

Molecular and Genetic Basis for Partial Resistance of Western White Pine against *Cronartium ribicola*

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Abstract

Western white pine (*Pinus monticola* Douglas ex D. Don) is an important forest species in North America. Forest genetics programs have been breeding for durable genetic resistance against white pine blister rust (WPBR) caused by *Cronartium ribicola* in the past few decades. As various genetic resistance resources are screened and available from breeding programs, we are interested in understanding the genetic mechanisms at the molecular level. This will facilitate a breeding strategy of pyramiding several resistance mechanisms in white pine elite stocks, which would make durable resistance possible for effective and long-term WPBR management.

Both major gene resistance and quantitative partial resistance have been identified in *P. monticola* populations. In contrast to the *Cr2*-mediated major gene resistance that occurs on pine needles by the hypersensitive response (HR), quantitative partial resistance was observed in stems after *C. ribicola* infection as slow canker growth, or bark reaction. Quantitative stem resistance was displayed with various phenotypes in different seed families, ranging from complete susceptibility (rust dead) to complete stem resistance (stem symptom-free), including normal canker development, partial bark reaction with incomplete inhibition of fungal growth, complete bark reaction without fungal activity in the bark, delayed stem infection, fewer stem infections, or longer time to mortality as compared to susceptible controls. Partial resistance is believed to be a heritable and polygenic resistance trait that allows greater survivability of infected white pine trees. Based on phenotypic data collected yearly from western white pine seed families sowed in 2003 and inoculated with *C. ribicola* in 2004, partial resistance levels were analyzed and ranked for each seedling.

Using these plant materials, we used a candidate gene-based association study to reveal what genomic DNA variants underlie phenotypic variation of white pine partial resistance. A set of pathogenesis-related (PR) genes was selected as candidates, including defense-related genes encoding for β -1,3-glucanases (PR2), chitinases (PR3), thaumatin-like proteins (PR5), cytosolic nuclease-like proteins (PR10), and anti-microbial proteins (AMPs). Genomic DNA sequences of these genes were determined in white pine trees. DNA sequence data of selected candidate genes showed rich single nucleotide polymorphisms (SNPs) in white pine seed families. We will report on the genetic variations of these genes. Development of DNA markers will be discussed for marker-assisted selection of partial resistance to speed up of white pine breeding programs.

Defense responses of white pine trees with partial resistance were also investigated by measuring PR protein accumulation post *C. ribicola* infection. Using Pm-AMP1 as a biochemical indicator, a few patterns were documented for protein regulation in white pine seed families. Our results revealed that different molecular mechanisms may be responsible for various phenotypes of partial resistance in white pine populations. Cross-pollination between seed families with different resistance mechanisms would produce progeny with more durable resistance against *C. ribicola*.

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