

🕓 de 13h à 14h

SÉMINAIRE

Complex genomic landscape of inversion polymorphism in Europe's most destructive forest pest

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In many species, polymorphic inversions underlie complex phenotypic polymorphisms and appear to facilitate local
adaptation in the face of gene flow. Multiple polymorphic inversions can co-occur in a genome, but the prevalence, evolutionary
significance and limits of complexity of genomic inversion landscapes remain poorly understood. I will present our recent study in
which we examined genome-wide variation in one of Europe's most destructive forest pests, the spruce bark beetle lps
typographus, scanned for polymorphic inversions and tested whether inversions are involved in key adaptations in this species.
We discovered a genomic landscape that not only represents one of the most complex genomic inversion architectures described
to date, but is also enriched in odorant receptor genes involved in host plant, mate and symbiotic fungal recognition pathways.
Our results raise questions about the limits of complexity of genomic architecture and the consequences of having inversion-rich
genomes, which I will briefly discuss at the end of my talk.