# IMPROVING THE ASSOCIATION MAPPING PIPELINE IN A LOBLOLLY PINE POPULATION WITH A COMPLEX PEDIGREE THROUGH INCREASED MARKER COVERAGE VALIDATION USING DISEASE RESISTANCE DATA

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Next-generation sequencing technologies enables identification and detection of a large number of sequence variants or molecular markers. This allows a better characterization of genomic regions of interest in search for candidate genes of interest. In loblolly pine, resistance screening of fusiform rust and pitch canker diseases is routine in genetic improvement programs, as deployment of susceptible material would result in high economic losses to the timber industry. The CCLONES (Comparing Clonal Lines on Experimental Sites) population at the University of Florida has been one of the best characterized loblolly pine populations at a phenotypic and genotypic level. This population consists of 71 full-sib families derived from a circular diallel mating design with 41 parents. Previous studies have used this population to identify significant associations with fusiform rust resistance, pitch canker, and other traits using over 4,800 polymorphic SNPs.

More recently we used next-generation sequencing to genotype this population and increased the genotypic data available to over 67,000 SNPs. Because of the large datasets, a script was implemented using R software to automate table processing and selection a subset of 400, 1000, and 5000 SNP markers based on differences between the homozygous classes for each SNP. Association analyses were then performed using BAMD (Bayesian Association with Missing Data), a program that evaluates all SNPs simultaneously, performs multiple imputations of missing SNP data and uses the posterior distribution to generate a confidence interval from which significant associations can be detected.

Phenotypic data from previous screenings for fusiform rust and pitch canker were used to test the table processing pipeline. Nine significant associations were obtained for both fusiform rust at confidence intervals of 90% or higher. Sequence comparisons between the contigs harboring the old and new sets of SNPs are in process to confirm common markers between the datasets and validate the location of the significant SNPs in the pine genome.

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