</i>
Mohamed Djawad Mohamed Hassani	Influence of ecological (season, site), and physiological (sex and age) factors on the diversity and prevalence of intestinal parasites in two populations of chimpanzee (<i>Pan troglodytes</i>) in southeastern Gabon
Vignal Emmanuel	Le séquençage d'ARNm sur cellules uniques appliqué à deux espèces de bivalves : une vision transcriptomique des populations hématocytaires.
Caro Audrey	Unexpected associated bacteria with <i>Crassostrea gigas</i> juveniles during mortality events
Froustey Nicolas	Small game's habitat management: an experimental approach in favour of Mediterranean avian biodiversity?
Alba Menendez Annia	Environmental parameters and vector competence in natural ecosystems: the microbiome and the snail host <i>Pseudosuccinea columella</i> as main actors
Lheraud Baptiste	Investigating <i>Wolbachia</i> symbiont-mediated host protection against a bacterial pathogen using a natural <i>Wolbachia</i> nuclear insert
Jean Louis Wilfrid	Compromis entre soins maternels et immunité chez <i>Forficula auricularia</i> , le perce-oreille.
Dellong Amélie	Human DNMT3A inhibitors are potential active epigenome modulators in invertebrates
Carole Vincent-Monégat	Compartmentalization in bacteriomes protects endosymbionts from their insect host immunity

Résumé des présentations (par ordre alphabétique)

Un certain nombre de résumés n'ont pas encore été déposés sur le site. Ils seront rajoutés ultérieurement.



Réconcilier Pasteur et Darwin

Samuel Alizon*¹

¹Centre interdisciplinaire de recherche en biologie – Collège de France, Institut National de la Santé et de la Recherche Médicale, Centre National de la Recherche Scientifique – France

Résumé

Le SARS-CoV-2 a fait la triste démonstration que l'évolution virale peut conduire à des catastrophes sanitaires. Antibiorésistance, VIH, grippe... Contrairement à l'optimisme majoritaire des années 60 qui envisageait la fin des maladies infectieuses, les fléaux persistent. Leur étude est assez divisée car au cours du XXe siècle, la biologie s'est scindée en deux branches, l'une s'attachant à comprendre le fonctionnement du vivant en répondant à la question "comment ?", l'autre étudiant les causes évolutives et le "pourquoi?". Le microbiologiste Louis Pasteur et le naturaliste Charles Darwin sont des figures emblématiques de ces deux biologies et de leurs différences. D'ailleurs, bien que contemporains, ils n'ont jamais échangé. Pourtant, de nombreux travaux démontrent comment la microbiologie peut apprendre des sciences de l'écologie et de l'évolution et réciproquement. En santé publique, seule une approche réconciliant ces deux visions de la biologie peut permettre d'avoir un temps d'avance dans notre course co-évolutive avec les microbes.

Mots-Clés: évolution, microbiologie, virus, bactérie, maladies infectieuses : écologie, virulence, résistance, traitements, santé publique

*Intervenant

Xenorhabdus : bactéries tueuses d'insectes et leurs métabolites

Noémie Claveyroles*¹

¹Diversité, Génomes Interactions Microorganismes - Insectes [Montpellier] – Université de Montpellier
– France

Résumé

Les produits phytosanitaires chimiques, utilisés contre les insectes ravageurs de culture, sont néfastes pour la biodiversité, l'environnement et la santé humaine. L'utilisation de petits vers ronds mangeurs d'insectes : les nématodes, est une piste prometteuse d'alternative biologique. Pour infester des insectes et se nourrir de l'intérieur de leurs corps, ces nématodes sont aidés par leurs bactéries symbiotiques : *Xenorhabdus*.

Ensemble, nématodes et bactéries ont un cycle de vie bien particulier : les nématodes pénètrent dans le corps de larves d'insectes par les orifices naturels puis libèrent les bactéries *Xenorhabdus* à l'intérieur de l'insecte, causant la mort des larves par septicémie. Les nématodes et bactéries utilisent le cadavre de l'insecte comme gîte et ressource nutritive pour se développer. Après reproduction, les nouveaux nématodes se réassocient avec leur bactérie. Enfin, ils quittent le corps de la larve et partent dans le sol en quête d'un nouvel insecte à infecter.

Au cours de leur cycle de vie, les bactéries *Xenorhabdus* produisent un arsenal de métabolites secondaires avec des fonctions variées : tuer l'insecte, se protéger, communiquer, se débarrasser des compétiteurs microbiens etc. Parmi ces molécules, une famille d'antimicrobiens nommés " PAX " pourrait présenter des fonctions multiples.

Mon sujet de thèse vise à comprendre les rôles de ces molécules PAX dans les différentes phases du cycle de vie de *Xenorhabdus* : dans la phase pathogène chez l'insecte, dans la phase cadavre de l'insecte (au cours de laquelle de nombreux acteurs microbiens et nématodes sont en interactions), et dans la phase de réassociation avec les nématodes hôtes. A cet effet, des approches de microbiologie, de biochimie, de pathologie sur différents modèles d'insectes ravageurs, et de nématologie sont utilisées.

Mots-Clés: bactéries entomopathogènes, métabolites secondaires, antimicrobiens, nématodes, bio-contrôle, insectes ravageurs

*Intervenant

Tolérance au stress hydrique, fonctionnement racinaire et flux de carbone optimisés, pour une amélioration du rendement chez le pois

Mathias Coulon^{*1}, Léo Bunel¹, Benoit Porcheron¹, Florence Thibault¹, Caroline Artault¹, Laurence Maurousset¹, Joan Doidy¹, Cecile Vriet¹, and Nathalie Pourtau¹

¹Sucres Echanges Végétaux-Environnement – Ecologie et biologie des interactions – France

Résumé

Le pois (*Pisum sativum*) est une plante d'intérêt agroécologique de la famille des légumineuses et cultivée pour la haute valeur nutritionnelle de ses graines. Ses rendements sont fortement impactés par des épisodes de sécheresse de plus en plus fréquents et précoces, du fait du réchauffement climatique.

En condition de contrainte hydrique, les relations source/puit sont modifiées et la réallocation du carbone dans la plante induit une compétition entre les deux organes puits, à savoir les racines et les graines. Ces modifications peuvent entraîner à terme, l'avortement des fleurs et des graines et conduire à une diminution des rendements.

L'objectif principal de notre étude est de mieux comprendre le rôle du développement racinaire et les mécanismes de réponse du pois au déficit hydrique, ainsi que les effets de produits biostimulants dont des microorganismes bénéfiques sur sa tolérance à ce stress.

Une première partie de ces travaux consiste à identifier des variétés de pois présentant des niveaux contrastés de tolérance au déficit hydrique, et d'explorer l'importance du développement du système racinaire dans la réponse du pois à ce stress.

L'objectif de la seconde partie de notre étude est d'identifier des produits biostimulants, dont des rhizobactéries bénéfiques de type PGPR ("Plant Growth Promoting Rhizobacteria"), capables de conférer une meilleure tolérance au déficit hydrique, potentiellement via un effet sur l'allocation des ressources carbonées vers les racines et la rhizosphère.

Enfin la troisième partie, se concentrera sur la caractérisation des acteurs moléculaires jouant un rôle majeur dans la tolérance du pois au déficit hydrique et d'explorer les modes d'action des produits biostimulants.

Ces travaux de recherche permettront d'identifier des marqueurs moléculaires qui contribueront à sélectionner de nouveaux génotypes du pois plus tolérants à la sécheresse.

Mots-Clés: Pois, Déficit hydrique, Architecture racinaire, Biostimulants, PGPR, Flux de carbone

*Intervenant

Découverte de nouvelles bactéries bénéfiques dans nos océans

François Delavat*¹

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Résumé

Les océans sont souvent pauvres en azote, élément chimique pourtant indispensable au fonctionnement de tout organisme vivant. Certaines bactéries jouent un rôle majeur dans le fonctionnement de ces écosystèmes, en étant capables d'introduire de l'azote utilisable par tous (animaux et plantes) à partir du diazote, non utilisable. De par leur importance écologique, ces bactéries bénéfiques ont été largement étudiées ces dernières décennies, et ces études montrent que des bactéries appelées Cyanobactéries sont responsables de ce métabolisme. Récemment, des approches ont révélé l'existence d'autres bactéries, capables d'introduire cet azote utilisable dans les océans. Cependant, leur mode de vie, leur fonctionnement et leur importance dans les écosystèmes marins sont encore largement méconnus. Une des questions qui se pose est notamment la suivante : comment ces bactéries sont capables de transformer le diazote, alors que cette transformation est inhibée par l'oxygène pourtant présente dans les océans ? Dans ce cadre, nous nous sommes intéressés à une de ces nouvelles bactéries, isolée d'un intestin d'oursin, afin de comprendre comment celle-ci pouvait croître dans un environnement pauvre en azote et de poser les bases d'une étude approfondie de cette activité. Grâce à des approches de microbiologie, nous avons pu montrer que cette bactérie va produire une matrice appelée biofilm, permettant de diminuer la diffusion de l'oxygène et donc permettant la production d'azote utilisable. Par ailleurs, elle est capable de vivre à des concentrations très faibles en oxygène, lui permettant de produire de l'azote utilisable, sans inhibition. Enfin, nous avons pu développer un outil permettant de rechercher les gènes bactériens impliqués dans cette transformation, qui ouvrent des perspectives extrêmement intéressantes sur l'étude de ces bactéries méconnues et de leur rôle dans nos océans.

