



Back to the wild: identification and genetic mapping of resistance factors to *Melampsora larici-populina* in *Populus nigra*

Véronique Jorge, Arnaud Dowkiw, Redouane El Malki, Elise Albert, Marie Pégard, Vincent Segura, Vanina Guérin, Celine Ridet, Patrick Poursat, Jose-Luis Almeida Falcon, et al.

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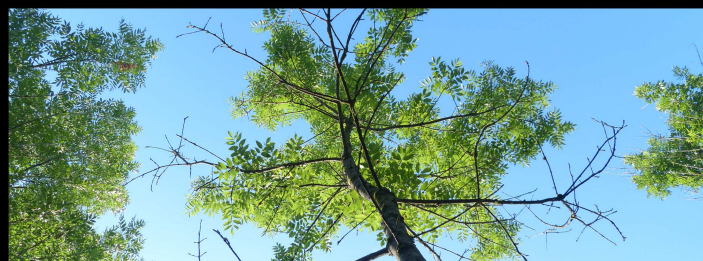
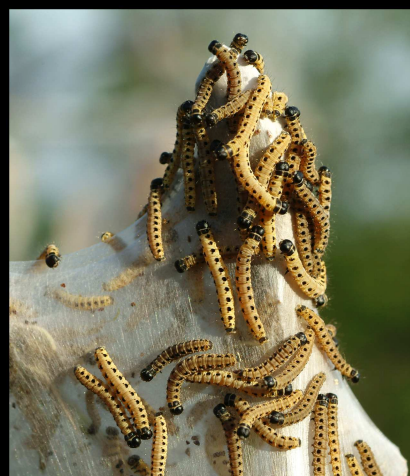
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Back to the wild: identification and genetic mapping of resistance factors to *Melampsora larici-populina* in *Populus nigra*

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In Europe, resistance to *Melampsora larici-populina* (*Mlp*) leaf rust is a major breeding objective for cultivated poplars. Up to now, qualitative resistances inherited from American species deployed in commercial hybrids were all overcome by the fungus. Breeder strategy has now switch to the identification of quantitative resistances in natural populations of black poplar (*Populus nigra*) coevolving with the populations of *Mlp*. The objective of the present study is to unravel the genetic determinism of partial resistance in *P. nigra* using a range of *Mlp* strains from cultivated areas and from natural populations and to locate and validate resistance factors in different genetic backgrounds. Artificial inoculation tests were carried out to measure three epidemiological components (latent period, uredinia number and size) using four *Mlp* strains in 7 *P. nigra* individuals from natural population and their F1 progenies organized in a factorial mating design. These F1 progenies were genotyped at high density in order to perform QTL detection. A quantitative variation of the resistance, a high genetic variability and significant genotype by strain interaction were observed in the parental genotypes and their F1 progenies. Major QTLs, with component and strain- specific effects, explained up to 86 % of the phenotypic variability observed for the epidemiological components. A fourth resistance component “pseudo-quantitative” expressing a hypersensitive reaction was identified. This reaction was observed for the first time in *P. nigra*. The QTL involved in the genetic control of the different components were located in genomic regions rich in NBS-LRR resistance genes, contributing to blur the line between qualitative and quantitative resistance.

Keywords

Populus nigra L., *Melampsora larici-populina* Kleb., leaf rust resistance, partial resistance, strain-specificity, QTL mapping