

# A holistic approach of host-pathogen interactions

Eve Toulza – Caroline Montagnani – Benjamin Gourbal – Guillaume Mitta

# **IHPE – UMR 5244**

## Scientific objectives

Emerging theories of evolution highlight the importance on host fitness of the interaction with its microbial associates. Host and its interacting microbiota are referred to as the holobiont. The collective genome of this entity, the holo(epi)genome, is a source of phenotypic variability which represents a material for multi-level selection.

Despite its importance for organism adaptability in a context of environmental changes, extended studies of the hologenome composition and functioning are still limited and usually take into account only the bacterial composition without considering other symbionts (protists and viruses) neither their functions nor the (epi)genomic diversity of the different partners in interaction. With the development of omics, it has now become possible to investigate the role of microbes in host adaptive capacities, not only in terms of taxonomic composition but also in terms of gene content and activity.

A major axis of our research aims at characterizing the relative contribution of host and microbial community's responses to the fitness of the holobiont in a broad sense. Our models include aquatic invertebrates of medical, ecological or economic importance. More precisely, we investigate the role of microbiota (i) in the disease outcome of oyster mortality syndromes (ii) in the interaction between schistosome parasites and their intermediate snail hosts and (iii) in the response of the coral holobiont to temperature stress. We are particularly interested in the underlying immune interactions, and we are also starting to explore transmission and intergenerational effects of the microbiota.

We implement holistic and multi-layered approaches combining experimental as well as field studies to investigate the molecular mechanisms underlying organisms' responses to environmental changes, accounting for genomic modifications, epigenetic reprogramming and modifications of the microbiota (including bacteria, protists and viruses).

Finally, we are seeking to implement close collaborations with mathematicians and stakeholders to predict the outcome of changing interactions between organisms and their environments to propose management measures.

### Link to Major Themes of Research of TULIP

This project is mainly linked to MTR2 (organism-organism interactions) and MTR3 (environment effect on interactions between organisms) and has some extensions in MTR4 (interactions within populations and communities) as our systems involve more than two partners as well as the effect of the natural environment on holobiont functioning and response to changes.

### ETPs involved on the project

7 ETP, 6 non-permanent staffs