GENOMIC ASSEMBLY COMPARISONS OF FOUR FLORIDA *FUSARIUM CIRCINATUM* ISOLATES

Katherine E. Smith [1], James C. Fulton [2], Jose C. Huguet-Tapia [3], Tania Quesada [4], Jeremy Brawner [5]

[1] Biological Science Technician, Southern Institute of Forest Genetics, Southern Research Station, USDA Forest Service, Saucier, MS, USA, 39574 (smithk@ufl.edu);

[2] Postdoctoral Associate, [3] Assistant Scientist, [5] Assistant Professor, Department of Plant Pathology, University of Florida, Gainesville, FL, USA 32611;

[3] Assistant Research Scientist, Forest, Fisheries, and Geomatics Sciences, University of Florida, Gainesville, FL, USA 32611

Pitch canker disease incited by the fungus *Fusarium circinatum*, causes economic losses to the pine timber industry all over the world. Screening seedlings by measuring lesion length following controlled inoculation is used to provide estimates of pine tolerance and isolate virulence. Four isolates that demonstrated differences in virulence when screening slash and loblolly seedlings were selected for further study. To understand the genetic basis for the differences, we used Oxford Nanopore long-read sequencing combined with Illumina short-read sequencing to achieve high quality, nearly chromosome level, genome assemblies. The assemblies were checked for completeness using BUSCO (Benchmarking Universal Single-Copy Orthologs) and aligned to the publically available reference genome (NCBI: GCA_000497325.3). *Fusarium* species are known to transfer pathogenicity genes and whole "pathogenicity chromosomes" between and within species. Variation in virulence may derive from gene content as well as structural differences in the genome. We located genes in the assembled genomes using annotation software and employed various other techniques to a take a closer look at which genes differ between isolates. In addition, we examined the extent of structural differences among the genomes by locating and quantifying the number of sequence inserts, deletions and rearrangements across the genome. This study has identified genomic differences among *Fusarium circinatum* isolates that may be useful for characterizing isolate virulence, monitoring pathogen populations and identifying where different resistance mechanisms should be deployed across the landscape.