COEVOL MULTI-SCALE COEVOLUTION

EVOLUTIONARY GENETICS OF INTERACTIONS GROUP

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Research interests

The goal of my research is to bring an evolutionary perspective to the study of symbiosis, through the understanding of molecular interactions between partners.

Animals live in symbiosis with controlled bacterial communities in contrasting and changing environments. Symbionts can impact the phenotype of their host positively (*e.g.*, by providing nutrients or protecting their host from pathogens) or negatively (by imposing a fitness cost). These partner interactions evolve in response to different selection pressures, making the associations dynamic along the continuum between parasitism and mutualism, and may also vary the degree of dependence between partners. I am particularly interested in the evolution of these symbiotic associations in response to different selection pressures, and in characterizing the molecular mechanisms underlying these changes.

Recent projects

Understanding the interactions between the bedbug and its microbiota, to control its populations by breaking the symbiotic association

Funding Pack Ambition Recherche (
région Auvergne Rhône-Alpes)
2019-2024 / SymBed Project/ Collaboration with
BF2i
and
IZInovation
/ PhD Marius Poulain and Raphaël Jorge.

Funding
ANR PRC
2021-2025 / FBI Project / Collaboration with
BF2i
and
LECA
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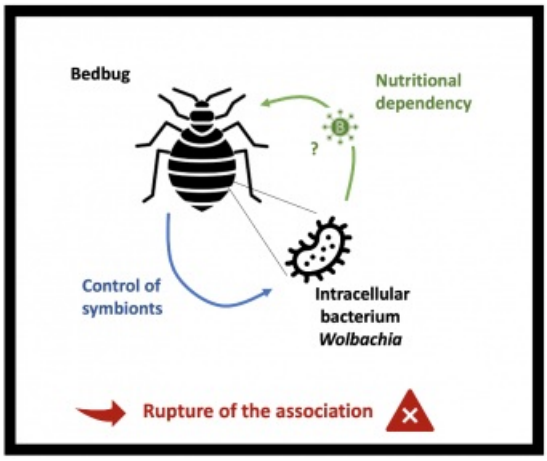
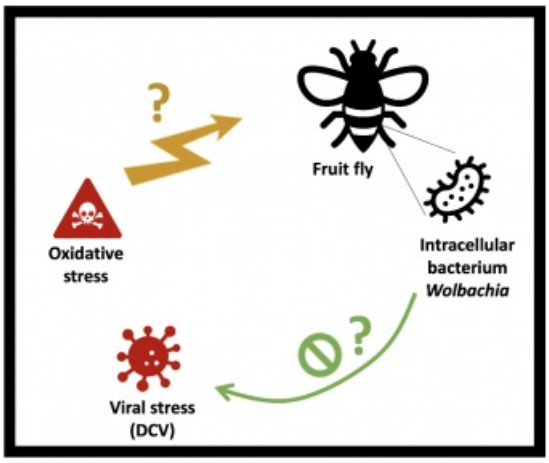


Bedbugs have increased significantly over the last ten years, mainly due to the increase in human migration and resistance to insecticides. In the short term, the study of resistance determinants (project of Julien Varaldi / Jean-Philippe David) will allow to target the use of insecticides. In parallel, we are studying the interactions between the bedbug *Cimex lectularius* and its obligate bacterium *Wolbachia* in order to break the symbiotic association and control bedbug populations by alternative methods to pesticides. Indeed, *Wolbachia w*Cle bacteria synthesize B vitamins that are necessary for the development and fertility of bedbugs. Using transcriptomics, metabolomics and microscopy approaches, we are studying in detail the interactions between the insect and its nutritional symbionts, in order to identify molecular mechanisms involved in the regulation of bacterial density and in the dependence of the bedbug on its symbiont.

Rapid Evolution of symbiotic interaction in response to stress

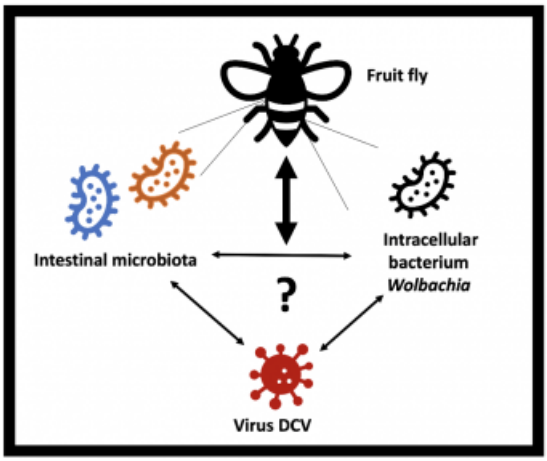
Funding JCJC
ANR
2017-2021 / RESIST Project / PhD Alexis Bénard



