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Living systems are made up of a multitude of interlocking levels of organization, involving cooperation and conflict. Cooperation and the selection of systems operating in a coordinated manner has allowed so-called "major" evolutionary transitions, towards new scales of individuality, such as the eukaryotic cell. Nevertheless, natural selection continues to operate at all scales, generating possible evolutionary conflicts between the different components of the individual.

Our research is in line with this perspective, and aims to better understand the nature and evolutionary implications of the interactions between the multiple components of organisms, from genes to symbiotic bacteria, viruses and transposable elements. We also explore the impact of these interactions on the dynamics of genetic information, through horizontal transfer, or on genetic innovation and adaptation, through domestication. Our research, mainly experimental, but also theoretical, is implemented on arthropod models, and is mainly related to genetics and evolutionary genomics.

The team is structured along two main axis:

### > **Intragenomic interactions: transposable elements (resp. Marie Fablet)**

Ex1: The evolutionary dynamics of transposable elements (TEs) in genomes, in relation to their natural variability. Our models include natural populations of *Drosophila melanogaster* and *D. simulans*, as well as species of agronomic or societal interest, such as the invasive species *D. suzukii* or the tiger mosquito *Aedes albopictus*.

Ex2: Interactions between ET control and anti-viral immunity. We are studying the molecular mechanisms of RNA interference at the origin of the entanglement of these two processes, as well as the co-evolutionary implications, using experimental infections of different viruses on several *Drosophila* lines.

*People involved : CV, MB, MF*

### > **Symbiosis, the driving force of evolution (resp. Natacha Kremer)**

Ex1 : Certain symbiotic bacteria provide metabolic capacities that the insect lacks. We are analysing these interactions in haematophagous insects (bedbugs, ticks) and phytophagous insects (the whitefly *Bemisia tabaci*) using approaches combining phenotype analysis, genetics, physiology and metabolomics.

Ex2: Parasitoid insects have domesticated viral genes enabling them to bypass the immune responses of their hosts. We are studying the frequency and adaptive significance of these events and, more generally, looking into the factors structuring horizontal transfers in host-parasitoid communities.

*People involved: NK, LM, LZ, JMD, JV, FV, SC*