

Genetic Architecture of Quantitative *Melampsora larici-populina* Leaf Rust Resistance in Poplars (*Populus* spp.)

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Poplar (*Populus* spp.) leaf rusts caused by *Melampsora* species are considered among the most crucial sanitary problems threatening poplar stands worldwide. Several major resistance factors specific to poplar rusts have been identified, each of them discovered by using a single *Melampsora* species. Most of them are inherited from *Populus* species that did not co-evolve with the pathogen. The origin and function of such “exapted” resistance are thus called into question.

The purpose of this presentation is to compare the genetics of exapted and co-adapted resistance to *M. medusae* f. sp. *deltoideae* (*Mmd*) and to *M. larici-populina* (*Mlp*), respectively. To achieve this, resistance quantitative trait locus (QTL) against *Mlp* was studied in two pedigrees. The first, an F2 *P. trichocarpa* × *P. deltoides* family, was previously evaluated for resistance to *Mmd*, and a major gene for resistance, *Mmd1*, inherited from the *P. trichocarpa* grandparent, was mapped. The second pedigree was an F1 *P. nigra* family.

In the F2 pedigree, 17 QTLs were detected that are involved in the 3 components of quantitative resistance to the 5 *Mlp* strains inoculated in laboratory. These QTLs explain between 3 and 30 percent of the phenotypic variance. None of these QTLs has a broad-range

effect. No major resistance factor against *Mlp* was identified in this pedigree, showing that *Mmd1* is not functional against *Mlp* strains tested.

In the *P. nigra* family, 11 QTLs explaining between 2 and 60 percent of the phenotypic variation observed after inoculation with the two *Mlp* strains were detected. All except one of these QTLs were trait- or strain-specific. A major QTL inherited from the most resistant parent and located at the end of LG I explained more than 60 percent of uredinia size variation after inoculation with one *Mlp* strain and showed a moderate effect after inoculation with the other strain. Genomic mining of the QTL region revealed a cluster of 25 NB-LRR genes. Those results confirm in *P. nigra* the gene-for-gene model suggesting specific interactions between QTLs for quantitative resistance and *Mlp* strains.

The results presented will be compared and discussed together with results of previous studies on *Melampsora*/Salicaceae pathosystems.

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