

## MARKER-ASSISTED SELECTION FOR TRAIT IMPROVEMENT IN LOBLOLLY PINE (*PINUS TAEDA* L.)

**W. Patrick Cumbie<sup>1</sup>, Dudley A. Huber<sup>2</sup>, Victor C. Steel<sup>1</sup>, William Rottmann<sup>1</sup>, Les Pearson<sup>1</sup> and Michael Cunningham<sup>1</sup>**

A set of 900 clonally replicated loblolly pine varieties (*Pinus taeda*, L.) from 35 full-sib families were assessed for growth, stem form, and disease resistance after 6 growing seasons. Using a set of more than 5000 SNPs we identified 3340 SNPs that were informative in this population and were subsequently used in genetic analyses. SNP markers were used for the estimation of genomic relationships and significant SNP associations were identified for height growth, volume, rust resistance and stem straightness. Resistance to fusiform rust infection caused by *Cronartium quercuum* (Berk) Miyabe ex Shirai f.sp. *fusiforme* was heritable ( $H^2=0.44$ ) and highly significant SNP associations were identified using a Bayes CPI analysis. The five most significant (5) SNP loci accounted for 45% of the total variance for fusiform rust infection. Current results and potential applications will be discussed.

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<sup>1</sup> ArborGen, Inc., Ridgeville, SC

<sup>2</sup> Quantitative Genetic Services, Toccoa, GA