



## Adaptation of poplar rust to the poplar varietal landscape

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## **Adaptation of poplar rust to the poplar varietal landscape**

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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 plantations, with pathogen populations swamped by virulent genotypes<sup>1</sup>. 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, with regions heavily planted with poplar resistance type R7 continuing to be dominated by the corresponding virulence type, along with virulence types that “hitch-hiked” 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 additionally describe plans to, using the information learned from objective 1, and with experimental tests of trade-offs in pathogen virulence, reproduction, and spread in response to quantitative resistance (resistance measured by degree), forecast the ability of the pathogen to evolve resistance to the future deployment of quantitative resistance types. 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 the understanding of host-pathogen coevolution as a whole.

<sup>1</sup>Xhaard C *et al.*, 2011. *Molecular Ecology* 20, 2739-2755.

*Key words:* landscape genetics, durable resistance, pathogen evolution