

MULTIPLE APPROACHES TO DISSECT FUSIFORM RUST RESISTANCE IN *PINUS TAEDA* L.

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Mapping the specific loci that regulate phenotypic traits in conifers is a major undertaking because of their very large genomes. However, the release of the annotated loblolly pine (*Pinus taeda* L.) genome may allow fine-mapping of Mendelian traits that are economically critical, such as for disease-resistance. Here we present the results of work mapping Fusiform rust resistance locus 1 (*Fr1*) in elite rust resistant loblolly pine trees. 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 United States. Rust galls cause yield losses that exceed US\$100M/year. 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 transcript from RNA-sequencing data and a TIR-NB-LRR protein, thus identifying it as a candidate *Fr1* gene. In order to further characterize the *Fr1* locus, we assembled the transcriptomes of 92 elite rust-resistant loblolly pine genotypes from five pine-growing regions, identifying candidate resistance genes in the process. Next we aligned these transcripts to the loblolly pine genome and calculated population genetic parameters. These results enable analysis of the diversity and conservation of resistance genes that interact with Cqf and present a foundation for further characterization of *Fr1* and other resistance loci.

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