Mots-Clés: écosystème marin, azote, bactérie

*Intervenant

La croisière en mer des agents pathogènes

Delphine Destoumieux-Garzón*¹

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Résumé

La circulation des agents infectieux a augmenté significativement au cours de la dernière décennie avec la propagation et l'émergence d'épizooties, de zoonoses et d'épidémies. Alors que les océans et les mers couvrent les deux tiers de notre planète, le milieu marin reste peu exploré au travers du prisme One Health (une seule santé). Nous ignorons largement à quel point il contribue et pourra contribuer au risque infectieux à l'échelle planétaire. Les invertébrés marins, qu'ils soient sauvages ou élevés, habitent les écosystèmes marins côtiers, dans lesquels ils subissent les contaminations biotiques et abiotiques d'origine anthropique, des proliférations d'algues toxiques et le changement climatique. Des crises majeures les affectent depuis plusieurs années causant d'importants dommages aux écosystèmes ainsi que des pertes économiques conséquentes. Nous nous sommes concentrés sur les bivalves marins qui sont d'excellents indicateurs de la santé environnementale en tant qu'organismes filtreurs. Nous avons caractérisé la nature polymicrobienne du syndrome de mortalité de l'huître du Pacifique, qui affecte l'espèce *Crassostrea gigas* à l'échelle mondiale et est fortement dépendant de la température. Les travaux sur cette maladie ont montré que les populations d'huîtres de la côte atlantique française sont des réservoirs de virus avec une grande diversité génétique et que les transferts d'animaux contribuent à la propagation de l'agent causal de la maladie, le virus OsHV-1, à travers la France. Une dispersion similaire a été observée à l'échelle européenne pour un autre agent pathogène important des huîtres, *Vibrio aestuarianus* causant des mortalités chez les huîtres adultes. Encore plus surprenant, il a été observé que des cancers transmissibles affectant les moules se sont propagés au travers des océans, vraisemblablement à la faveur des transports maritimes. Tout récemment enfin, une prévalence importante de gènes de résistance aux antibiotiques a pu être mise en évidence dans les milieux marins côtiers, y compris dans la faune sauvage et dans les coquillages d'élevage. Une meilleure connaissance des conséquences des activités humaines et du changement global sur les milieux marins côtiers est désormais nécessaire pour comprendre la dynamique des agents infectieux en milieu marin et mieux gérer le risque sanitaire.

Mots-Clés: One Health, zoonose, espèce sentinelle

*Intervenant

Transmission de la peste de l'écrevisse dans les populations naturelles en France

Maud Laffitte*¹ and Grandjean Frederic¹

¹Ecologie et biologie des interactions – Université de Poitiers, Centre National de la Recherche Scientifique – France

Résumé

Parmi les trois espèces d'écrevisses autochtones présentes en France métropolitaine, l'écrevisse à pattes blanches *Austropotamobius pallipes* est la plus largement répartie sur le territoire. Cette espèce, aujourd'hui menacée par de nombreux facteurs d'origine anthropique dégradant la qualité et la quantité d'eau, fait partie de la liste rouge nationale UICN. Ce déclin s'explique également par l'introduction d'espèces d'écrevisses invasives plus compétitives que l'écrevisse à pattes blanches entraînant un remplacement progressif des populations. Par ailleurs, ces espèces allochtones sont porteuses saines d'un pathogène, *Aphanomyces astaci*, qui est responsable de la maladie appelée peste de l'écrevisse laquelle décime les populations autochtones qui y sont hautement sensibles. Face à ce risque épidémique, il est urgent de mieux comprendre les mécanismes impliqués dans la transmission du pathogène ainsi que ses impacts sur les populations autochtones. Dans ce contexte, nous avons mené une approche épidémiologique afin d'étudier les taux de prévalence du pathogène dans les populations d'écrevisses allochtones en milieu naturel ainsi que leur rôle dans les mortalités d'écrevisses autochtones. Dans un second temps, nous nous sommes intéressés aux réponses immunitaires d'une espèce autochtone, *Astacus astacus* suite à une infection, en condition contrôlée afin d'obtenir des profils d'expression de gènes impliqués dans la réponse immunitaire. Ces résultats permettront de mieux comprendre les mécanismes d'infection et de transmission du pathogène en milieu naturel et d'orienter la gestion et la protection des populations d'écrevisses autochtones en France.

Mots-Clés: Ecrevisses, Peste de l'écrevisse, Transmission, Prévalence, Immunité

*Intervenant

Modelling vaginal microbiota community dynamics

Tsukushi Kamiya¹ and Samuel Alizon^{*1}

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Résumé

Human vaginal microbiota stands out because of its composition, evolution, and impact on health. Studies identified 5 main community state types (CST), most of which are dominated by a single *Lactobacillus* species. One of these, CST-IV, stands out because of its high diversity, high pH, and abundance of anaerobic bacteria such as *Gardnerella*, *Prevotella*, or *Atopobium*. Furthermore, this CST is also associated with higher health risks. Although some factors have been associated with vaginal microbiota composition, we still lack a clear picture of the community dynamics that can be observed within a year. We developed a community ecology model that captures the interaction between a *Lactobacillus* CST and a CST-IV. We show how lactic-acid-mediated and glycogen-mediated interactions can lead to changes in dominance throughout the menstrual cycle. We also use data from the PAP-CLEAR clinical study that followed 149 women for a median duration of 290 days to validate the findings of the model. Overall, this better understanding of the community state types variation calls for models with additional levels of details to include more populations, and for more detailed metabolomic data to validate our findings.

Mots-Clés: vaginal, microbiota, diversity, environment, bacteria, mathematical model

*Intervenant

Testing for an effect of multiple infections on the evolution of the rice yellow mottle virus (RYMV) in Burkina Faso

Estelle Billard^{*1}, Abalo Itolou Kassankogno², Drissa Sérémé², Issa Wonni², Nils Poulicard¹, Mathilde Hutin¹, Martine Bangratz¹, Aurore Comte¹, Sebastien Cunnac¹, Gaël Thebaud³, Olivier Cotto³, Phonsiri Saengram¹, Abdoul Kader Guigma², Agnès Pinel¹, Eugénie Hébrard¹, and Charlotte Tollenaere¹

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Résumé

Pathogens actually share host plants with a myriad of other microbes, some of them being pathogenic. Multiple infections, or ‘co-infection’, occur when a single host plant is infected by various pathogen species, or genotypes. This is known to affect symptom expression and pathogen multiplication in various pathosystems. However, the population-scale consequences remain poorly explored. Our current project aims at testing whether multiple infections impact the evolutionary trajectories of pathogen populations and drive epidemiological outcome.

We focus on rice in Sub-Saharan Africa, a crop of increasing importance because of human population growth and change in food habits, and two major rice pathogens: the Rice yellow mottle virus (RYMV) and the bacteria *Xanthomonas oryzae* (*Xo*). Our preliminary results showed within-plant interactions between these two pathogens in case of experimental co-infection, identified hotspots of the two diseases in Burkina Faso, and initiated the follow-up of genetic and pathogenic diversity of these pathogens. We investigate population-scale consequences of inter-species (RYMV-*Xo*) and intra-species (various RYMV genotypes) co-infections.

To this purpose, a two-year survey was performed in two sites. Simultaneous molecular detection of RYMV and *Xo* is ongoing for all collected samples (ca 3 000 samples). Further molecular work will allow to describe the genetic structures of RYMV and *Xo* populations, and to test whether co-infections affect the population genetic structure of the pathogens involved. In addition, we will use experimental infections to further document the diversity of outcome in co-infection, and to follow-up the evolution of viral RYMV populations in different contexts (mono *vs* co-infections).

Overall, this project integrates each pathogen in the microbial community of its host, with a population-scale approach, and a particular focus on evolution and epidemiology. As it applies to a pathosystem of strong agronomic importance, we expect valuable results for integrated control of crop diseases in Sub-Saharan Africa.

*Intervenant

Chemical cues from bark boring beetle larvae trigger the proliferation of *Brenneria goodwinii*, the main bacterial pathogen in Acute Oak Decline

Marine Cambon^{*1,2}, Gareth Thomas³, Michael Crampton⁴, John C. Caulfield³, James Doonan⁵, Usman Hussain¹, Sandra Denman⁴, Vuts Jozsef³, and James McDonald²

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Résumé

Interactions between insects and bacteria often play a key role in plant disease, and bacteria can produce chemical signals which influence insect behaviour. However, little is known about the impact of insect chemical cues on bacteria in plant pathosystems. Here, we investigated these inter-kingdom interactions in a tree disease called Acute Oak Decline (AOD). AOD is characterised by stem bleeds, bacterial inner bark necrosis and larval galleries of the bark-boring beetle *Agilus biguttatus*, eventually leading to tree death. The tissue necrosis is mainly due to *Brenneria goodwinii*, a bacterium known to possess several putative virulence genes. These genes are over-expressed in tree hosts that are invaded by the bark-boring beetle *Agilus biguttatus*. In this study, we characterised the chemical cues produced by the beetle larvae using liquid chromatography and gas spectrometry. We then tested their effect on bacterial growth and gene expression using *in vitro* cultures and RNAseq. Our results show that chemical cues from the beetle larvae are bioactive toward the bacterial pathogen. They increase its growth rate, increase its final density, and we are investigating the modifications in its gene expression profile including putative virulence genes. Our work confirms that this multi-kingdom interaction plays a significant role in the establishment of the disease and may require more attention in our attempts to mitigate AOD. We also show that bacteria can respond to chemical cues from insects, which have rarely been studied and may be important in other plant diseases.

Mots-Clés: oak decline, insect, bacteria interaction, RNAseq, plant pathogen

*Intervenant

Ecology of free-living amoebae and varying predation capacity against pathogenic vibrios in Mediterranean costal environments.

