

## GENOME SEQUENCE-ENABLED IDENTIFICATION OF AVIRULENCE GENES IN THE FUSIFORM RUST FUNGUS

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*Cronartium quercuum* f.sp. *fusiforme* (*Cqf*), the causative agent of fusiform rust disease has been damaging southern pine forests for decades. A complete *Cqf* genome sequence is currently under assembly at the Joint Genome Institute that will greatly facilitate identification of avirulence genes. Amerson and colleagues (manuscript in prep) have mapped 9 resistance genes (*R* genes) in loblolly pine suggesting that at least 9 corresponding avirulence genes (*Avr* genes) should exist in the fungus. The resistant reaction (i.e., no gall condition) requires the match of at least one *R* gene with its corresponding *Avr* gene for each spore that challenges the tree. Precise identification of these avirulence genes will provide the most accurate markers for measurement of allelic frequencies in various geographic locations. Frequency measurements can be used to guide selection of the most appropriate resistant pine genotypes. These kinds of preventive measures can now be realized more quickly with the aid of the *Cqf* genomic sequence. For example, the avirulence gene, *Avr1*, is known to specifically interact with the *Fr1* resistance gene. This avirulence gene exists within an 8.62 cM interval (about 0.3% of the genome), defined by 14 DNA markers: six Random Amplified Polymorphic DNA (RAPD) and eight Amplified Fragment Length Polymorphism (AFLP). The DNA fragments amplified by these markers have been sequenced and, for the AFLPs, the opposite parental allele has also been sequenced. Genomic sequence scaffolds will be bioinformatically screened with these fragment sequences to zero in on the target locus. Once identified, the locus can be fine mapped to pinpoint the *Avr1* gene. As additional markers are found to be linked to the other avirulence genes, their identification can proceed more easily using this method.