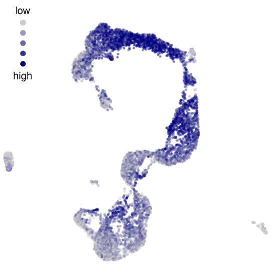

External seminars – IGFL

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Invité par/Invited by **Eglantine Heude**

Date **29/01/2026**

Titre de la présentation/Title of the presentation
Convergent evolution of genomes and phenotypes in birds

Résumé/Short abstract

Functional evolutionary genomics studies can bring insights into the selective pressures and molecular mechanisms that drive the emergence (or loss) of biological functions and of phenotypes. In this talk, I illustrate how comparative genomics approaches can bring insights into the genomic basis of convergent phenotypic evolution, in the avian model system. The avian clade displays a spectacular diversity of phenotypes. Numerous instances of convergent phenotypic evolution are known in birds, such as the convergent loss of flight or the parallel gain of vocal learning. In this presentation, we will focus on one peculiar case of convergent morphological evolution : the loss of the intromittent male phallus. Although an intromittent phallus was likely present in the ancestor of all amniotes, this organ was reduced or entirely lost in multiple avian lineages. The evolutionary processes that led to phallus reduction or loss are still unclear, as are the genomic consequences of this major phenotypic change. Taking advantage of the availability of hundreds of avian genomic sequences, we have performed large-scale evolutionary analyses of protein-coding gene sequences and of non-coding regulatory elements, searching for genomic changes that occur in parallel with phenotypic changes. We found that hundreds of protein-coding genes and non-coding regulatory elements underwent an acceleration of their rate of evolution following this major phenotypic change. We also identify numerous gene expression differences between bird species that have retained the intromittent phallus and species that have lost this organ. While we cannot claim that these changes in expression patterns and regulatory programs are causal to the loss of the phallus, our findings illustrate the genome-wide consequences of this major phenotypic change.

Mini-CV/Short CV (+ Picture of you)

2008: PhD at the University of Lyon. My PhD reseach topic was the evolution of DNA base composition.

2009 – 2012: Post-doctoral fellowship, University of Lausanne. I participated in pioneering comparative transcriptome sequencing studies. I focused on the evolution of protein-coding gene expression levels and on the evolution of long non-coding RNAs.

2012 – 2016: Junior group leader, Ecole Polytéchnique Fédérale de Lausanne. I continued my work on long non-coding RNA evolution and became interested in developmental genomics.

2016 – present: CNRS researcher at the LBBE, Lyon. My main research interest is the evolution of gene expression regulatory mechanisms and its relationship with the evolution of phenotypes.