

Sassera research activity

Evolution of symbiotic relationships and of infectious agents

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My focus of study are the interactions between organisms. My two main research lines in this field are the study of symbiosis and the evolution of infectious agents.

Symbioses are broadly defined as interactions between different organisms, starting from the simplest interactions, such as host-parasite and host-pathogen, to the study of the more complex ones, involving several protagonists. One example is the Midichloria system, which involves various species of vertebrate hosts, a parasitic arthropod (the tick *Ixodes ricinus*), an intracellular organelle (the mitochondrion) and a unique intramitochondrial symbiont. The study of symbiosis is necessarily multidisciplinary, and thus requires integrated methodological approaches. Starting from molecular, ultrastructural and serological methodologies, I specialized in the latest -omics technologies, using proteomics and above all genomics and transcriptomics approaches for the study of different symbiotic systems.

Currently the main project on which I am working is the funded project HFSP 2016, in the context of which I lead an international team (Institut Pasteur, Walter and Eliza Hall Institute, Koln University) to understand the mechanisms of interaction between Midichloria and mitochondria. In the context of this project, the collaboration of researchers with different expertise has allowed to design a research plan that merges genomics, parasitology, cellular biology, biochemistry and bioinformatics with the final goal to understand Midichloria to understand mitochondria. Connected to the HFSP project, a collaboration is ongoing with the ONIRIS research center in Nantes, on the effect of antibiotic treatments on the presence of the *M. mitochondrii* symbionts in populations of the host tick *I. ricinus*. The aim of the study is to obtain aposymbiotic populations and to evaluate changes in their fitness parameters. The project is funded with a doctorate scholarship from the Italian-French University.

I am also currently involved in three bioinformatics projects that use genomics and bioinformatics to study parasites and pathogens.

The SpARK project, funded by European funds, gathers researchers from 5 countries for a genomic epidemiology approach on the nosocomial pathogen *Klebsiella pneumoniae*. Through a capillary sampling in the Pavia area, followed by the most advanced genomic, bioinformatic and statistical analyses, SpARK aims to understand the ways and means of transmission of clones and genes in bacteria of the genus *Klebsiella*.

In collaboration with the San Matteo Hospital and the University of Milan, I am involved in the Skynet platform, which aims to implement continuous microbiological genomic surveillance and integrate it with metadata on patients (including their movements) in the Lombardy health system.

This ambitious goal could allow monitoring, and potentially preventing, the spread of bacterial pathogens in hospitals. Currently two pilot studies focusing on *Klebsiella pneumoniae* and *Staphylococcus aureus* are ongoing.

In a research project funded by the Ministry of Health (Finalizzata 2016), I collaborate with Roman and Pavia researchers for the development of innovative diagnostic methods for cystic echinococcosis. The role of my unit is to analyze *Echinococcus* -omics data to develop a protein that will allow us to test the antigenic characteristics of a set of proteins and peptides of this parasite, with the aim of obtaining serological diagnostic methods with high sensitivity and specific for the different stages of the disease.