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Evolution and control of host-microbe symbiosis in arthropods: an RNAseq-based transcriptomic analysis

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Symbiotic interactions between microbes and eukaryotic organisms are widespread in nature and exhibit different features ranging from parasitism to mutualism. However, despite their different outcomes, parasites and mutualists microbes share mechanisms of infection, proliferation and defense within hosts: the molecular dialog between microbial mutualists or parasites and their hosts appears to have common bases.

To decipher common but also specific molecular mechanisms underlying the functioning of intimate interactions, we have developed a comparative transcriptomic approach using RNAseq in four symbiotic systems exhibiting different features, but all involving arthropod hosts associated with endosymbiotic vertically-transmitted bacteria. Three species are associated with *Wolbachia*: the hymenopteran wasp *Asobara tabida,* where *Wolbachia* appears necessary for oogenesis completion, the mosquito *Aedes albopictus*, where cytoplasmic incompatibility-inducing *Wolbachia* are close to commensal and the isopod *Armadillidium vulgare* where *Wolbachia* induces feminization generating a strong nucleo-cytoplasmic conflict. The fourth species is the cereal weevil Sitophilus oryzae, which shares an obligate trophic relationship with a gamma-proteobacteria called SPE (*Sitophilus* primary endosymbiont).

RNAseq analyses have been performed on ovaries of infected and uninfected individuals. In this talk, we will present the bioinformatics pipeline that has been set up for exploitation of transcriptomics data on these non-conventional organisms. The identification of genes differentially expressed between infected and uninfected individuals and their comparison across four invertebrate species will permit to unravel common and distant molecular mechanisms involved in symbiotic interactions.

Keywords: Bacterial-arthropod symbioses, Functional pathways in symbiosis, RNA sequencing