

GENETIC PARAMETER ESTIMATES FROM A LARGE CLONED POPULATION OF LOBLOLLY PINE

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Cloned progeny tests provide the ability to test the same genotypes in multiple environments. Compared to seedling progeny testing, cloned tests are more expensive but provides more reliable prediction of the genetic merit of individuals. The aim of this study was to estimate genetic parameters and predict breeding values for a large clonal population of elite loblolly pine.

This study included a clonal population obtained from 51 full-sibling crosses made from 24 elite parents of loblolly pine from the US Atlantic Coastal Plain. About 45 full-sib progeny per cross were cloned via rooted cutting techniques and planted at eight locations in the southeastern US. Each clone had one copy per location. An incomplete block row-column experimental design was used. Tree height, diameter at breast height, stem straightness, and the incidence of fusiform rust disease (caused by *Cronartium quercuum* f. sp. *fusiforme*) and forking were measured at age six. Individual tree models were fit to partition observed phenotypic variance into genetic and environment effects. Several variance-covariance structures were evaluated to model the clone by environment interactions, including compound symmetry, heterogeneous genetic, and factor analytic structures. The residual variance structure was allowed to be heterogeneous by site.

Results for height are reported here. More complex genetic covariance structures generally improved model fit statistics, indicating that heterogeneity in the data was better explained. However, the effect of variance-covariance structures on the precision of the breeding value predictions was modest. Overall standard error of difference between predicted genetic merit of clones was 5.1 for the compound symmetry and decreased to 5.0 for the factor analytic model. Sites had large differences for additive genetic and residual variances. The ratio of additive genetic variance over the residual variance at sites ranged from 0.16 to 0.65, indicating substantial differences in test site uniformity. However, the estimated clone mean heritability estimate was very high (0.97).

The extended factor analytic structure proved to be the best fitting model. This model explained 92% of genetic variance within sites. Genotype by environment interaction was generally negligible between sites. Additive genetic correlations between pairs of sites was generally well above 0.75, with an exception between site three and five (0.58). These results showed a high efficiency of selection from cloned progeny testing in loblolly pine, especially when utilizing advanced variance-covariance structures to model tree measurements.

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