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Résumé

Free-living amoeba (FLA) diversity, population dynamics and niche specialization in marine environment remain poorly described. In a previous study, we observed a low diversity of amoebae in oyster farming area in the Thau lagoon in the south of France, with mostly Vannellid amoebae. Herein, we wondered whether this low diversity is particular to this oyster farming environment and whether the presence of pathogenic vibrios potentially resistant to grazing can shape FLA communities. To address these questions, we sampled FLA monthly over an entire year along the Mediterranean coast, in three distant and contrasted sites, using various nutritive sources to follow FLA dynamics and predation capacity. By performing 18S barcoding, as well as clonal isolation, we found a diversity of amoebae belonging to *Vannellidae*, *Tubulinea*, *Rhizamoeba*, *Vermistella*, *Flabellulidae* and *Paramoebidae* families, and isolated a total of 301 clones representing this diversity. Our results reveal that beyond seasonal variations the overall FLA diversity found in the sediments is higher and different from the diversity found in the water column. Moreover, FLA diversity found in the sediment is specific for each sampling sites on the contrary to the FLA diversity found in the water column. Finally, we observed different predation capacity of phylogenetically related groups of FLA against different vibrios, that are bivalve opportunistic pathogens, suggesting complex predator-prey interactions that could play a role in pathogen dynamics in these environments.

Mots-Clés: microbial ecology, predator prey interactions, pathogen dynamics

*Intervenant

Le microbiote intestinal du forficule européen ne favorise pas la socialité de son hôte

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Résumé

Les animaux portent au sein de leur tractus entérique une large diversité de microorganismes communément appelé microbiote intestinal. Alors que ses fonctions métaboliques pour son hôte ont été largement étudiées, de récentes théories lui associent un rôle majeur dans l'évolution de la socialité. La modulation du comportement de l'hôte par les parasites est déjà bien connue. De ce fait, les communautés microbiennes ne pourraient-elles pas aussi inciter leur hôte à se regrouper avec d'autres individus pour favoriser leur propre transmission? Cette hypothèse n'est restée que théorique et n'a jamais été étudiée empiriquement. Dans cette étude, nous proposons de la vérifier sur le modèle du forficule européen (*Forficula auricularia*), un insecte à la vie sociale facultative, pouvant être solitaire ou social. La variabilité inter-individuelle et la compréhension de ces choix de comportements entre socialité ou solitude restent marginalement étudiées et restent non-élucidées. Nous avons donc mesuré dans un premier temps la variabilité inter-individuelle du comportement d'agrégation et sa consistance chez 385 forficules européen femelles afin de tester si la variabilité de ce comportement reflétait la variabilité de son microbiote intestinal. Enfin, via une expérience de transmission de contenu intestinal, nous avons cherché à vérifier si l'acquisition de microorganismes provenant d'individus grégaires pouvait augmenter la grégarité d'individus receveurs à tendance solitaire. Contrairement à nos prédictions, les communautés microbiennes entériques n'étaient pas expliquées par le degré de grégarité de leurs hôtes. Par ailleurs, le nouveau degré d'agrégation observé chez les individus à tendance solitaire n'était pas déterminé par le degré de socialité du donneur. De ce fait, nos résultats suggèrent que la socialité chez le forficule européen n'est pas due à l'action directe de son microbiote intestinal. De façon plus générale, cette expérience placée au référentiel de l'individu hôte suggère que le microbiote intestinal semble jouer un rôle limité d'un point de vue intrinsèque sur la transition d'une vie solitaire à groupée chez les insectes.

Mots-Clés: Socialité facultative, Agrégation, Microbiote intestinal, Transplantation intestinale, Dermaptère

^{*}Intervenant

Plant-mediated effects of the entomopathogenic fungus *Beauveria bassiana* on *Spodoptera littoralis*

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Résumé

Beneficial microorganisms are able to promote plant growth and defence barriers, offering a valuable alternative to synthetic agrochemicals. *Beauveria bassiana* is one of the most important entomopathogenic fungi that can colonize a wide variety of plant species as an endophyte, limiting the growth and survival of plant pests and pathogens. Here we contribute to this research topic by studying the effect of tomato plants colonization by *B. bassiana* on the survival, development, and immunity of *Spodoptera littoralis* (Lepidoptera, Noctuidae). Endophytic colonization of plants did not affect the survival of larvae feeding on them, which showed a weight increase associated with a higher pupal mortality and a lower adult fecundity. Interestingly, encapsulation and nodulation responses of larvae fed with *B. bassiana* colonized plants were reduced, while, in contrast, phagocytosis slightly increased. These larvae proved to be more sensitive to *B. bassiana* or *Bacillus thuringiensis* infection, given their reduced immune competence. "Omic" studies on tomato plants and *S. littoralis* larvae aim to unravel the molecular mechanisms underlying these changes. Our study provides key findings toward the understanding of mechanisms underlying this intricate plant-insect-microbe interaction interconnecting the below-ground and above-ground environments. It also sheds light on the evolution of the entomopathogenic lifestyle in soil fungi.

Mots-Clés: soil microbiota, insect immunity, plant protection, multitrophic interactions, pest management

*Intervenant

Infection with an acanthocephalan helminth reduces anxiety-like behaviour in crustacean host

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Résumé

Trophically transmitted heteroxenous parasites of diverse clades can decrease or reverse antipredator behaviours in their intermediate hosts, thereby increasing their chances of reaching their final hosts. Such behavioural alterations could result from compromised cognitive abilities affecting fear- or more generally stress-related neurophysiological pathways. We tested this hypothesis in a key model system in the study of parasitic manipulation, the fish acanthocephalan parasite *Pomphorhynchus tereticollis* and its intermediate crustacean host *Gammarus fossarum*, using the ‘threat of electric shock’ paradigm. We exposed uninfected and infected *G. fossarum* to chronic and/or acute electric shock programs at two different intensities (voltage), and then quantified their sheltering behaviour as a proxy for anxiety-like state. Infected gammarids did not express anxiety-like response to electric shocks, while uninfected gammarids hid more when exposed to acute treatments, and when exposed to the high intensity chronic treatment. Interestingly, the lack of response in infected gammarids depended on parasite developmental stage. Our results support the hypothesis that this acanthocephalan parasite impacts the general anxiety-like circuitry of their intermediate host. Further studies are needed to investigate whether it involves inappropriate processing of information, impaired integration, or altered activation of downstream pathways initiating behavioural action.

Mots-Clés: anxiety, Crustacea, host manipulation, parasite, induced phenotypic alteration, stress

*Intervenant

Immune senescence as a function of environmental-mediated changes in growth duration

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Résumé

Central to the evolution of life history is the principle of resource allocation, which posits that individuals should optimally allocate their limited resources between growth, reproduction, and survival to maximize fitness. The Disposable Soma Theory of Ageing is based on the principle that growth and reproduction are costly functions that compete with somatic protection and maintenance, including the immune system, leading to a progressive decline in survival. Whereas trade-offs between reproduction and immunity are relatively well known, those involving growth are less well documented. In contrast to slow growth, rapid growth might be resource-demanding, but it may have the advantage of reducing exposure to parasitism and thus the need for immunity. Moreover, while overall immunity suffers from age-related deterioration (immune senescence), the different components of the immune response seem to age differently. We hypothesized that investment among the many arms of the immune system is finely adjusted to the resource cost of growth and the related risk of parasitism. We tested this hypothesis in the insect *Tenebrio molitor*, which exhibits large environmental-dependent variation in growth duration. We experimentally modified growth duration by raising larvae at different temperature (21.5, 24.5, and 28.5°C; 85%RH) and relative humidity conditions (55, 70, and 85% HR; 24.5°C). Once reaching the pupal stage, each individual was then individually kept at the standard condition of 24.5°C and 70% RH. The different components of the cellular, enzymatic, and antibacterial immune defences in the haemolymph of adult males and females were assessed early (15 ± 3 days post-eclosion) or late (45 ± 3 days post-eclosion) in life before and after a standard bacterial immune challenge. The longevity of the insects was then recorded. The findings will be discussed in relation to *T. molitor* ecology and the Disposable Soma Theory.

Mots-Clés: ageing, immunity, cost of growth, disposable soma theory, experimental manipulation

*Intervenant

Caractérisation de la diversité cytologique, transcriptomique et fonctionnelle des hémocytes de *Crassostrea gigas*

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Résumé

Les épisodes de mortalités d'huîtres dans les élevages conchylicoles surviennent de plus en plus fréquemment et les connaissances actuelles montrent que ceux-ci résultent principalement d'infections bactériennes ou virales. Pour lutter contre ces infections, l'huître *Crassostrea gigas* (*C. gigas*) possède un système immunitaire inné composé d'hémocytes circulants capables d'initier une réponse antimicrobienne cellulaire, par phagocytose, pièges extracellulaires d'ADN et agrégation, ou par voie humorale via la sécrétion de cytokines, de chimiokines, de peptides anti-microbiens et d'espèces réactives de l'oxygène. Ces deux voies de réponses immunitaires impliquent plusieurs types cellulaires possédant des spécificités fonctionnelles diverses. Cependant, malgré la diversité des approches qui ont été utilisées depuis de nombreuses années pour caractériser les différents types cellulaires circulants dans l'hémolymphe des huîtres, il n'existe pas aujourd'hui de consensus concernant leur classification et leurs spécificités fonctionnelles. Cette méconnaissance des cellules du système immunitaire chez ce bivalve représente un verrou majeur pour accéder à un niveau supérieur de compréhension des interactions immuno-biologiques dans ce modèle complexe d'interaction entre huîtres, virus et bactéries. L'objectif de nos travaux est donc de caractériser d'un point de vue cytologique, fonctionnel et transcriptomique les populations d'hémocytes de *C. gigas* afin de créer un atlas hémocytaire de référence. Grâce à la mise en œuvre conjointe de méthodes de fractionnement cellulaire et de tests fonctionnels ainsi que l'utilisation de RNAseq sur cellules uniques, il nous est possible aujourd'hui de caractériser finement aux niveaux cellulaire et moléculaire la diversité des populations hémocytaires chez l'huître creuse *C. gigas*. Ces travaux vont permettre de définir le rôle respectif de chaque sous-population hémocytaire dans les mécanismes de défense de l'hôte. Nous espérons ainsi pouvoir identifier les populations hémocytaires spécifiquement impliquées dans les interactions avec les pathogènes viraux, bactériens ou encore les parasites eucaryotes, mais également d'explorer le support cellulaire de la mémoire immunitaire innée chez ce mollusque. Enfin, ces travaux pourront contribuer au développement de nouvelles approches diagnostiques des infections chez *C. gigas* afin d'en améliorer le suivi et le contrôle.