Symbionts can promote or constrain rapid host adaptation to environmental changes. In response to global changes (temperature, precipitation; air, water and soil quality; biological invasions…) and to anthropization (intensive agriculture; urbanization…), it is therefore important to study the impact of these changes at the holobiont scale, *i.e.,* the host and its microbial communities. In the RESIST project, we studied more precisely: to what extent do stresses associated with the presence of pesticide (paraquat) and/or virus (DCV) impact flies of the genus *Drosophila melanogaster*, directly or indirectly via an impact on their *Wolbachia* symbionts? How does the symbiotic association evolve and more particularly if the presence of *Wolbachia* allows a rapid adaptation to these stresses? And what molecular and metabolic mechanisms are involved in the response to viral and/or oxidative stress?

Impact of commensal and endosymbiotic bacteria on viral infection in insects

Funding
Labex Ecofect
2017-2019 / ComEndoVir Projet/ Co-PI with
F. Leulier
(IGFL) / Post-doc Vincent Raquin



The complex relationships between different microbial communities and how these communities can impact their host remain poorly studied. In the ComEndoVir project, we therefore characterized the impact of polymicrobial associations on *Drosophila* physiology. To this end, we created an artificial holobiont model, composed of two commensal bacteria of the digestive tract (*Lactobacillus plantarum* and *Acetobacter pomorum*), the intracellular bacterium *Wolbachia* and the pathogenic virus *Drosophila C virus* (DCV), and measured several life history traits related to the physiology of the host and the microbes. We showed that the multipartite interactions detected within the host impact host physiology, with multiple bacterial interactions notably allowing for improved tolerance to viral infection.

Previous research

Post-doc - Establishment and maintenance of the squid/vibrio symbiosis

2010-2014. University of Madison-Wisconsin, USA. Supervision : Margaret McFall-Ngai

During my post-doc, I worked on the mutualistic association between the sepiola *Euprymna scolopes* and the bioluminescent bacterium *Vibrio fischeri*, acquired anew each generation from the surrounding water. *V. fischeri* represents less than 0.1% of the bacterioplankton, but surprisingly, it is the only bacterium able to efficiently colonize the light organ of the squid. As the initiation of symbiosis can be easily reproduced in the laboratory, this association constitutes a particularly interesting model to study, in real time, the initial communication between the two partners of the symbiotic association. Using comparative transcriptomics and functional approaches, I characterized the first molecular dialogue between the two partners, just after their first contact.
Another interesting question is to understand how this symbiotic association is maintained, since we observe a daily phenomenon of expulsion then recolonization of bacteria in the light organ. This daily rhythm is associated with a coordinated change in gene expression in both the host and the bacteria, and it has been shown that the symbiotic population is maintained under hypoxic conditions. My second project was therefore to understand how the oxidative environment controls, and is controlled, by the symbiosis.

PhD - Evolution of dependancy in *Wolbachia* symbioses

2005-2009. University Lyon 1, Lyon, France. Supervision : Fabrice Vavre

During my thesis, I worked on the intracellular bacterium *Wolbachia*, which induces a wide range of phenotypic effects on its hosts, from facultative reproductive parasitism in arthropods to obligate mutualism in nematodes.
The hymenopteran *Asobara tabida* is one of the few species where *Wolbachia* is required for the ovogenesis of its arthropod host. It thus constitutes a particularly relevant study model to investigate the mechanisms underlying this recent evolutionary transition.
I first investigated the variability of *Wolbachia* dependence within the genus *Asobara*. Using various transcriptomic approaches, I then characterized the molecular mechanisms involved in the dependence between *A. tabida* and *Wolbachia*, and highlighted processes associated with oxidative stress, programmed cell death, and development. Finally, I examined the extent to which *Wolbachia* impacts the physiology of its host by studying iron metabolism in various symbiotic associations.
These studies revealed that dependence is not always associated with the contribution of new functions. Rather, it may reflect compensatory mechanisms in the host, in response to physiological perturbations induced by the presence of the symbiont. More generally, these results invite us to consider the effects and consequences of the presence of symbionts beyond the mechanisms that allow their persistence within populations.