

Institut Jean-Pierre Bourgin

# Séminaire

Lundi 25 juin 2018, à 14h00

**Dr. Korbinian Schneeberger**

*Genome Plasticity and Computational Genetics  
Max Planck Institut, Cologne, Allemagne*

## **Phylogenetic association mapping and a simple, sequencing-based method to assess meiotic recombination landscapes**

During the past years, great progress has been made in the development of association methods for GWAS or QTL mapping. However, methods to map the variation that can be found between species are still sparse. We have developed a genomics-based method for between-species (or 'phylogenetic') association mapping (PAM), which can find signals even in highly re-arranged genomes of different species. In my presentation, I will show how we used PAM in a panel of 47 closely-related plant species to map the genetic underpinnings of differences in the mutational profiles that we found in these species. In the second part of my talk I will present a new method that reveals meiotic recombination landscapes in a single, sequencing experiment. Using sequencing data from ultra-long molecules extracted from hybrid pollen we can precisely estimate the location of hundreds of crossing-over events. We assess our method using a pool of recombinant plants which also have been whole-genome sequenced individually. Ultimately, we plan to use this method to phenotype recombination landscapes across our 47 plant species and use it as a trait for PAM.

[Korbinian Schneeberger groupe webpage](#)

Invité par **Christine Mézard & Raphaël Mercier**  
Ce séminaire aura lieu dans l'Amphithéâtre Bât. 10