ALTERNATIVE APPROACHES TO BREEDING VALUE PREDICTIONS WITHIN FAMILY

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The goal of this study is to increase the selection intensity within loblolly pine breeding programs, by assessing the relationship between unique patterns of family gene expression and parental breeding values (BV). We hypothesize that selection intensity can be increased in pine breeding programs under two conditions -first, that there are genetic differences among families in gene regulatory networks, and second, that those differences are correlated with family mean performance in field tests of progeny. Currently, selections for advanced generations of loblolly pine are made on the basis of family mean phenotype, where phenotypically superior individuals are selected from top-performing families, and progeny tested to screen for those trees that have the best BVs. However, there is little confidence that phenotypically superior selections from a progeny test will carry forward the traits intended from the family, because many traits of interest to breeders have low individual-tree heritability.

In order to estimate the BV of a tree, a BLUP (Best linear unbiased predictor) analysis is conducted where phenotype and pedigree data are utilized to help define the genetic covariance among a set of families from a mating design. It is reasonable to suspect that variation in family mean phenotypes can be partially accounted for by differences in gene structure, and partially by gene regulation patterns. Sequencing DNA copies of messenger RNA is a means to collect information on both types of differences. Using covariance structures based on variation in gene structure or gene regulation in a BLUP analysis instead of, or in addition to, the standard numerator relationship matrix, may provide a higher prediction accuracy of BV's.

To test this hypothesis, we have chosen 43 different parents, from a wide geographic distribution, with pre-existing progeny phenotype data available from field tests across multiple sites. Seeds (open-pollinated or pollen-mix in 37 cases, controlled-cross in 6 cases) from each of these parents were grown in a greenhouse, and seedlings were harvested at 3 months for RNA extraction and sequencing, which is still underway. The RNA expression results from these families will be used to create covariance matrices reflecting shared genetic variation in coding sequences on one hand, and shared variation in gene regulatory networks on the other. Cross-validation of BLUP models using these covariance matrices, as well as a standard numerator relationship matrix, will be used to test the hypothesis that phenotypic variation can be accurately modeled by covariance of these classes of genetic variation. This analysis should provide insight into the value of using RNA expression patterns as another screening effort in selecting individuals as parents for future breeding populations.

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