Mots-Clés: *Crassostrea gigas*, Immunité, Hémocytes, Cytologie, Séquençage d'ARNm sur cellule unique, Biologie Fonctionnelle

*Intervenant

Invasive success of *Drosophila suzukii*: Is *Wolbachia* playing a role?

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Résumé

Invasive species constitute a worldwide issue, jeopardizing biodiversity and engendering important economic losses. A better understanding of how they can establish under environmental conditions that are different from those they encounter in their native range is necessary. *Drosophila suzukii* is an invasive pest worldwide, originating from Asia. Because of its impressive abilities to develop in new environments, it became a precious model organism to understand invasive success. Among the traits that may have contributed to its success are (1) a highly polyphagous diet allowing the fly to develop within several fruits species all year round; and (2) the female's ability to lay eggs in healthy fruits, a niche neglected by other Drosophilidae. Moreover, *D. suzukii* hosts the *Wolbachia* strain *wSuz*, the role of which is still under study. Hypotheses include towards a mutualistic role. We conducted experiments to better understand how *Wolbachia* affects *D. suzukii* fitness, thermal biology and metabolism. In stressful conditions (e.g., fluctuant thermal regime, diet change), flies infected with *Wolbachia* had a higher survival, a lower thermal preference and a lower metabolic rate. This presentation questions whether *wSuz* played a role in *D. suzukii* invasive success, specifically linked with its polyphagy and thermal preference.

Mots-Clés: Ectotherm, Endosymbiont, Metabolism, Polyphagy, Thermal Biology

*Intervenant

Genetic and physiological insights into the diazotrophic activity of a non-cyanobacterial marine diazotroph

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Résumé

Nitrogen (N₂) fixation, or diazotrophy, supports a large part of primary production in oceans. Culture-independent approaches highlighted the presence in abundance of marine non-cyanobacterial diazotrophs (NCD) but their ecophysiology remains elusive, mostly because of the low number of isolated NCD and because of the lack of available genetic tools for these isolates. Here, a dual genetic and functional approach allowed unveiling the ecophysiology of a marine NCD affiliated to the species *Vibrio diazotrophicus*. Physiological characterization of the first marine NCD mutant obtained so far was performed using a soft-gellan assay, demonstrating that a *DnifH* mutant is not able to grow in nitrogen-depleted media (Fig. 1). Furthermore, we demonstrated that *V. diazotrophicus* grows as single cells under micro-oxic conditions and produces a thick biofilm under fully aerated conditions, suggesting biofilm production as an adaptive response of this NCD to cope with the inhibition of nitrogen-fixation by molecular oxygen. Finally, the genomic signature of *V. diazotrophicus* is essentially absent from metagenomic data of Tara Ocean expeditions, despite having been isolated from various marine environments, unveiling potential hidden diazotrophic diversity. We think that the genetically tractable *V. diazotrophicus* strain used in this study may serve as an ideal model to study the ecophysiology of these overlooked procaryotic group.

Mots-Clés: *Vibrio diazotrophicus*, N₂ fixation, *nifH*, bacterial genetics, biofilm

*Intervenant

Impact of drought on biotic interactions in grapevines: a physiopathological approach

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Résumé

Climate change, particularly the increased frequency and severity of drought, has a significant impact on pathogen aggressiveness, plant physiology, and their interactions. Consequently, plant mortality and yield losses are escalating worldwide in both natural and agroecosystems. However, our understanding of the underlying causes is limited due to the intricate interplay between abiotic and biotic factors. This is particularly evident in viticulture, where grapevines have been experiencing declining yields and increased mortality over the past two decades. Our research focuses on grapevine hydraulic functioning, which lies at the heart of the interaction between biotic and abiotic factors. Specifically, we investigate (i) the influence of vascular diseases on xylem hydraulic integrity and (ii) the interaction between drought, climatic conditions, and fungal diseases, both in controlled environments and in the field. During the presentation, I will present how we integrate ecophysiology and plant pathology to provide novel insights into the role of plant physiology and microbial communities, as well as their interaction with climate, as key drivers of grapevine decline.

Mots-Clés: climate, drought, microbial communities, fungal pathogens, vascular disease, *Vitis vinifera* L., xylem

*Intervenant

Peaceful relationships in an old symbiotic couple

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Résumé

Parasitic wasps of the *Cotesia* genus, which larvae develop within caterpillars, have been used worldwide as biological control agents of Lepidoptera, as an alternative to chemical pesticides. One of the critical factors for parasitoid wasp impact on pests is the bracovirus, the symbiotic virus originating from the integration of a nudivirus genome in the germline of an ancient wasp. Bracovirus particles produced in the ovaries and injected in caterpillar larvae with the wasp eggs are used as a tool to transfer virulence genes into host cells allowing the production of proteins inhibiting immune response against the parasite.

We have determined a *Cotesia congregata* genome sequence at chromosomal scale. This study has provided for the first time a very detailed view on how bracovirus sequences are organized within a wasp genome. Genes encoding virulence factors introduced in host cells by the bracovirus following wasp oviposition were clustered in 5 loci, the major one encoding 77% of the genes. Conversely viral genes involved in particles production the so-called "nudiviral genes" that are not packaged in bracovirus particles were widespread in the genome. Some nudiviral genes have undergone a large expansion such as *fen* and *chondroïtine lyase* genes (or "odv-e66") with respectively 7 and 35 copies detected in *C. congregata* genome respectively. Transcriptomic data showed that genes involved in viral transcription were expressed earlier than the other viral genes during pupal development. Moreover, they were shown to evolve under notably strong conservative selection, which suggests that they play a critical role in particles production, as in a regular nudivirus cycle. Strikingly, the expression of genes involved in anti-viral immunity was not induced in the ovaries, suggesting the virus is not recognized as foreign by the wasp although massive production of particles is ongoing. Altogether these data suggest that a viral entity recognized as such by the wasp still exists but that conflicts no longer remain between partners probably because the wasp/virus association is very ancient (approx. 100 million years old).

Mots-Clés: parasitoid wasp, polydnnaviruses, nudiviruses, wasp, virus symbiotic association

^{*}Intervenant

Efficiency of immune priming by oral route or septic wounding in *Tenebrio molitor*

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Résumé

Since the discovery of immune priming in arthropods, many studies (mainly concerning insects) have focused on the ability of these animals to resist infection following a non-lethal contact with the same pathogen as that involved in the infection. The demonstration of this phenomenon often relies on an immunisation procedure of individuals by septic wounding; however, the natural route of infection may also include an oral contamination route by pathogens. Furthermore, as juvenile insects tend to invest more in immunity than adults due to their much higher residual reproductive value, the effectiveness of immune priming should be age-dependent. In addition, an adult that has already reproduced (and therefore has a low residual reproductive value) should invest less in priming compared to a virgin adult of the same age. The experiments we conducted on the mealworm beetle (*Tenebrio molitor*) aimed to compare the efficiency of the immune priming response considering two routes of contamination in larvae: wounding with dead bacteria, or orally with food contaminated with either live or dead bacteria. We also compared the efficiency of the immune priming response by septic wounding in larvae, virgin adults and reproducing adults. We observed that consumption of contaminated food only protects larvae for a very short period, and that the effectiveness of this protection varies according to the pathogen involved. Priming by wounding is effective in protecting adults from subsequent reinfection, but less effective in larvae. However, contrary to predictions, we did not find any effect of the reproductive status of adults. Moreover, larvae showed a much stronger constitutive resistance than adults, and were therefore better protected from injuries. These results seem to confirm that the effectiveness of immune priming depends on the developmental stage at which the first infection occurs, but also on the route of infection.

Mots-Clés: cost of reproduction, immune priming by septic wounding, oral immune priming, developmental stage, *Tenebrio molitor*

*Intervenant

Pesticides impair gut bacterial diversity in honeybee queens (*Apis mellifera*)

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Résumé

Honeybees (*Apis mellifera*) face multiple environmental stressors that have consequences on their physiology, fitness and health. Among them, pesticides are a major threat to pollinators due to direct mortality or sublethal effects on a wide variety of traits. Honeybees are exposed to pesticides mainly by foraging and ingesting resources, such as pollen and nectar, often contaminated with numerous agrochemical compounds. Most of the studies on pesticides and gut microbiota (e.g., bacterial diversity, community structure) were conducted on worker bees. Gut microbiota is involved in digestion, immunity and pathogen protection for example, and therefore plays a major role in honeybee health. However, to our knowledge, the effects of pesticides on queens' gut microbiota are unknown. Honeybees are social insects in which a single individual, the queen, produce all the offspring. Moreover, the fate and performance of the colony is highly dependent on queen health. In this study, we investigated the consequences of concentrations of pesticides found in the environment on queen gut microbiota. Queens were exposed to the insecticide cypermethrin, either alone or in combination with two fungicides, in the laboratory for two days after emergence. Queens were then released in hives and collected after two weeks to assess their gut bacterial community. We observed changes in the structure and composition of gut bacterial community in queens exposed to pesticides. Alpha-diversity indexes (observed richness, Shannon, inverse Simpson) were not significantly affected. However, we found significant impact of insecticide and fungicides on beta-diversity (Bray-Curtis and Jaccard indexes). Brief oral exposure to sublethal doses of pesticides can therefore alter the relationship between the queen and its microbiota, with potential effects on queen vital functions, health and reproductive performance, and ultimately on colony weakness and losses.

