FUNGAL EFFECTORS OF *CRONARTIUM QUERCUUM F.SP. FUSIFORME*

Katherine E. Smith[1,2], Daniel Ence, Nicolas Feau, Amanda Pendleton, Richard Hamelin,
C. Dana Nelson, Mark Yandell and John M. Davis

[1]School of Forest Resources and Conservation, University of Florida, Gainesville, FL; [2]Southern
Institute of Forest Genetics, USDA Forest Service, Southern Research Station, Saucier, MS

The genomic sequence of *Cronartium quercuum f.sp. fusiforme* (Cqf), the rust fungus that causes fusiform rust disease on southern pines, has been determined. The genome assembly contains 13,903 genes, 1,140 of which are predicted to be secreted from the fungus. Some of these proteins are secreted during infection stages and therefore potentially influence pathogenicity. Effectors are pathogen proteins that alter host cellular function and morphology to accommodate infection and fungal growth. They are at the heart of understanding how Cqf is able to overcome host defenses and live within plant tissues without killing the plant. Small secreted proteins (SSPs) fewer than 300 amino acids are considered to be good candidate fungal effectors since proteins must be secreted during the infection process to exert a direct effect on the host. Cqf gene expression during pine and oak infection was studied using microarrays. Proteins encoded by genes showing significant differential overexpression in one host over the other were greatly enriched for SSPs and included homologs of known effectors. A subset of effectors conform to predictions made by the gene-for-gene hypothesis, meaning they are avirulence genes with alleles that specifically interact with host resistance gene alleles resulting in a non-disease phenotype. A physical location for the Cqf avirulence gene 1, Avr1, was determined using two different genetic marker approaches. Exact genomic locations for avirulence genes allow perfect markers to be made that can precisely identify alleles present in fungal samples. This ability can lead to better studies aimed at understanding the nature of Cqf virulence and ultimately a greater level of control of fusiform rust disease. Experiments that measure the presence of virulent and avirulent alleles in the field can elucidate how virulence changes geographically and over time.