Identification of Pathogen Avirulence Genes in the Fusiform Rust Pathosystem

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Abstract

The *Cronartium quercuum* f.sp. *fusiforme* (*Cqf*) whole genome sequencing project will enable identification of avirulence genes in the most devastating pine fungal pathogen in the southeastern United States. Amerson and colleagues (unpublished) have mapped nine fusiform rust resistance genes in loblolly pine, suggesting that at least nine corresponding avirulence genes likely exist in the fungus. Identification of these avirulence genes would greatly facilitate selection of resistant pine genotypes for deployment to forest plantations. Based on work in other rusts, we anticipate avirulence genes may encode secreted effector proteins that interact directly or indirectly with host resistance proteins. As a step toward testing this hypothesis, we genetically mapped the *Cqf* avirulence gene *Avr1*, which specifically interacts with the *Fr1* resistance gene, with the goal of integrating this map with the *Cqf* genome sequence assembly so that *Avr1* can be identified. Once *Avr1* is identified, we want to determine its allele frequency across geographically defined hazard maps for fusiform rust, to help guide genotype deployment by growers. We view identification of *Avr1* as our initial case study, guiding our strategy to efficiently identify additional avirulence genes in *Cqf* that in turn can be used to guide plantation deployment of all genotypes currently represented in southern pine breeding programs.

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