30
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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 Ips 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.