

## NLR DIVERSITY AND CANDIDATE FUSIFORM RUST RESISTANCE GENES IN LOBLOLLY PINE

Daniel Ence<sup>1</sup>, Katherine E. Smith<sup>2</sup>, Leandro Gomide Neves<sup>3</sup>, Robin Paul<sup>4</sup>, Jill Wegrzyn<sup>5</sup>, Matias Kirst<sup>6</sup>, Jeremy Brawner<sup>7</sup>, Gary Peter<sup>8</sup>, C. Dana Nelson<sup>9</sup>, and John M. Davis<sup>10</sup>

<sup>1</sup> Postdoctoral Associate, University of Florida, Gainesville, FL, USA 32611 (d.ence@ufl.edu)

<sup>2</sup> Biological Science Technician, Southern Institute of Forest Genetics, Southern Research Station, USDA Forest Service, Saucier, MS, USA, 39574

<sup>3</sup> Chief Executive Officer, Rapid Genomics, Gainesville, FL, USA 32601

<sup>4</sup> Bioinformatics Research Scientist, St. Jude Children's Research Hospital, Memphis, TN, USA 38105

<sup>5</sup> Associate Professor, University of Connecticut, Storrs, CT, USA 06269

<sup>6</sup> Professor, University of Florida, Gainesville, FL, USA 32611

<sup>7</sup> Assistant Professor, University of Florida, Gainesville, FL, USA 32611

<sup>8</sup> Professor, University of Florida, Gainesville, FL, USA 32611

<sup>9</sup> Research Geneticist/Project Leader, USDA Forest Service, Lexington, KY, USA 40546

<sup>10</sup> Senior Associate Dean for Research, IFAS/University of Florida, Gainesville, FL, USA 32611 (jmdavis@ufl.edu)

Fusiform rust causes substantial mortality and productivity losses in pine plantation yields across the southeastern United States. Breeding for genetically resistant families has reduced rust infection. Pine control resistance to the fusiform rust pathogen, *Cronartium quercuum* f.sp. *fusiforme*, in a classic gene-for-gene system. In gene-for-gene interactions, disease symptom expression is conditioned by pathotype-specific genetic interactions between resistance gene alleles and pathogen genotypes harboring specific (a)virulence alleles. Early resistance gene mapping in the loblolly pine (*Pinus taeda*) family 10-5 identified markers for a major fusiform rust resistance gene, *Frl* (Wilcox et al. 1996; Kuhlman and Powers 1988). More recent work identified markers associated with resistance that mapped to a full-length gene model in version 1.01 of the loblolly pine genome encoding for an NLR protein (Neale et al. 2014). In plants, NLR proteins play key roles in disease resistance to biotrophic pathogens. Given the importance role of NLRs in gene-for-gene disease resistance in model and crop species, their identification and diversity are key targets of research directed at mining in other plant genomes. We hypothesize that elite loblolly pine families selected for disease-resistance and other desirable traits possess novel NLR genes that are not present in the reference genome and that a sequencing strategy targeting novel NLR genes will identify SNP alleles associated with disease resistance. We combined transcriptome mining with sequencing of targeted loci to identify novel NLR genes and map SNPs that reliably segregate with fusiform rust resistance in half-sibling loblolly pine progeny. The novel NLR genes identified here are the first characterization of intraspecies NLRs diversity in a gymnosperm. The SNPs segregating with rust resistance and in novel NLR genes derived from transcriptomes, can be applied to the breeding and deployment of resistant pine seedlings.