## THE CRONARTIUM QUERCUUM F. SP. FUSIFORME GENOME PROJECT

Katherine E. Smith, <sup>1</sup> Thomas L. Kubisiak, C. Dana Nelson, and John M. Davis

<sup>1</sup>School of Forest Resources and Conservation, University of Florida, Gainesville, FL

Cronartium quercuum f.sp. fusiforme (Cqf) is the causative agent of fusiform rust disease of southern pines. A complete Cqf genome sequence is currently under assembly at the Joint Genome Institute (JGI) that will identify all of the genes in this important forest pathogen. One biological objective of the project is to gain new insights into the relative number and nature of genes involved in Cqf host alternation, i.e., the requirement that particular spores produced on oaks can only infect pines and vice versa. Another objective is to identify virulence/avirulence genes so that managers can select appropriate genotypes for plantation establishment based upon allele frequencies in the local rust population. Cqf genome size was estimated by flow cytometry to be ~90 Mb (Anderson et al. 2010). For genome sequencing and to facilitate genome annotation, materials were collected for DNA and RNA extraction. DNA from the reference genotype was collected from pycnial droplets pooled from a single gall infected in the field near Saucier, MS. The sample contained single alleles only (i.e., there was no evidence for a mixture of genotypes) at six SSR loci. This suggests the sample is a haploid representation of the Caf genome, which should aid assembly because there is no allelic variation in the sample. RNA was extracted from aeciospores (from pine), the hymenial layer from which pycnia were being produced in the fall (from pine), the hymenial layer from which aecia were being produced in the spring (from pine), basidiospores (from oak), teliospores (from oak) and diseased leaves containing vegetative mycelium, teliospores and basidiospores (from oak). Transcript assembly was performed to identify messenger RNAs encoded by Cqf genomic loci, and will be used to complement ab initio gene identification in the genomic assembly. BLAST analysis provides an estimate of host transcriptome representation in the transcript assembly, and generates an early glimpse of the *Cqf* "parts list."