

Candidate Gene-Quantitative Phenotype Associations for Resistance to Fusiform Rust and Pitch Canker in Loblolly Pine

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Pitch Canker, caused by the necrotrophic fungus *Fusarium circinatum*, is a fungal disease that has been detected in loblolly pine plantations since 1974 where it causes excessive pitch production and shoot dieback. Fusiform rust, caused by the biotrophic fungus *Cronartium quercuum* f. sp. *fusiforme*, has been a major disease of southeastern conifer plantations since the early 1920's. We are seeking to identify genes that determine quantitative resistance and genetic markers that can be used in resistance breeding. Single nucleotide polymorphisms (SNPs) in candidate genes conferring resistance to these pathogens were identified based on direct DNA sequencing. Candidate genes for disease resistance are categorized as: *Positional Candidates*, referring to candidate genes that are near QTLs for cell wall chemistry like phenylpropanoid pathway genes and cellulose synthase genes, *Expression Candidates*, referring to genes identified by expression analyses (chitinases and myb and WD40 class transcription factors), *Functional Candidates*, referring to genes and regulatory regions whose roles in disease resistance have been identified in other plant systems through sequence homology to loblolly pine ESTs and bioinformatics. A total of 57 candidate loci have been screened first for identification of polymorphic locations that might lead to physiological changes in the disease resistance phenotype, and then selected SNPs have been inquired for their relevance to the variation observed in the phenotypes via association testing of these polymorphisms over an association population of 960 individuals. Progress to date on the successful associations made will be presented; two pathosystems will be compared and contrasted regarding allelic associations of the loci detected to be associated with resistance.

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