COEVOL MULTI-SCALE COEVOLUTION

EVOLUTIONARY GENETICS OF INTERACTIONS GROUP

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Almost 50% of our genome is made of transposable elements, which are sequences able to move and multiply along the chromosomes. Among these sequences, endogenous retroviruses are remnants of ancient viral infections, which are now transmitted from one generation to another in a gene-like manner.

Within and between species dynamics of transposable elements

Our group is interested in the dynamics of these sequences in the genomes of natural populations, based on the twin species model D. melanogaster / D. simulans. The amount of transposable elements in the genomes of these natural populations is highly variable, as are the activity and regulation of these sequences. This allows a powerful comparative approach to dissect the involved mechanisms.

In order to understand the observed variability, we are investigating the epigenetic control of TEs, particularly via the piRNA class of small interfering RNAs. We are exploring the link between differences in TE dynamics and variability in the regulation by piRNAs, using sequencing data as well as laboratory experiments.

Epigenetics and genome stability: how the environment affects transposable element stability

We study genome stability through the diversity of the epigenetic pathways controlling TEs, in normal conditions and when the environment changes. We use fresh Drosophila samples coming from temperate (France) and tropical (Brasil) areas, that are submitted to various environmental stress. We then characterize TE content and activity as well as epigenetic regulation using NGS technologies.

Endogenous Retroviruses and Immunity

We want to investigate the interplay between the host immune responses to arbovirus (Arthropod Borne virus) infections and the TE and Endogenous Retroviruses (ERV) genomic control mechanisms (RNA interference: piRNA and siRNA pathways) using Drosophila as an in vivo model system. To this end, we will take advantage of the natural variability existing between and within species for ERVs (copy numbers, activities, and control by the piRNA pathway).