GENOMICS RESEARCH AND FUSIFORM RUST DISEASE

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Two of the major goals of our fusiform rust disease research are to identify resistance genes in pine selections and to monitor fungal virulence in the field as a tool to predict the best selections to plant. Advances in high-throughput sequencing and bioinformatics have provided new methods for achieving these goals. The 23.2 gigabase loblolly pine genome is approximately 232 times larger than the 100 megabase genome of *Cronartium quercuum*, the causative fungus, yet we have a genomic reference for both, as well as, RNA sequence data to support gene annotation. Ongoing research in the pine host includes: 1. Employing known SNP (single nucleotide polymorphism) data and specialized target selection with high-throughput sequencing to fine map the Fr1 locus; and 2. Identifying resistance genes expressed in elite families by leveraging the large depth of known RNA sequences to select resistance gene candidates. On the fungal pathogen side of the interaction, a genomic location for the Avr1 gene has been identified using previously obtained marker sequences and high-throughput re-sequencing techniques. Advances in the assembly of genomes using longer reads and improved software have made it feasible to sequence the Cqf genome using the Pacific Biosciences sequencing platform. These data are being used to improve the Cqf reference sequence and to more accurately pinpoint the Avr1 gene. Progeny of the fungal isolate P2 were sequenced in order to locate the Avr1 locus. Sequencing of P2 progeny resulting from inoculation on pine families segregating for resistance gene alleles corresponding to Avr2 and Avr3 can be used to locate these avirulence genes. This reinforces the importance of maintaining germplasm of relevant pine families and fungal isolates.

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