

Adaptation of Poplar Rust to the Poplar Varietal Landscape

K.J. Hayden^{1, 2}, C. Xhaard^{1, 2}, B. Fabre^{1, 2}, F. Halkett^{1, 2}, and P. Frey^{1, 2, *}

¹ Institut National de la Recherche Agronomique, Interactions Arbres–Microorganismes, Champenoux, France

² Université de Lorraine, Interactions Arbres–Microorganismes, Vandoeuvre-les-Nancy, France

* pascal.frey@inra.fr

The breakdown of host resistance to plant pathogens is of critical concern in agriculture, forestry, and the management of natural systems. Evolution of the fungal poplar rust pathogen *Melampsora larici-populina* has been shown to have been dramatically influenced by the deployment of resistance genes in commercial poplar (*Populus* spp.) plantations, with pathogen populations inundated by virulent genotypes (Xhaard et al. 2011). The deployment and subsequent breakdown of resistance genes in poplar plantations provide an experimental system for understanding the dynamics of pathogen evolution in response to resistance breeding, which will be critical to formulating effective management strategies in the future.

We describe a combined retrospective and prospective approach, integrating population genomics, landscape epidemiology, and evolution of life history traits of the poplar rust fungus. First, the records of poplar genotypes deployed across France over the last 17 years, along with genotypes of *M. larici-populina* collected across France, have been used to make overlaying maps of host and pathogen resistance and virulence genotypes. We demonstrate that the virulence landscape continues to be dominated by the sweep described by Xhaard et al. (2011); regions heavily planted with poplar resistance type R7 are still dominated by the corresponding virulence type, along with virulence types that “hitchhiked” across the landscape

during the original sweep. These genotypes persist, despite a reduction in planting of R7, and a near-absence of resistance types corresponding to the hitchhikers. In addition, the beginnings of a new sweep are emerging in regions in which a recently overcome resistance type (R8) has been more widely planted. We also describe plans to forecast the ability of the pathogen to evolve resistance to the future deployment of quantitative resistance types. To accomplish this objective, we will use the information learned from objective 1, and experimental tests of tradeoffs in pathogen aggressiveness, reproduction, and spread in response to quantitative resistance (resistance measured by degree). These forecasts will provide a framework for the future management of poplar and other forest plantations, and will also provide testable hypotheses with which to continue to improve understanding of host–pathogen co-evolution.

REFERENCES

Xhaard, C.; Fabre, B.; Andrieux, A.; [et al.]. 2011. The genetic structure of the plant pathogenic fungus *Melampsora larici-populina* on its wild host is extensively impacted by host domestication. *Molecular Ecology*. 20: 2739–2755.

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.