



Association mapping of resistance to rust disease in poplar

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Population Genetics and Genomics of Forest Trees: From Gene Function to Evolutionary Dynamics and Conservation

A joint conference of IUFRO Working Groups **2.04.01** (*Population, ecological and conservation genetics*) and **2.04.10** (*Genomics*), and COST Action **E-28** (*Genosilva: European Forest Genomics Network*)

PROGRAMME and CONFERENCE ABSTRACT BOOK

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■ Association mapping of resistance to rust disease in poplar

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The foliar rust caused by the fungus *Melampsora larici-populina* Kleb. is the most devastating disease affecting the European poplar plantations. We have identified a factor of quantitative resistance, *Rus*, inherited from the genotype *Populus trichocarpa* 101-74, which can reduce by 60% the level of infection in laboratory and which has a significant effect in field. This factor is localized on the genetic map of *P. trichocarpa* 101-74 based on the analysis of one F1 inter-specific family *P. deltoides* x *P. trichocarpa*. Map based cloning of *Rus* is under development, fine mapping and construction of BAC contig are underway. The alignments with the sequence of *P. trichocarpa* Nisqually-1 makes it possible to target the area of interest. We defined an exploratory zone of approximately 400 kb on which we already detected 28 genes. Ten of them are re-annotated as Resistance Gene Analogs (RGAs). Predicted genes have been investigated as candidate genes for fine mapping and association study. Association between *Rus* and those candidate genes has been first investigated in a collection of 94 individuals of *P. trichocarpa*. The collection was phenotyped for rust resistance under control conditions and in the field. The individuals have been genotyped by EcoTILLING.

NOTES:

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