

# IMPLEMENTATION OF GENOMIC PREDICTION IN A LOBLOLLY PINE BREEDING POPULATION

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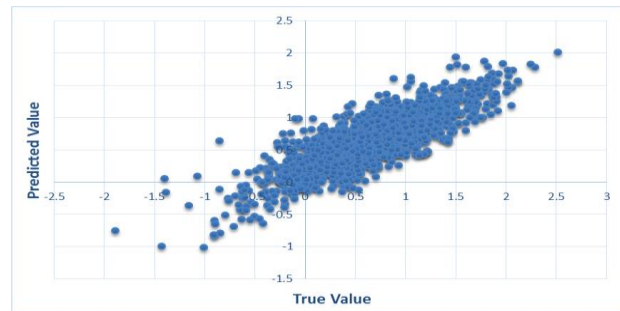
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The application of genomic based breeding and selection is not a one size fits all proposition. As ArborGen builds genomic information and resources we are exploring different approaches to incorporate genomic tools to accelerate the breeding and selection of superior genotypes of loblolly pine. A population of 1850 clonally replicated varieties was genotyped with 50,000 single nucleotide polymorphisms (SNPs) for genomic analysis. The Bayes Cpi model appeared to be successful in identifying significantly associated SNPs for all traits in this population (Table 1). The number of significantly associated SNPs ranged from 63 for fusiform rust (with 3 large effect SNPs) to 327 SNPs for volume (with no large effect SNPs). There were 58 SNPs in common between volume, height, and DBH suggesting some SNPs may have biological meaning. Modeling efforts to incorporate genomics for trait improvement show promise for parental and varietal selection but pedigrees must be represented in the training population. The prediction model worked well in this population with a correlation of 0.83 (Figure 1). A sub-sampling exercise in which 30 individuals were randomly removed from the population yielded correlations for true vs. predicted ranging from 0.63 to 0.97. The application of this technology could significantly reduce the testing and selection timeline for forest trees and improve selection intensity by pre-screening of test seedlings to remove the predicted poor performers and allow field testing of trees with a higher probability of desirable phenotypes.

**Table 1.** Significant SNPs and true vs. predicted correlations for each trait from Bayes Cpi modeling in the Coastal varietal population.

Trait	Significant SNPs	Correlation True vs. Pred.
Height	201	0.81
DBH	103	0.76
Volume	327	0.83
Rust	63	0.84
Straight	147	0.89
Forking	300	0.90



**Figure 1.** True vs. predicted values ( $r = 0.83$ ) for age 6 volume in the Coastal varietal population. A total of 1523 samples out of the 1850 were used in the training model.