

IDENTIFICATION OF CANDIDATE INTERACTING RESISTANCE AND AVIRULENCE GENES IN THE FUSIFORM RUST PATHOSYSTEM

Daniel Ence¹, Katherine E. Smith², Amanda L. Pendleton³, Thomas L. Kubisiak⁴, Claire L. Anderson⁵, Asaf Salamov⁶, Andrea Aerts⁶, Robert W. Riley⁶, Alicia Clum⁶, Erika A. Lindquist⁶, Nicolas Feu⁷, Robin Paul⁸, Braham Dhillon⁹, Michael C. Campbell¹⁰, Zev Kronenberg¹¹, Igor Grigoriev⁶, Mark Yandell¹², Richard C. Hamelin⁷, Matias Kirst¹, Leandro Neves¹³, Jill Wegrzyn¹⁴, C. Dana Nelson¹⁵, John M. Davis¹⁶

¹School of Forest Resources and Conservation, University of Florida, Gainesville, FL; ²USDA Forest Service, Southern Research Station, Gainesville, FL; ³Purdue University, West Lafayette, IN, USA 47907; ⁴retired Southern Institute of Forest Genetics, USDA Forest Service, Southern Research Station, Saucier, MS; ⁵Research School of Biology, Australian National University, Canberra, ACT 0200, AU; ⁶Joint Genome Institute, US DOE, Walnut Creek, CA; ⁷Department of Forest and Conservation Sciences, University of British Columbia, Vancouver, BC, CA; ⁸Indiana University School of Medicine, Bloomington, IN; ⁹Department of Plant Pathology, University of Arkansas, Fayetteville, AR; ¹⁰10X Genomics, Pleasanton, CA; ¹¹Pacific Biosciences, Menlo Park, CA; ¹²Department of Human Genetics, School of Medicine, University of Utah, Salt Lake City, UT; ¹³Rapid Genomics, Gainesville, FL; ¹⁴Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT; ¹⁵Forest Health Research and Education Center, USDA Forest Service, Southern Research Station, Lexington, KY; ¹⁶IFAS, University of Florida, Gainesville, FL

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 yield losses that exceed US\$100M/year. A high priority for breeders and forest managers is to identify candidate resistance genes in loblolly pine (*Pinus taeda* L.; *P. taeda*) and avirulence genes in *Cqf*. However, identifying the specific loci that regulate phenotypic traits in conifers is a major undertaking because of their very large genomes. During the process of annotating the genome of *P. taeda*, an expressed sequence tag (EST) was identified that contains a single nucleotide polymorphism (SNP) mapping to Fusiform rust resistance locus 1 (*Fr1*), which interacts with the *Cqf* gene, Avirulence locus 1 (*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. Here we present the results of work mapping *Fr1* in the *Pinus taeda* genome and *Avr1* in the *Cronartium quercuum* genome. We conducted bulk segregant analysis of next-generation sequence data from both host and pathogen. In pine, half-sibling progeny from a resistant mother were phenotyped as either resistant or susceptible to *Cqf*. These progeny were sequenced with a custom sequence-capture method targeting a genomic region linked to resistance by prior work. In *Cqf*, analysis of whole-genome sequence of rust grown on resistant or susceptible seedlings identified a 200kbp region containing several likely effector proteins. By identifying candidates for an interacting avirulence and resistance gene pair in this conifer-rust pathosystem, we will discover markers that will guide breeding and deployment of resistant pine.