

PREDICTION OF GENETIC MERIT IN A CLONAL POPULATION OF LOBLOLLY PINE

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Cloned progeny testing provides more reliable predictions of individual-tree breeding values than does seedling progeny testing. In this study, we analyzed a large cloned progeny test established by the NC State University Tree Improvement Program. The main objective of the study was to identify superior genotypes for breeding. From each of 51 full-sib families of loblolly pine (*Pinus taeda* L.), an average of 46 progeny were cloned using rooted cutting techniques. A total of 2362 clones were tested in seven test sites across the southeastern United States using an incomplete block row-column design. Growth measurements (height and diameter at breast height), stem straightness, and forking were assessed at tree age 4 years; only the results for height are presented here.

Linear mixed models were used for the statistical analysis. Predictions of genetic merit of clones for tree height were obtained using various G and R covariance structures that account for heterogeneity and genotype by environment interactions. Models were compared through fit statistics (Akaike Information Criterion, Bayesian Information Criterion, Log Likelihood). Best linear unbiased predictions of clones were compared using rank correlations, Pearson's correlations, and overall standard error of predictions. To estimate the aggregate genetic merit of clones from the multi-environmental trial analysis, weights for each site were obtained from separate analyses of individual trials.

Among the fitted models for the genetic analysis of height, factor analytic models G structure combined with a separable autoregressive structure of first order for the residuals at each site were superior based on the Akaike information criterion. However, the model was computationally demanding and required good starting values to converge. On the other hand, factor analytic G structure combined with block diagonal covariance R structure for the residuals was robust for modeling genotype by environment interactions. The model was parsimonious, informative, and could be fit without running into convergence problems since the computational burden of the mixed model analysis is greatly reduced.

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