Temporal and spatial partitioning of retrotransposon niches in Drosophila melanogaster

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Résumé

The Transposable Elements (TEs) are parasitic DNA sequences present in almost all sequenced genomes. They are able to move within a genome by a mechanism known as transposition. This mobility can induce mutations that can be beneficial for the host, by allowing genetic diversity, a potential source of evolution, or deleterious by inducing diseases such as cancer. Thus, several repression mechanisms against TE activity have been selected. In the germline, specific defense pathways are activated by the host to counteract TE expression, keeping the transposition rate at a low level to ensure genomic integrity of the progeny. Nevertheless, these TEs represent a fair amount of the genome (up to 15% in the genome of *Drosophila melanogaster*) and have a high sequence diversity, classifying them in hundred families.

How these families are maintained within genomes and coexist is the question I aim to answer in my thesis. My working hypothesis is that each of these families exploits not only features of the host genome, but also features specific to the different stages of their transposition cycle.

To test this, my laboratory engineered a *Drosophila* line to induce the expression of several TE families in the follicular somatic cells that surround the germline. This TE expression induction was correlated with an increase in inheritable new TE insertions after one generation (Barckmann et al. 2018). The lab has induced this TE expression over 70 generations and using long-read DNA sequencing and a bio-informatic pipeline established in the laboratory (TrEMOLO,https://github.com/DrosophilaGenomeEvolution/TrEMOLO), we have precisely determined the new TE integration sites and highlighted the families concerned by this increase. Two Endogenous RetroVirus families (ERV), ZAM and gtwin, have seen their number of insertions increase significantly.

By analyzing numerous published Omics datasets on different features of the Drosophila genome (ChIP-seq, ATAC-seq, single cell ATAC-seq), I was able to demonstrate that these two families choose different landing sites characterized by specific epigenetic marks in the host genome. In addition the timing of ERV integration during Drosophila embryogenesis is not the same. Finally, these two families show different expression profiles in ovaries and embryos.

Overall, my data suggest that the different TE families have different ecological niches within a host, allowing them to coexist.

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Mots-Clés: Transposable elements, Drosophila, Epigenetics