

Genomics, Transcriptomics, and Effectoromics of the Poplar Leaf Rust Fungus *Melampsora larici-populina*

B. Petre^{1, 2, 3}, S. Hacquard^{1, 2, †}, A. Persoons^{1, 2}, N. Saveleva^{1, 2}, E. Tisserant^{1, 2}, E. Morin^{1, 2}, C. Delaruelle^{1, 2}, J. Petrowski^{1, 2}, M. Pernaci^{1, 2}, B. Fabre^{1, 2}, S. De Mita^{1, 2}, F. Halkett^{1, 2}, A. Hecker^{1, 2}, N. Rouhier^{1, 2}, P. Frey^{1, 2}, and S. Duplessis^{1, 2, *}

¹ Institut National de la Recherche Agronomique/Université de Lorraine Interactions Arbres/Micro-organismes, Centre INRA Nancy Lorraine, Champenoux, France

² Université de Lorraine/Université de Lorraine Interactions Arbres/Micro-organismes, Faculté des Sciences et des Technologies, Vandoeuvre-lès-Nancy, France

³ Norwich Research Park, the Sainsbury Laboratory, Norwich, United Kingdom

[†] Current address: Max Planck Institute for Plant Breeding Research, Department of Plant-Microbe Interactions, Cologne, Germany

* sebastien.duplessis@inra.fr

Melampsora larici-populina is causing leaf rust disease in poplar (*Populus* spp.) worldwide and poses serious problems to poplar breeders in France and in northern Europe. As with other rust fungi, its obligate biotroph status hinders laboratory investigations. Understanding the biology of rust fungi and deciphering the molecular mechanisms underlying biotrophy have long been a problem. Most of the knowledge gained was largely descriptive and limited to a few rust species; only recently has substantial progress been made in the characterization of avirulence determinants of the flax rust *Melampsora lini*.

The pioneer sequencing of the genomes of the poplar rust fungus *M. larici-populina* and of the wheat stem rust fungus *Puccinia graminis* f. sp. *tritici* in 2011 has opened great perspectives for the molecular study of this group of fungi. Comparative analyses with recent reports have confirmed the typical profile of rust fungi genomes. These genomes are rather large (>89 Mb) and contain many repetitive and transposable elements (~50 percent of the genome) and a very large number of predicted genes (>16,000), including many large gene families of unknown function with no homology outside the Pucciniales. Within the genomes are several hundreds of genes encoding candidate effectors that are likely to be involved in the fungal virulence. These effectors are small secreted proteins specifically expressed *in planta*.

In the present talk, we will briefly introduce some basics about the poplar rust genome. We will provide an overview of our current knowledge gained by genome-wide oligoarrays and RNA-Seq on *M. larici-populina* gene expression at different stages of the complex lifecycle of this heteroic and macrocyclic rust, particularly during successful infection of the telial host (poplar) and of the aecial host (larch, *Larix* spp.). We will present our current strategy to characterize virulence effectors and illustrate a few candidates under investigation. Finally, we will provide an overview of ongoing genomics projects including the refinement of the genome assembly through the construction of a genetic map and a population genomics approach to identify the gene(s) responsible for a breakdown in the major gene resistance in poplar plantations.

ACKNOWLEDGMENTS

We acknowledge the support of public grants overseen by the French National Research Agency (ANR) as part of the “Investissements d’Avenir” program (ANR-11-LABX-0002-01, Lab of Excellence ARBRE) and the Young Scientist Grant POPRUST to Sébastien Duplessis (ANR-2010-JCJC-1709-01) and by the Région Lorraine (Researcher Award to Sébastien Duplessis). We also acknowledge the support of poplar rust genomics by the U.S. Department of Energy Joint Genome Institute through the 2014 Community Science Program.

In: Schoettle, Anna W.; Sniezko, Richard A.; Kliejunas, John T., eds. 2018. Proceedings of the IUFRO joint conference: Genetics of five-needle pines, rusts of forest trees, and Strobosphere; 2014 June 15–20; Fort Collins, CO. Proc. RMRS-P-76. Fort Collins, CO: U.S. Department of Agriculture, Forest Service, Rocky Mountain Research Station. 245 p.

Papers published in these proceedings were submitted by authors in electronic media. Editing was done for readability and to ensure consistent format and style. Authors are responsible for content and accuracy of their individual papers and the quality of illustrative materials. Opinions expressed may not necessarily reflect the position of the U.S. Department of Agriculture.