

Expression Patterns of *Pinus* Defense Genes During Host-Pathogen Interactions

A.M. Morse¹, K.E. Smith², D.A. Huber¹, S.F. Covert³, K.D. Hunt⁴,
C.D. Nelson⁵, and J.M. Davis⁶

¹ Research Faculty, ⁶Associate Professor
School of Forest Resources and Conservation, University of Florida, Gainesville, FL

²Biological Sciences Technician
Southern Institute of Forest Genetics, USDA Forest Service, Gainesville, FL

³Associate Professor, ⁴Graduate Student
Daniel B. Warnell School of Forest Resources, University of Georgia, Athens, GA

⁵Research Geneticist and Project Leader
Southern Institute of Forest Genetics, USDA Forest Service, Saucier, MS

Cronartium quercuum infects the stems and branches of certain pines and leads to the development of fusiform rust disease. Gall formation is associated with alterations in host metabolism, morphology and development as well as fungal propagation, all of which are likely to be associated with changes in host gene expression. Genetic resistance to fusiform rust exists and controlled inoculation studies have revealed the evolution of specific (gene-for-gene) resistance in pine-*Cronartium* interactions. In slash pine, families can not only be classified as susceptible or resistant to fusiform rust based on gall presence/absence, but also on gall morphology. Small galls on young slash pines often ‘disappear’ as the tree matures, a phenomenon that has been referred to as partial resistance.

To identify candidate genes for conditioning fusiform rust gall morphology and possibly partial resistance, we probed our pine defense-associated array with cDNA derived from RNA isolated from either large or small galls on slash pine. The arrays were statistically analyzed as six pairwise contrasts to distinguish between host tissue and pathogen regulation. A total of 158 genes were identified as significantly regulated in one or more of the contrasts.

Hierarchical cluster analysis comparing transcript abundance for the probes significantly expressed in one or more of the contrasts identified five prominent clades. Two of the clades represent host tissue regulation and contain genes differentially expressed between xylem and phloem. The remaining three clades represent different patterns of pathogen regulation.

A number of genes significantly regulated by fusiform rust had been previously identified as significantly regulated by pitch canker, a disease incited by the necrotrophic fungal pathogen *Fusarium circinatum*. Of particular interest is the fact that a number of defense genes were regulated in opposite directions in the two disease states. Genes encoding chitinase and peroxidase enzymes were suppressed in fusiform rust galls and induced in pitch canker lesions. This result is consistent with the emerging view that biotrophic pathogens, such as *C. quercuum*, actively suppress host defenses in order to complete their lifecycles and cause disease.