



12
MAI.
2023

🕒 de 13h à 14h

📍 Salle Legay -

SÉMINAIRE

Polydnavirus chromosomal integration and inheritance in lepidopterans

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Increasing numbers of horizontal transfer (HT) of genes and transposable elements are reported in insects. Yet the mechanisms underlying these transfers remain unknown. Here I will first summarize some of our recent results showing that polydnaviruses (PDV) of parasitoid wasps undergo massive chromosomal integration in somatic cells of their hosts upon parasitism.

Polydnaviruses are domesticated viruses injected by wasps together with their eggs into their hosts in order to facilitate the development of wasp larvae. We find that each haploid genome of parasitized hosts suffers between 12 and 85 integration events (IEs) on average after parasitism. Almost all IEs are mediated by DNA double strand breaks occurring in the host integration motif (HIM) of PDV circles. We show that despite their independent evolutionary origins, PDV from both Campopleginae and Braconidae wasps use remarkably similar mechanisms for chromosomal integration. We further find that while reproducing host adults that resisted to parasitism can bear an average of nearly two PDV integrations per haploid genome, none of these integrations were retrieved in 500 of their offspring using Illumina sequencing. This suggests either that host gametes are less targeted by PDVs than somatic cells or that gametes bearing PDV integrations are nonfunctional. Interestingly, we uncovered that PDVs can massively integrate into the chromosomes of other lepidopteran species that are not normally targeted by the wasp in the wild, including one which is divergent by at least 100 million years from the natural host. Finally, our similarity search performed on 775 genomes reveals that PDVs of both Campopleginae and Braconidae wasps have recurrently colonized the germline of dozens of lepidopteran species through the same mechanisms they use to integrate into somatic host chromosomes during parasitism. We found evidence of HIM-mediated HT of PDV DNA circles in no less than 124 species belonging to 15 lepidopteran families. Thus, this mechanism underlies a major route of HT of genetic material from wasps to lepidopterans with likely important consequences on lepidopterans.