Mots-Clés: microbiota, sublethal effects, environmental concentrations, insecticide, fungicides

*Intervenant

Nudivirus domestication in Campopleginae parasitoid wasps

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Résumé

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.

By comparing endogenized alphanudiviruses of *V. canescens* and *Campoplex capitator*, a parasitoid wasp of an important vineyard pest, we investigated whether core viral functions have been retained following viral domestication and whether different evolutionary trajectories led to VLP production. The expression dynamics of alphanudivirus genes was monitored by RNA-seq and the functional role of *lef* genes, predicted to encode the viral RNA polymerase, was investigated by RNA interference. As described for baculovirus infections, a transcriptional cascade involving early and late expressed alphanudivirus genes could be observed. *Lef* gene expression was required for the expression of late viral genes allowing correct particle formation. Together with previous literature, the results show that endogenization of nudiviruses in parasitoid wasps has repeatedly led to the conservation of the viral RNA polymerase function, allowing the production of functional VLPs. Electron microscopy and proteomic approaches revealed that the particles produced by the two related 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.

The description of new viral endogenization events in other phylogenetically related Campopleginae wasps will allow to further refine research on processes involved in viral domestication.

Mots-Clés: parastoïde, virus, domestication, virulence

*Intervenant

Impact of within-vertebrate host parasitaemia on the temporal dynamics of *Plasmodium* in mosquitoes

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Résumé

Vector-borne parasites have to interact with their environment in dynamic ways to cope with different pressures exerted by both the host and the vector. For *Plasmodium* parasites, most studies focused on the traits underpinning its dynamics within the vertebrate host and their sources of variation. Comparatively, little attention has been given to those underpinning the parasite's dynamics within the vector. Using the avian malaria system, we aimed to investigate whether the intensity of infection in the vertebrate host drives the intensity of infection and the extrinsic incubation period (EIP) of *Plasmodium* within the vector. EIP represents the time it takes for the parasite to develop from its ingestion until it invades the salivary glands. We have shown that mosquitoes that blood-fed on highly infected vertebrate hosts were infectious as soon as four days post blood meal. However, biting on highly infected vertebrate host does not seem to affect the intensity of parasite infection within the mosquito: the number of oocysts did not vary according to the vertebrate host parasitaemia. We hypothesize the density-dependent processes occurring both during the gametocytes-to-ookinetes and the ookinetes-to-oocysts associated with non-competitive strategy in the mosquito resources exploitation might underpins the formation of sporozoites, affecting either their growth rate or their quality. Studying the timing of infection under varying conditions and understanding how it shapes sporozoites development and to what extent this drives malaria transmission potential is needed to reassess the approaches of disease control programs.

Mots-Clés: Avian malaria, *Plasmodium*, Extrinsic Incubation Period, EIP, Transmission

*Intervenant

Genetic diversity of the Ostreid Herpesvirus type 1

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Résumé

The use of next generation sequencing (NGS) is essential for studying and monitoring pathogens in bivalve mollusks in order to anticipate the emergence of new genotypes or species. The improvement of knowledge and approaches to characterize their genome allows for a better understanding of their life cycle, host interactions, and capacity for adaptation or evolution.

Ostreid Herpevirus 1 (OsHV-1), a pathogen of the Pacific oyster *Crassostrea gigas*, is responsible for significant mortality of larval and juvenile oysters each year. The study of its genome is complicated by the inability to culture the virus in vitro. Currently, 52 OsHV-1 genomes are available in public databases. This emphasizes the need for the development of diversity and phylodynamic analyses, which are key elements in understanding the spatial and temporal viruses diffusion.

Through the use of "ultra-deep" short-read sequencing on individual moribund oysters, combined with a new bioinformatics pipeline, 440 de novo OsHV-1 genomes were assembled. By combining the genetic variations quantification, phylogenetic analysis, and ancestral state reconstruction of discrete traits, the connectivity of OsHV-1 viral populations between oyster farming areas was assessed. The results suggest that some oyster aquaculture areas have higher OsHV-1 diversity than others. The phylogenetic study indicates samples clustering according to host, location, and time. This work demonstrates that phylodynamic approaches can be applied to aquatic DNA viruses to determine how epidemiological, immunological, and evolutionary processes act and interact on viral diversity.

Mots-Clés: OsHV, 1, diversity, molecular epidemiology, phylogeography

*Intervenant

Un parasite peut en cacher un autre !

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Résumé

Le parasitisme est présent naturellement chez la plupart des grands herbivores sauvages du monde, avec des taux d'infection qui se maintiennent à des niveaux acceptables pour la survie des individus hôtes. En condition de captivité, la charge parasitaire peut augmenter jusqu'à devenir dangereuse pour la santé des animaux. C'est le cas des parasites gastro-intestinaux : lors de fortes infections, on observe par exemple des pertes de poids et des occlusions intestinales chez l'hôte, voir sa mort.

Afin de prévenir ces symptômes, les vétérinaires utilisent des antiparasitaires. Leur nature varie selon le type ou la forme de parasite ciblé. Les autorités vétérinaires françaises recommandent de changer de famille de molécule active à chaque application d'antiparasitaire afin d'avoir un plus grand spectre d'efficacité mais aussi afin de réduire l'apparition de résistances.

Chez les équidés, 2 types de parasites gastro-intestinaux principaux sont connus : les nématodes (dont les strongles digestifs et les ascaris), et les protistes (dont les coccidies). Dans cette étude, nous avons suivi mensuellement la charge parasitaire du plus grand groupe de zèbre de Grant (*Equus quagga boehmi*) d'Europe pendant 6 mois. Après 3 mois d'observation, les zèbres ont reçu un traitement antiparasitaire ciblant les nématodes.

Nos résultats montrent la présence d'ascaris, de strongles et de coccidies. Malgré la présence avérée des coccidies chez les herbivores côtoyant les zèbres, celles-ci n'avaient jamais été décrites auparavant chez les zèbres de Grant en milieu naturel à notre connaissance, et une seule fois en captivité dans une étude de 1978. Après traitement antiparasitaire, nous avons observé une diminution significative de la charge parasitaire en strongles et une augmentation significative de la charge parasitaire en coccidies, avec une corrélation entre les dynamiques d'excrétion des œufs et des oocystes.

Cette étude nous amène à nous questionner sur l'utilisation des vermifuges, et pousse à approfondir nos recherches pour mieux comprendre les mécanismes qui régissent l'écologie des parasites au sein d'un même hôte.

Mots-Clés: Zèbres, Parasites gastro-intestinaux, Coccidies, Anthelminthiques, Parc zoologique

*Intervenant

Larval ecology, bacterial microbiota and mosquito vectorial capacity

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Résumé

In animals with distinct life stages such as holometabolous insects, adult phenotypic variation is often shaped by the environment of immature stages. In mosquito vectors of human pathogens, this means that the larval environment may influence the vectorial capacity of adult females. In this talk, I will describe how bacteria present in larval habitats affect adult traits underlying pathogen transmission by mosquitoes. I will present experimental evidence for a functional link between larval ecology, environmental microbes and adult phenotypic variation in a holometabolous insect vector.

Mots-Clés: Mosquito, Vectorial capacity, Microbiota, Carryover effects, Gnotobiotic

*Intervenant

Early modulation of the jasmonate pathway in rice (*Oryza sativa*) by the oral microbiota of *Spodoptera frugiperda* larvae

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Résumé

Herbivorous insect pests cause 18 to 20% of yield reduction in crops worldwide. *Spodoptera frugiperda* (Lepidoptera: Noctuidae), a polyphagous insect native to the Americas, has recently spread throughout the world, posing a threat to global food security. It is mainly detected on *Poaceae* such as maize (*Zea mays*) and sporadically on rice (*Oryza sativa*). The recognition of the insect attack by the plant will be done through the Damage Associated Molecular Patterns (DAMPs) produced at the time of the wound and the Herbivore Associated Molecular Patterns (HAMPs) present in the oral secretions (OS), which will lead to the induction of defense response. Recent studies have shown that some insects can circumvent these defenses via the oral microbiota by suppressing the jasmonate (JA) pathway central to the herbivory response. Our objective is to determine whether the oral microbiota of *S. frugiperda* modulates the JA pathway in rice and to identify the microbial and molecular players in this tripartite interaction and to investigate the advantage of the insect in suppressing this pathway. To this end, we simulated a caterpillar attack on rice leaves via mechanical wounding followed by OS deposition and analyzed the modulation of rice defense responses by global transcriptomic analysis (RNA-seq). We identified a set of genes whose expression is specifically induced by the response to DAMPs, HAMPs and co-modulated by DAMPs and HAMPs. We then characterized the OS microbiota via a metabarcoding approach and identified *Enterococcus mundtii* as the prevalent bacterium. To study the impact of the microbiota on the JA pathway, we fed the larvae an antibiotic-treated artificial diet and harvested dysbiotic OS that we deposited on rice leaves. We thus obtain a low transcriptomic impact of the dysbiotic microbiota with a modulation of 33 genes. However, an HPLC approach showed us a strong biochemical impact with a suppression of the JA pathway by the microbiota. A contact between insects and WT and mutant JA-deficient rice showed a reduced effect of JA on the insects' weight gain. The next step will be to determine the bacterium responsible for this suppression with *E. mundtii* as the first candidate.

