**Interacting Genes in the Pine-Fusiform Rust Forest Pathosystem**

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Fusiform rust (FR) disease of pines, caused by *Cronartium quercuum* f.sp. *fusiforme* (*Cqf*), is the most destructive disease in pine plantations of the southern U. S. The NCSU fusiform rust program, in conjunction with the USDA-Forest Service in Saucier, MS and Athens, GA, has research underway to elucidate some of the genetic interactions in this pathosystem.

Major genes (R genes) for FR resistance, primarily in loblolly pine and to a lesser degree in slash pine, are being recognized and tagged with genetic markers. These genes, termed *Fr* genes, are being defined in resistant selections (clones) whose progeny segregate 1:1 for the presence or absence of galls when challenged with specific isolates of *Cqf*, i.e., the selections are heterozygous with regards to a given R gene. Thus the resistance (R) and the non-resistance (r) alleles of these *Fr* genes can be followed within specific pedigrees with genetic markers linked to the R genes. Typically 1 or 2 different heterozygous *Fr* genes have been found in a given selection and to date 8 different *Fr* genes (*Fr1-Fr8*) are known among several different resistant loblolly selections. The *Fr* genes were discovered in first generation, plantation or equivalent Forest Service selections, but some of the *Fr* alleles are now being followed in advanced generation selections (elite trees) using the previously identified markers.

Some of the loblolly *Fr* genes are being used to investigate virulence composition in pathogen populations. In that work, progeny from selections segregating for 1 or 2 different *Fr* genes are challenged with *Cqf*, either artificially in greenhouse studies (using inocula collected from various field sites) or naturally in field studies. Infection of progeny with a genetic marker defined resistance allele (R1, R2, R3 etc.) denotes virulence in the pathogen population against the specific R-allele of a given *Fr* gene. The percentage of R-individuals infected, for a given *Fr* gene, provides a measure for the level of virulence in a particular inoculum. The artificial inoculations have been very informative, showing that the effectiveness of a given R allele may vary greatly from site-to-site, indicative of site-to-site virulence variation. Some R alleles are frequently overcome by virulence in the test inocula at multiple sites while others confer good levels of resistance at many sites.

In concert with genetic marker mapping of *Fr* genes, and as another approach to analyze virulence composition, an effort is underway to genetic marker map the avirulence gene (pathogenicity locus) *Avr1* that corresponds to the *Fr1* gene in loblolly pine. Once markers tightly linked with *Avr1* are obtained, we expect to identify the avirulence gene sequence and develop internal markers for allele discrimination. This should allow us to assess *Avr1* vs. *avr1* allele frequencies in spore populations of *Cqf* as a guide for prescribed *Fr1* deployment. Upon demonstrating success of this approach, other *Avr* genes will be similarly investigated. A discussion of the work outlined here will be the focus of our presentation.

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