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Association of two co-occurring mutations at the *AvrMlp7* avirulence locus in poplar rust during the breakdown of *RMlp7* resistance gene

Clémentine Louet, Méline Saubin, Axelle Andrieux, Antoine Persoons, Mathilde Gorse*, Jérémy Pétrowski, Stéphane De Mita**, Bénédicte Fabre, Sébastien Duplessis, Pascal Frey and Fabien Halkett

Université de Lorraine, INRAE, IAM, F-54000 Nancy, France

*Present address: INRAE, AgroParisTech, Université Paris-Saclay, BIOGER, F-78850 Thiverval-Grignon, France

**Present address: INRAE, Cirad, IRD, Montpellier SupAgro, Université de Montpellier, PHIM, F-34000 Montpellier, France

ABSTRACT

The deployment of plant varieties carrying resistance (*R*) genes exerts strong selection pressures towards pathogen populations. Several studies reported the rapid evolution of avirulence (*Avr*) genes to escape *R*-mediated plant immunity and identified a variety of mechanisms leading to virulence. The poplar rust fungus *Melampsora larici-populina* is the most damaging pathogen of poplars. A major adaptive event occurred in 1994 with the breakdown of *RMlp7* resistance gene in poplar. Population genomics studies identified a locus in the genome of *M. larici-populina*, which likely corresponds to the *AvrMlp7* candidate avirulence gene. We used a population genetics approach combined with dedicated qPCR assays on a comprehensive set of 281 isolates, covering 27 years (encompassing the resistance breakdown event), to validate the candidate locus and to assess its polymorphism. We found two mechanisms, a point mutation and a deletion, that allowed the pathogen to escape *RMlp7*-mediated resistance. Six diploid genotypes were thus characterized at the candidate locus (three avirulent and three virulent). In addition, a temporal analysis revealed that the two virulence alleles pre-existed (harboured as avirulent heterozygous genotypes) since the early samplings and were found in association (as virulent genotypes) at the time of the resistance breakdown. Our study documented that, in a diploid pathogen, combining virulence determinants is adaptive.

Keywords

Melampsora larici-populina, molecular evolution, gene-for-gene interaction, pathogen, fungi