Mots-Clés: 'Plant, insect, bacteria interaction' 'Spodoptera frugiperda' 'Microbiota' 'Rice' 'Defense response' 'Oral secretion'

*Intervenant

Trans-generational immune priming occurs after oviposition in the European earwig

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Résumé

Protecting offspring from pathogen infection is an important function of parental care. In insects, a key mediator of this protection occurs during egg formation through trans-generational immune priming (TGIP), a powerful process by which parents transfer their own immunological experience to their eggs, and thus to future offspring, before oviposition. However, it is not known whether this can also be more plastic and occur after egg formation. Here, we addressed this knowledge gap using the European earwig, a Dermapteran insect in which mothers care for their eggs and juveniles for several months after oviposition. We primed 246 mothers caring for their eggs with either heat-killed solutions of the bacterium *Serratia marcescens*, PBS (a buffer solution) or no injection (control). We then tested whether this priming helped the mothers to be better protected against a future infection (immune priming) and whether they could transfer this improved protection to their offspring during post-oviposition care (TGIP). Our results support both predictions but, somewhat surprisingly, only for PBS-primed mothers. These mothers survived infection with live bacteria better than control mothers, whereas bacteria-primed mothers survived overall less well than control and PBS-primed mothers. Moreover, adults who had previously been cared for by PBS-primed mothers survived bacterial infection better than adults who had previously been cared for by the three other types of mothers. Overall, our results show that the effects of building up an immune defence in earwig mothers range from costly to beneficial in terms of resistance to future infection, depending on whether the priming is caused by dead bacteria or simple wounds. It also shows that these beneficial immunological changes in mothers can be transmitted to their offspring after oviposition, confirming that TGIP is a dynamic process that can occur throughout offspring development and may therefore play an important – but currently neglected – role in the evolution and maintenance of family life in insects.

Mots-Clés: Immune defence, Insects, *Forficula auricularia*, Parental care

*Intervenant

TRANSPORT DE SUCRES ET RESISTANCE A B. CINEREA CHEZ LA VIGNE

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Résumé

La compréhension des mécanismes de défenses des plantes est essentielle au développement de solutions alternatives dans la lutte contre les maladies cryptogamiques. Parmi ces mécanismes, de plus en plus d'études soulignent le rôle important des transporteurs de sucres et des invertases dans la résistance des plantes face aux agents pathogènes. Dans nos travaux précédents, nous avons démontré génétiquement que l'expression du transporteur d'hexoses STP13, localisé dans la membrane plasmique, favorise la résistance basale de la plante *Arabidopsis thaliana* contre le champignon nécrotrophe *Botrytis cinerea*. Notre hypothèse est que STP13 pourrait améliorer la résistance en privant le pathogène de ressources et en alimentant les réponses de défenses de la plante. Toutefois, comme cela a été démontré chez le blé et l'orge, ce type de transporteur pourrait également jouer un rôle négatif dans la résistance en favorisant la prolifération de champignons ayant un autre mode trophique, par exemple les biotrophes. Sur la base de ces études, nous élargissons nos recherches aux plantes d'intérêt agronomique, telles que la vigne. Pour explorer le rôle des gènes du transport de sucres lors de l'infection par *B. cinerea*, nous utilisons une approche dans laquelle le plus proche homologue de STP13 chez la vigne est exprimé sous le contrôle d'un promoteur constitutif fort. Ici, nous présentons l'analyse phénotypique de l'expression ectopique de ce candidat. Nos résultats indiquent que le contrôle des sucres apoplastiques, par l'activité des transporteurs d'hexoses localisés dans la membrane plasmique, peut constituer une stratégie de défense de l'hôte en limitant la prolifération fongique.

Mots-Clés: Vigne, *Botrytis cinerea*, Transport de sucres, Sensibilité, Maladies cryptogamiques

*Intervenant

Systeme de secretion de type III : un autre rôle que la virulence ? Le couple ormeau-*Vibrio harveyi* comme modèle.

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Résumé

Vibrio harveyi ORM4 est une bactérie marine pouvant induire jusqu'à 80% de mortalité chez les populations naturelles d'ormeaux européens *Haliotis tuberculata* (1). L'importance de la température et de l'état physiologique de l'animal a déjà été démontrée chez ce couple infectieux (2), mais les mécanismes de virulence mis en œuvre par la bactérie restent encore inconnus.

Le système de sécrétion de type III (T3SS) est associé à la sécrétion de protéines cytotoxiques, lesquelles perturbent la machinerie cellulaire de l'hôte avec des conséquences diverses. L'étude du génome de *V. harveyi* ORM4 a révélé la présence d'un cluster de 49 gènes homologues à celui codant le T3SS1 chez *V. parahaemolyticus* RIMD2210633. Par une approche de mutagenèse ciblée, nous avons évalué l'importance de ce système dans la virulence de *V. harveyi* ORM4 envers l'ormeau européen, en délétant le gène *exsA* codant le régulateur principal du T3SS. La délétion de ce gène a engendré une perte totale de la virulence envers *H. tuberculata*, révélant ainsi que le T3SS est essentiel à l'infectiosité de la bactérie (3). Pour aller plus loin, nous avons caractérisé la capacité du mutant *exsA* à coloniser l'animal et avons démontré que la délétion de ce gène impacte la capacité de la bactérie à se maintenir sur les branchies de l'animal. Ces organes étant identifiés comme voie de pénétration de *V. harveyi* ORM4 dans l'hémolymphe de *H. tuberculata* (4), nos résultats mettent en lumière l'importance du T3SS dans la colonisation de l'animal.

Parallèlement, une étude transcriptomique visant à identifier les gènes impliqués dans la formation de biofilm par *V. harveyi* ORM4 a révélé la surexpression de 18 gènes appartenant au cluster du T3SS, dont certains codant des protéines potentiellement excrétées. La délétion du gène *exsA* n'ayant pas impacté la formation de biofilm de *V. harveyi* ORM4 en conditions dynamiques, d'autres investigations devront être mises en place afin d'étudier l'implication de ce système dans la formation de biofilm.

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Mots-Clés: *Vibrio harveyi*, T3SS, virulence, biofilm

*Intervenant

Phages of plant pathogenic bacteria: ecology, evolution and biocontrol

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Résumé

Phages are part of the plant microbiota and promising biocontrol agents against bacterial pathogens, but numerous challenges and questions remain: What is the impact of phages on the diversity and pathogenicity of microbial communities in agriculture? Can we identify the optimal conditions (when and how) to apply biocontrol measures? Can we predict if phages will protect for a long time or will resistance inevitably arise? We currently work on phage interactions with three bacteria responsible for major plant diseases: *Ralstonia solanacearum*, *Pseudomonas syringae* and *Erwinia amylovora*. By bringing evolutionary biology, community ecology and molecular microbiology together, we aspire to unveil the role of phages for plant bacterial pathogens and to advance their development as therapeutic agents in agriculture.

Mots-Clés: Phages, biocontrol, evolution, community ecology

*Intervenant

Environmental parameters and vector competence in natural ecosystems: the microbiome and the snail host *Pseudosuccinea columella* as main actors

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Résumé

The environment is a major component of host-parasite interactions that can influence the ecological fitness, immune reactivity/virulence of hosts/parasites and the ultimate compatibility and transmissibility of the infection. The impact of fasciolosis on livestock and as a zoonosis worldwide has been on the rise, related among other factors, to different environmental perturbations including biological invasions. For instance, the flash expansion of *Pseudosuccinea columella* snails from North America to other world regions (reaching Europe and spreading in France) boosted *Fasciola* transmission in the invaded areas through successful parasite spill-backs. Noteworthy, although *P. columella* is one of the main intermediate hosts of *F. hepatica* with most individuals being susceptible (S) to infection, a few field-occurring populations (in Cuba) are strictly resistant (R; 0% prevalence) to the parasite at the expenses of a fitness cost. By profiting from this exceptional model, we aim at answering how abiotic and biotic (in the field and within the snails) factors associate with the susceptibility/resistance of *P. columella* and how the immune competence of the snail varies depending on the environment. Ecological characterization (*in situ* measurement of ecological factors), eDNA (from water and sediment) and snail sampling in contrasted environments from Cuba (highly contrasted sites where resistant and/or susceptible *P. columella* occurs), France (introduced susceptible *P. columella* in natural habitats) and Zimbabwe (invasive susceptible *P. columella* in an artificial lake) were carried out. Microsatellite markers and 16S metabarcoding analyses were used to describe the population genetics of *P. columella* and the trematode fauna, food resources and microbial communities to snail population/each site, and were associated with the ecological factors to depict differential ecological patterns. RNAseq analyses were used to assess the immune competence of the snails in the different environmental settings. From this, we gauge the contribution of the environment in shaping the differential patterns of vector competence of *P. columella*.

Mots-Clés: vector competence, snail resistance, microbiota, trematode infection, ecology, environment

*Intervenant

Unexpected associated bacteria with *Crassostrea gigas* juveniles during mortality events

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Résumé

Crassostrea gigas pacific oysters are recurrently affected by mortalities at the juvenile stage both on the atlantic and mediterranean coast since 2008. Thau lagoon (south of France) is an important farming area, producing between 7000 and 5000 tonnes of oysters each year. However, the recurrent juvenile oysters mortality , ranging from 35% to 70%, causes important economic losses.

The disease involves an herpes virus (OsHv-1 μ var) that causes immunosuppression in juveniles, leading to bacterial dysbiosis, then followed by opportunistic bacterial colonization and final death. The underlying mechanisms that triggers mortality, depending both on host and environment interaction, remains still unknown.

In " Microlag project " conducted in Thau lagoon, we investigated the changes in the microbiome composition in juveniles oysters from several months before mortality starts, during the mortality event, and till 2 months later to determine if the microbiome characteristics could help in understanding the outcome of oysters. We also investigated the impact of moribund oysters on their immediate environment (water and sediment) as we suspected the role of the environment in these recurrent episodes of mortalities.

The microbiome of juveniles oysters (alive and moribund) was investigated by 16rRNA sequencing, from february to august 2021. At the same time, OsHv-1 herpes virus was quantified by qPCR, aside with a suspected primary pathogen (*Vibrio aestuarianus*).

The results showed unexpected associated bacteria with juvenile oysters : the Mycoplasmatacea family, that dominated quite constantly juveniles' microbiome, and a more discreet pathogen : *Vibrio aestuarianus*, mainly present during the mortality event. These bacteria were also detected in the environment. The role of these permanent or transient bacteria in oysters in relation with the farming environment will be discussed in the context of oysters mortality.

