

GENETIC DIVERSITY IN CANDIDATE DISEASE-RESISTANCE GENES IN *PINUS TAEDA* L.

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Fusiform rust is a disease incited by the fungus *Cronartium quercuum* f.sp. fusiforme (*Cqf*) on southern pines (where it causes galls on stems and branches) and on oaks (where it causes minimal leaf damage). Fusiform rust is a major disease threat to the timber industry in the US. Rust galls cause annual yield losses that exceed US\$100M. The genome annotation of loblolly pine (*Pinus taeda*) has become an essential resource for understanding the genetic basis of resistance to fusiform rust disease (Neale et al. 2014 and Wegrzyn et al. 2014). During the genome annotation process, an expressed sequence tag (EST) was identified that contains a single nucleotide polymorphism (SNP) mapping to the locus (*Fr1*) that interacts with the fungal avirulence gene, *Avr1*. This EST aligns to a full-length transcript from RNA-sequencing data and a TIR-NB-LRR protein, thus identifying it as a candidate *Fr1* gene. In order to understand the population genetic context of this and other pine resistance genes, we sequenced and assembled RNA sequencing data from 92 elite rust-resistant loblolly pine genotypes from five pine-growing regions, identifying candidate resistance genes in the process. Next we aligned the assembled transcripts to the loblolly pine genome and calculated population genetic measures. These results allow us to understand the diversity and conservation of resistance genes that interact with *Cqf* and in elite genotypes that are important to pine breeding for their fusiform rust resistance and growth traits.

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