



# Rustomics

## An integrated multi-omics approach to decipher the poplar-poplar rust interaction

Project leader: Sébastien Duplessis , UMR Interaction Arbre Micro-organismes (IAM) 1136

LabEx partners: Pascal Frey & Arnaud Hecker

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### Summary

*Context* — Rust diseases caused by fungi of the order Pucciniales cause significant damage to many crops and plantation trees such as poplar. The pathosystem established between poplar and *Melampsora larici-populina* is one of the most advanced models for the understanding of the mechanisms of interaction with Pucciniales, in particular because of the availability of host and pathogen genomes. Studies conducted in the last ten years have allowed progress in our understanding of the infectious process, however, our knowledge of the molecular mechanisms at play still needs to be improved.

*Objectives* — In order to clarify the determinants of infection in the fungus and the resistance and defense mechanisms implemented by poplar during the interaction with the pathogen, we propose to set up a multi-omics approach in the context of the infection of a poplar cultivar by avirulent (resistance process) and virulent (successful infection) isolates.

*Approaches* — Based on time-course infection produced in the lab (collection of 7 points between spore inoculation and symptoms at 7 days), mRNAs and small-RNAs will be extracted in order to perform a transcriptomic analysis by Illumina sequencing, proteins will be extracted in order to perform a proteomic analysis, and finally, metabolites will be extracted in order to complete the analysis by a metabolomic approach.

*Expected results and impacts* — The analysis of these three approaches, thanks to the reference genomes available, will give us for the first time access to the profiles of the genes and proteins expressed, as well as the metabolites produced. The integration of all these data will be particularly powerful to generate a more complete view of the molecular events that take place during the interaction. These new results will guide future work to find new methods to control Pucciniales.