Mots-Clés: Oysters, Microbiome, Mycoplasmatacea, Herpes virus, Vibrio, Thau lagoon

*Intervenant

Human DNMT3A inhibitors are potential active epigenome modulators in invertebrates

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Résumé

The pacific oyster *Crassostrea gigas* is one of the most spreading mollusk species worldwide in aquaculture. *C. gigas* plays important roles in marine ecosystems by seawater filtration and reefs formation which enable to host many species and therefore, real ecosystems formation. Oyster farms are affected by many pathogens as bacteria and viruses which induce massive mortality episodes. Several biotic (alimentation, age...) and abiotic (water temperature, salinity...) factors can influence those disease outcomes but how environmental parameters are registered is not clearly understood. It has been shown that epigenetics mechanisms relay environmental information. The main carriers of epigenetic information are DNA methylation, histone post translational modifications and non-coding RNAs. It is already known that environment fluctuations impact DNA methylation but its function in chromatin structuration is unclear. One possibility to elucidate DNA methylation role is to use epigenome modulators able to inhibit DNA methylation. Those modulators are widely studied in cancerology as a possible treatment strategy. In the current study, we evaluate inhibitors of human DNMT3A for its activity on *C. gigas*. We tested three compounds for (1) their stability in sea water, (2) their *in vitro* effect against the activity of the DNA methyltransferase enzyme, (3) their *in vivo* effect on *C. gigas* global DNA methylation level. Active inhibitors will be used to modulate *C. gigas* epigenome and their effects on the oyster chromatin structure will be studied by multiomics approach (ATAC-seq and ChIP-seq).

Mots-Clés: Epigenetics, DNA methylation, Invertebrate, Environmental response, Epidrugs

*Intervenant

Small game's habitat management: an experimental approach in favour of Mediterranean avian biodiversity ?

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Résumé

In the French Mediterranean region, the progressive shrinking of traditional activities (i.e. grazing, extensive agriculture) results in scrubland expansion and landscape closure which induces some biodiversity loss. Hunters participate in environmental management mostly by scrubland opening for expanding small game species habitat. The aim of our study was to measure the contribution of such management to the conservation of non-target bird species. For this purpose, three 30-hectare managed and unmanaged areas of Mediterranean scrubland were investigated. Breeding birds were censused using the progressive frequency sampling (EFP) method. Species richness, a proxy for alpha diversity was estimated for comparing bird communities between pairs of areas. We also analyzed the occurrence of species according to their conservation status in the IUCN French list. Our results showed that small game habitat management was associated with a larger bird species richness including exclusive open-habitat specialists. The conservation status of species was significantly higher in managed areas, vulnerable species being four times more frequent there. So, hunters' small game management of scrublands can result in areas of high conservation value for non-target bird species. This study could support guidelines for the conservation of bird biodiversity.

Mots-Clés: scrubland opening, avifauna, species richness, conservation, southern France.

*Intervenant

Effects of metal contamination on fish-pathogen interactions

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Résumé

Environmental pollution is one of the major anthropogenic changes affecting ecosystems and biotic interactions. For example, metal contaminants from past mining activities can remain stocked in soil, biofilm and sediment of riverine ecosystems even centuries after the cessation of activities, with the potential to accumulate and cause adverse effects on wildlife health. However, their effects in aquatic systems and on fish-parasite interactions remain poorly known. In rivers, metals could potentially have direct effects on pathogen survival and/or through immunotoxic effects on fish physiology, thus altering fish-pathogen dynamics. In this study, we focused on the French Pyrenees mountains because of the long-standing legacy of past mining activities, and the spread of an emerging pathogen (*Tetracapsuloides bryosalmonae*) responsible for the deadly Proliferative Kidney Disease in wild brown trout (*Salmo trutta*). Using an extensive field approach, we investigated the implications of metal pollution on fish health and infection by *T. bryosalmonae* by measuring traits involved in immunity (e.g., neutrophils/lymphocytes ratio), genotoxicity (e.g., micronuclei), energy management (e.g., condition indices, muscle lipids), and parasite resistance/tolerance (e.g., pathogenic DNA in the fish body, haematocrit ratio, kidney/muscle ratio). Although preliminary, our results indicate that in the emerging field of evolutionary ecotoxicology, it is crucial to consider the impacts of metal pollution on host-pathogen interactions to achieve a comprehensive understanding of the disease dynamics and anticipate contamination effects on wildlife health.

Mots-Clés: Host, pathogen interaction, metal contamination, disease dynamics, wildlife, brown trout

*Intervenant

Compromis entre soins maternels et immunité chez *Forficula auricularia*, le perce-oreille.

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Résumé

In *Forficula auricularia*, care of the eggs is obligatory, unlike care of the young, which is optional. This care is often costly for mothers, because the energy they spend on it comes at the expense of other energetic investments in future reproduction or in their own survival. In this project, we propose to quantify these costs for the first time in the European earwig by investigating the link between immunity and maternal care. Immunity is a life history trait, and by measuring it and testing the survival of females injected with the pathogen *Serratia marcescens*, we will be able to observe whether there is a trade-off between maternal care and personal immunity in *F. auricularia* females. In our experiment, we allowed some females either to express care for their eggs, both eggs and juveniles, or to express no care. Several studies suggest that the level of investment individuals make in their immunity may depend on the presence of maternal care, and that the expression of maternal care depends on the presence of pathogens in the environment. It is therefore expected that the group that was not able to express maternal care will have a better survival rate and better immune competence than the others.

Mots-Clés: *Forficula auricularia*, social insect, Maternal care, Trade, off, Immunity, Survival.

*Intervenant

Functional analysis of interactions between bed bugs and their nutritional symbiont *Wolbachia*

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R sum 

Hematophagous insects are a global endemic threat that can spread disease or cause stress and anxiety. Because blood is an unbalanced diet that lacks certain B vitamins necessary for insect growth and fertility, strict hematophagous insects are all associated with nutritional symbionts that supplement their metabolism. In the bed bug *Cimex lectularius*, *Wolbachia wCle* is an intracellular bacterium that produces two B vitamins: riboflavin (B2) and biotin (B8), both required for bed bug fitness. Within the bed bug, the symbiont is found in two organs: in a specialized symbiotic structure, the bacteriome, and in the ovaries that ensure the vertical transmission of *Wolbachia* to developing eggs.

Bed bug infestations strongly increase in developed countries, mainly due to the evolution of insecticide resistance and globalization. Since there is an urgent need for an alternative strategy to pesticides to control bed bug populations, we propose to disrupt the obligate nutritional interaction between bed bugs and their endosymbiont. The development of such an alternative method requires a better understanding of the genetic and metabolic pathways necessary for both partners to maintain this symbiotic interaction.

The aim of my thesis project is thus to study the molecular and metabolic bases of this interaction. First, we propose to identify host and bacterial genes that are differentially expressed during the blood meal, using a DUAL-RNA sequencing approach. These data will be considered together with the results of a global metabolomics approach and a genomic reconstruction of the metabolic capacities of both partners. Based on these results, we will functionally characterize a few candidate genes using RNA interference, and study how the corresponding loss of function affects the metabolic transfer or the bacterial regulation. Through this project, we expect to better understand the interactions that may lead to the development of new strategies to control bed bug infestations.

Mots-Cl s: Symbiosis, Interaction, Nutritional symbiont, Bed bug, *Wolbachia*

*Intervenant

Investigating *Wolbachia* symbiont-mediated host protection against a bacterial pathogen using a natural *Wolbachia* nuclear insert

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Résumé

Wolbachia bacterial endosymbionts provide protection against pathogens in various arthropod species but the underlying mechanisms remain misunderstood. By using a natural *Wolbachia* nuclear insert (f-element) in the isopod *Armadillidium vulgare*, we explored whether *Wolbachia* presence is mandatory to observe protection in this species or the presence of its genes is sufficient. We assessed survival of closely related females carrying or lacking the f-element (and lacking *Wolbachia*) challenged with the bacterial pathogen *Salmonella enterica*. Despite marginal significant effects, the f-element alone did not appear to confer survival benefits to its host, suggesting that *Wolbachia* presence in cells is crucial for protection.

Mots-Clés: *Wolbachia*, Nuclear insert, Survival assay, Host protection, Arthropods

*Intervenant

Influence of ecological (season, site), and physiological (sex and age) factors on the diversity and prevalence of intestinal parasites in two populations of chimpanzee (*Pan troglodytes*) in southeastern Gabon

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Résumé

Parasites are involved in population dynamics, growth, and regulation and pose a threat to biodiversity conservation, particularly for chimpanzees (Sirima et al., 2021). Physiological, ecological, and behavioral factors strongly influence impacts on the health of their hosts

The diversity and prevalence of intestinal parasites in two groups of chimpanzees living in different environments: one in captivity at the Primatology Centre (CDP) and the other in the wild at the Léédi Park in south-eastern Gabon and The impact of ecological (season, site) and physiological (age, sex) factors on the diversity, prevalence, and risks of infestation.

For the purpose of this study, we analyzed faeces from a population of 87 chimpanzees. Two methods were used for parasite detection: MacMaster flotation with a saturated salt solution (400 g diluted in 1 L of distilled water) as solvent and sedimentation with a 0.9%NaCl solution. The Chi-square test (χ^2) and Fischer's exact test were applied to compare the different prevalences with a confidence level of 5%. We also used a multivariate analysis (logit) model (logistic regression) to assess the influence of risk factors (site, sex, age, season) on chimpanzee infestation.

