COMPARING AND VALIDATING ASSOCIATION MAPPING FOR DISEASE RESISTANCE IN TWO LOBLOLLY PINE POPULATIONS USING INCREASED MARKER COVERAGE

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Association genetics is a powerful approach to identify markers in genes related to traits of interest. Association genetic analyses were used loblolly pine to identify single nucleotide polymorphisms (SNPs) significantly associated with fusiform rust and pitch canker resistance in two populations: an association population composed of over 400 largely unrelated individuals (ADEPT2 population), and a population with known structure composed of 71 full-sib families derived from a circular diallel mating design with 41 parents (CCLONES - Comparing Clonal Lines on Experimental Sites). We conducted association tests between over two million polymorphic SNPs in the ADEPT 2 population and over 67,000 SNPs in the CCLONES population to identify candidate genes for pitch canker and fusiform rust resistance. Analyses were done using PLINK, an open-source toolset for whole-genome association and population-based analyses. For pitch canker resistance phenotypic data, obtained by measuring lesion length, we detected eight significant SNPs in the ADEPT 2 population at 90% confidence using PLINK. This number was similar to previously published data obtained the platform BAMD. However, when used in the CCLONES population, which has known structure, we obtained 1,695 significant SNPs at 90% confidence. For fusiform rust, the number of significant SNPs varied between two and 499 at 90% confidence, depending on whether gall score (presence/absence - a binary trait) or gall length (a quantitative trait) were used as phenotypic data. Gall score showed more differences in the number of significant SNPs obtained using different platforms (PLINK and BAMD). However, no overlap was observed between the SNPs significant for pitch canker or rust across the CCLONES and ADEPT2 populations; however, whether these significant SNPs are in linkage disequilibrium remains to be determined. Future steps involve the annotation of such significant SNPs and validation across platforms.