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Fondation Innovations en Infectiologie

Endogenization of Drosophila retroviruses: a cellular and populational approach

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Exogenous retroviruses infect somatic cells , but some can also infect germline cells and once they have done so and have been transmitted to the next generation, they are termed endogenous retroviruses (ERVs). ERVs are present in animal's genomes: recent genomic data indicates that 8% the human genome is derived from ERVs. Hence, the impact of ERVs on function and evolution of genomes is critical.
However, the process of infection of the germline, i.e. endogenisation, by retroviruses remains unknown, mainly because *in vivo* observations of endogenisation in real-time are very rare. Among the host organisms, *Drosophila melanogaster* is probably one of the most powerful models for the study of the genesis and impact of ERVs, since its genome contains the highest percentage of active full-length endogenous retroviruses among animals studied until now. We consider that the question of endogenisation should be addressed at the cellular level, in order to understand the assembly and transfer of ERVs particles, and at the populational level, in order to estimate the selective forces which maintain the coding capacities of ERVs.
We will present recent data which illustrate the process of endogenisation considering the gypsy ERV in *Drosophila melanogaster* laboratories strains, and the tirant ERV in a natural population of *D. simulans*.