Coprological examination enabled us to identify 19 parasitic genera, 6 protozoa (*Pseudolimax butschlii*, *Endolimax nana*, *Entamoeba coli*, *Entamoeba histolytica*, *Balantidium coli* and *Troglodytella* spp.) and 13 helminths (*Ascaris* spp., *Ancylostoma* spp., *Enterobius* spp., *Mamomonogamu* spp, *Necators* spp, *Oesophagostomum* spp, *Spirure* sp, *Strongyloides* sp, *Trichostrongylus* sp, *Toxocara* sp, *Trichuris* spp, *Fasciola hepatica* and *Hymenolepiss* spp.) including 2 parasites potentially identified for the first time in chimpanzees (*Fasciola* spp and *Toxocara* spp.). Parasite diversity was higher in the captive group (17 parasite genera) compared to the free-ranging group (11 parasite genera). The overall prevalence is 95.40%, with 98.38% in the free-ranging group and 92.68% in the captive populations. The mathematical model used positively influenced the risk factors studied. It revealed that the risk of infestation is high in the dry season for males and young chimpanzees. Depending on the site, the risk of infestation seems to be 3 times higher at L'édi than at CDP.

Mots-Clés: Chimpanzee, Intestinal parasites, Host, parasite, environment interactions, Gabon

*Intervenant

Coffee trees, floral scents and wild entomofauna or how to successfully pollinate in a new agricultural landscape?

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Résumé

Studies to understand the adaptability of plants to new environments and all of the interactions that allow this adaptability were conducted on *Coffea arabica* which was spread around the world from a genetic material of very reduced origin, and consequently presents with a poor genetic base which is also attributed to its autogamous reproduction. Its low genetic diversity jeopardizes the evolution of *C. Arabica* populations in response to environmental changes, consequently reducing their chances of persisting in the long term. On the other hand, *Coffea canephora* (robusta), which has lower ecological requirements and a greater genetic diversity, proves to be more tolerant to current temperature increases than the *C. arabica* coffee tree. It was with the aim of mixing these two species within the same plant, that emerge the idea of creating the interspecific hybrid *Coffea x arabusta*. The significant genetic diversity of the hybrid obtained allows it to be cultivated in varied environmental conditions. It was introduced into French Guiana and planted *in situ*, in very contrasting environmental conditions. It was able to be shown that the environment (rainfall, light, température) has an influence on the fertility of *C. arabusta* hybrids. More interestingly, their reproductive mode may be a limiting factor in the case of introduced plants. *C. arabusta* hybrids inherited a different percentage of allogamy from their parents according to the share inherited from the autogamous *C. arabica* or the allogamous *C. canephora*. Similarly, their grain production is highly variable, certainly due to their reproductive mode which for some of them, requires the intervention of a regular pollinator (managed bee), absent in their new growing environment. Scents produced by flowers attract a diverse fauna of insects. The small size of plots and their proximity to the surrounding wild forest, offers coffee plants access to local natural entomofauna. The effectiveness of pollination by these new local "pollinators", is studied and tested to better understand variations in grain production among hybrids. The observation of pollination only due to wild pollination auxiliaries shows that the management of these agro(eco)systems for an ecologically *stable* production can only occur on a landscape scale.

Mots-Clés: Coffea, Floral scents, wild insect population, non bee pollinators, agro(eco)logical landscape

*Intervenant

Alien introductions and the increase of snail-borne diseases in Europe: the case of trematode spill-back by lymnaeid snails

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Résumé

The invasion of freshwater snails, commonly associated to human activities, usually have negative effects on native species or disease transmission. The Lymnaeidae (Mollusca: Gastropoda) is a commonly introduced group of freshwater snails with several species displaying a multi-continent distribution. Lymnaeids are commonly known for their role in fasciolosis transmission worldwide, a parasitic disease that causes severe public and veterinary health problems. Lately, Europe has been the target of at least three exotic lymnaeids. Chronologically, the North American *Pseudosuccinea columella* was first sighted in the banks of the Lot river in France back in 2004. More recently, two species were added in the Spanish region of Deltebre since 2010: the neotropical *Galba cubensis* and the Australasian *Orientogalba viridis*. In the case of *P. columella* we have recently recorded several established populations along the Canal du Midi down to the Mediterranean coast in the Bagnas Natural Reserve as well as in southern Corsica. The other two species maintain stable populations at their introduction site with *O. viridis* colonizing adjacent areas. Given that the three species are recognized as major hosts of fasciolosis in their native range, we conducted experimental infections using field-derived populations of European *P. columella* and *O. viridis*. Local isolates of the liver fluke *Fasciola hepatica* (Camargue, Corsica, and Pyrenees) and the rumen fluke *Calicophoron daubneyi* (Pyrenees) were used to expose the snails. Both species were highly susceptible to *F. hepatica* (> 60% prevalence) and *C. daubneyi* succeeded to infect *P. columella* (40%). Survival post-exposure remained over 88% and all assays rendered viable cercariae that successfully encysted into metacercariae (infective form to mammal hosts). Noteworthy, the epidemiology of these parasitic diseases usually follow a marked seasonality determined by the ecology of the snail host, which in Europe is mainly maintained by the lymnaeid *Galba truncatula*. With the recent additions of tropical species to the European scenario and in the context of a changing climate, shifts in the epidemiological risks of transmission is foreseeable. Surveillance, proper identification, and further bio-ecological research should be conducted to support adjusted managing strategies of livestock in order to prevent outbreaks of strong zoonotic potential.

Mots-Clés: biological invasions, Lymnaeidae, experimental infections, liver fluke, parasite spill, back

*Intervenant

Le séquençage d'ARNm sur cellules uniques appliqué à deux espèces de bivalves : une vision transcriptomique des populations hémocytaires.

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Résumé

Les changements environnementaux liés au réchauffement climatique participent aux épisodes de mortalités chez les huîtres et les moules en favorisant le développement ou la sélection de certains pathogènes. Si l'identification de ces agents est importante pour détecter des maladies, la caractérisation des défenses immunitaires des bivalves est également indispensable afin de mieux comprendre l'interaction entre ces pathogènes, leurs hôtes, leurs pathologies, et proposer des marqueurs de leur état de santé et de leurs capacités immunitaires. Pour se défendre face aux pathogènes, ces invertébrés marins possèdent un système hémolympatique ouvert dans lequel circule des cellules immunitaires appelées hémocytes. Les bivalves ne possèdent qu'une composante immunitaire innée mais sont néanmoins capables de répondre très efficacement à des stress biotiques ou abiotiques. Chez l'huître et la moule, les hémocytes constituent une population très diverse et peu caractérisée de cellules. Bien que la réponse immunitaire de ces deux mollusques ait fait l'objet de nombreuses études aux niveaux transcriptionnel et moléculaire, la diversité des lignages hémocytaires et la caractérisation des sous-populations restent encore méconnues. Les avancées dans le domaine du séquençage massif permettent maintenant de travailler sur de très faibles quantités d'acides nucléiques et rendent possible le séquençage des ARNm d'une seule cellule. Nous avons donc utilisé une technique de séquençage d'ARNm sur cellules uniques (Drop-Seq scRNA-Seq) afin de caractériser la diversité hémocyttaire de deux espèces de bivalves (*C. gigas* et *M. edulis*). Nos résultats valident l'approche de scRNA-Seq chez ces animaux et montrent un nombre de clusters transcriptomiques différents chez ces deux espèces de bivalves. Les données obtenues permettent ainsi de construire un atlas transcriptomique des hémocytes. A partir des gènes surexprimés dans chaque cluster nous sommes en capacité d'obtenir des informations fonctionnelles et d'identifier des gènes marqueurs de chaque cluster pour chaque espèce. En conclusion, l'approche de scRNA-Seq chez les bivalves est possible et permet de révéler l'hétérogénéité cellulaire de leur système immunitaire d'un point de vue transcriptomique. Ces données permettent de proposer des marqueurs moléculaires potentiellement utilisables afin de suivre par qPCR les changements de populations cellulaires en réponse à des stress biotiques ou abiotiques.

Mots-Clés: Bivalves, Hémocytes, scRNAseq, Immunité, Transcriptomique

*Intervenant

Compartmentalization in bacteriomes protects endosymbionts from their insect host immunity

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Résumé

Mutualistic symbioses with intracellular bacteria (endosymbionts) are a common strategy for insects to acquire essential nutrients in nutrient-poor habitats. The establishment of an equilibrium between excessive host colonization by the symbiont and chronic activation of the host immune system is essential in such symbiotic relationships, as the former would be detrimental for host survival, while the latter would result in symbiotic damage and host fitness reduction.

As many other insect endosymbionts, the bacterium *Sodalis pierantonius* is housed in specialized cells, the bacteriocytes, contained in a specialized organ – the bacteriome – at the foregut-midgut junction of its host, the cereal weevil *Sitophilus oryzae*. Previous evidence showed that the bacteriome is immune-responsive to insect bacterial challenge, and that artificial injection of *S. pierantonius* in the host hemolymph triggers insect systemic immunity, showing that *S. pierantonius* injection in the host hemolymph triggers *S. oryzae*'s immune system. Hence, bacteriomes not only participate in the immune response to external pathogens but also protect the host against chronic immune activation, raising the question of how endosymbionts overcome such host immune response. We conducted a dual transcriptomic analysis of *S. oryzae*'s bacteriomes subjected to immunogenic peptidoglycan fragments, thus mimicking a pathogen attack. We confirmed that the bacteriome actively participates in the innate immune response mainly via a burst of antimicrobial peptides, but also showed that endosymbionts do not undergo any transcriptomic changes, indicating that this potential threat goes unnoticed. Immunohistochemistry of selected antimicrobial peptides showed that they are secreted outside the bacteriome, excluding direct contact with the endosymbionts.

In summary, the compartmentalization of endosymbionts in the bacteriome is an efficient evolutionary strategy that fulfils two important functions: protection of the host by preventing overactivation of the immune system, and isolation of endosymbionts from competition with pathogens intruders.

Mots-Clés: mutualistic symbiosis, innate immunity, insect

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