

IBIOL Seminar Series



30 September 2026



12:15-13:30 PM



F200

Come for cool science,
stay for cookies and
coffee!



Sam Horsfield

Simulating evolution of eukaryote pangenomes

Many eukaryotes have pangenomes - this is the observation that their populations have far more genetic diversity than that present in a single genome. In fungal species, the pangenome encodes a huge variety of important phenotypic characteristics, including drug resistance and virulence. However, we still don't have a good idea why pangenomes exist or how they are maintained. I'm working on a pangenome simulator, PansimNuc, which models a range of evolutionary mechanisms, including recombination, selection, Transposable Element (TE) movement and demographic changes such as migration, to understand how and why pangenomes evolve.

TALK n°1



Paula Escuer Pifarré

The epigenomic landscape across Lepidoptera and its role in chromosomal rearrangements

Karyotypic variability is common in holocentric organisms such as Lepidoptera, as a consequence of chromosomal rearrangements, and has been hypothesized its role as a barrier to gene flow and thus promote speciation. Repetitive elements have been proposed as drivers of rearrangements, yet they do not fully explain the rearrangements bursts observed in certain lineages. DNA methylation in insects, and particularly in Lepidoptera, remains largely unknown, as does its relationship with genome evolution. Here we characterize genome-wide methylation across 106 individuals from 60 Lepidoptera species, integrating its chromosomal breakpoint data. This work aims to shed light on the drivers of genomic rearrangements and the methylation landscape of Lepidoptera, with special attention to karyotypically variable lineages.

TALK n°2



Corentin Maslard

Decoding root barriers: from single cells to whole-root architecture

Plant roots are highly dynamic organs that constantly adjust their development to the surrounding environment. In grasses such as Brachypodium, specialized cell layers form protective barriers that control exchanges of water and nutrients between the soil and the plant. But how are these barriers formed and regulated? By combining single-nucleus RNA sequencing, cell-type-specific reporters, and AI-assisted root phenotyping, we explore root development from individual cell identities to whole-root architecture. This multiscale approach aims to uncover the molecular programs behind root barrier formation and understand how they contribute to plant adaptation to environmental stresses.

TALK n°3