

Association genetics of pitch canker resistance in loblolly pine

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Association genetics has been used for dissection of complex traits in species with large, outcrossing populations with high genetic diversity and low linkage disequilibrium. It relies on historical recombinations to identify statistical associations between phenotypic traits and genetic marker polymorphism. Association studies were performed on loblolly pine for resistance to pitch canker, an economically important disease that affects many pine species and is caused by the necrotrophic fungus *Fusarium circinatum*. Disease phenotyping was performed on 498 largely unrelated genotypes in a randomized incomplete block design with four resolvable replicates of each genotype. Lesion length measurements were taken 4, 8, and 12 weeks after inoculation with *F. circinatum* microconidia. Best linear unbiased predictions (BLUP) were estimated to correct for differences in number of observations and were used to identify highly susceptible and highly resistant genotypes. Clonal repeatabilities for the entire population ranged between 0.20 and 0.30; supporting previous evidence that pitch canker resistance is heritable. Tests for significant associations were performed using a two-step approach where 3,938 SNPs were evaluated singly for covariation with the phenotype, after which associations between the phenotype and the top 400 SNPs were detected simultaneously using BAMD (Bayesian Association with Missing Data), which also does multiple imputation for missing SNP genotypes. Many of the significant SNPs occur in genes annotated as having roles in disease resistance.

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