

# IMPACTS OF DIFFERENT LEVELS OF GENETIC HOMOGENEITY ON JUVENILE STEM CHARACTERISTICS AND POTENTIAL STAND-LEVEL VALUE IN LOBLOLLY PINE

J.J. Steiger<sup>1</sup>, B.P. Bullock, R.C. Abt, R.W. Whetten

<sup>1</sup>NC State University Cooperative Tree Improvement Program, Department of Forestry and Environmental Resources, NC State University, Raleigh, NC

The recent, wide-spread deployment of more genetically homogenous genotypes drives the demand for better understanding growth and uniformity in stands with varying levels of genetic diversity. We hypothesized that stands planted with more genetically homogenous genotypes would be more uniform for growth traits and sawtimber potential in juvenile loblolly pine. Our results indicate that less genetically diverse genotypes are not more uniform than the more genetically diverse genotypes, and in most cases genetic homogeneity actually led to more variation in growth traits.

Furthermore, we assessed and compared the predicted values of 9 genotypes using a scenario based on growth and yield projections using the LobDSS software package. Although volume is the primary driver of value, the quality of stems in a stand also plays a significant role. By incorporating predicted product class proportions and sawlog quality measures, we aimed to accurately predict and assess the overall stand value over a range of genotypes. Having access to reliable stand value data will play an important role for land managers that aim to increase the value of forested land. Our results show that by incorporating more accurate product class allocation and sawtimber quality measures, the value of stands can change dramatically. These results suggest that if the landowner is paid for the quality of their timber, not just the quantity, then some genotypes are better options than others.

## Materials and Methods

The study site was located at the Hofmann Forest in Jones and Onslow County, North Carolina (34°49.4'N, 77°18.2'W). The soil consists of a Pantego mucky loam (Fine-loamy, siliceous, semiactive, thermic Umbric Paleaquults). This soil series consists of very poorly drained, thick loamy deposits with a water table very near the surface. Due to the high water table, the site was bedded to give study trees optimum growing conditions. There are four levels of genetic control incorporated into the design (clonal, full-sib families (mass control pollinated), half-sib families (open-pollinated), and seed orchard mix). The following genetic entries were planted: two clones (C2 and C3); three full-sib families (FS1, FS2, FS3); three half-sib families (HS1, HS2, HS3); and one Seed Orchard Mix (SOM). The clonal material used in this study originated from top performing full-sib families and was propagated by somatic embryogenesis. Full-sib family seedlings were created by selecting and breeding superior well tested parents. The half-sib families (open-pollinated) were created by collecting seed from a single, well-tested orchard tree that was pollinated by wind-blown pollen. Finally, the seed orchard mix seedlings are second

generation selections from the coastal plain of Georgia and South Carolina that are a mix of parent trees that were wind pollinated. All full-sib and open-pollinated families in this study are among the top commercially available families, as verified by the NCSU Cooperative Tree Improvement PRS (Performance Ranking System) database.

The design was set up as a split-split-plot design with the two combinations of thinning being the whole-plots. Additionally, the two combinations of spacing were the sub-plots and each genotype was the sub-sub-plot. Each genetic entry was randomly assigned to each sub-plot within each whole-plot. Each measurement plot consisted of 68-108 measurement trees planted at either 1.5 m or 3 m within bed spacing. The measurement trees span 4-6 beds, spaced 6.1 meters apart and run for 9 to 20 trees in each bed. Buffers were installed to reduce any adjacency effects. In sum, there are a total of 558 trees per rep per family. The plot-level size for the 1.5 m and 3 m spacing treatments was approximately 1.66 hectares and 3.04 hectares, respectively. Furthermore, an attempt was made to keep the rectangularity of the plots to a minimum. Total test size is 25.84 hectares.

All trees were assessed at ages 5 and 6 for total height, diameter-at-breast height and survival. Individual tree volume was calculated according to Sherrill et al. (2011) from measurements taken at age 5. To get stand-level volume for each genetic entry, average tree volume was calculated, and then multiplied by trees per hectare which was generated using overall family survival. Sawtimber potential was assessed and each tree was given a score of 1 to 4, with 1 being high-quality sawtimber, 2 being sawtimber, 3 being pulpwood/some sawtimber, and 4 as non-merchantable. Additionally, to estimate the value of various loblolly stands at harvest, we used the Loblolly Pine Silviculture Decision Support System of the North Carolina State-Virginia Tech Forest Productivity Cooperative. Analysis of variance (ANOVA) was used to test for effects on height, DBH, volume, and sawtimber potential. Additionally, ANOVA was used to test for differences in the coefficient of variation (CV) among blocks, treatments, genotypes, homogeneity type, and interactive effects.

## **Results and Discussion**

At both planting densities, FS2 had the greatest total height while C2 had the shortest total height. Additionally, FS2 had the greatest diameter-at-breast height, 12.1 cm and 13.59 cm, respectively. Clones C2 and C3 had the smallest DBH in both spacing treatments. Moreover, the two clones in the study had significantly smaller DBHs than all other genotypes, with the one exception being C3 compared to the SOM in the wide-spacing treatment. FS2 had the greatest mean volume, but was only significantly greater than three of the other genotypes, two of which were the clonal families. In fact, compared to the top performing clone (C3), FS2 had a 41% greater volume when planted at 1.5 m x 6.1m and 26% more volume at 3 m x 6.1 m. Mean sawtimber scores were similar across genotypes and spacing treatments. However, the frequency of 1's and 4's varied dramatically. For example, 25.29% of trees in family FS2 had a sawtimber score of 1 in the tightly-spaced treatment, while only 9.77% had a score of 1 in the wide spacing

treatment. Interestingly, clone C3 had 19.88% of all sampled trees in the wide-spaced treatment receive a score of 1, more than any other genotype. On the contrary, 4.02% of trees from genotype FS2 in the tightly-spaced treatment were considered cull trees (score of 4) and only 1.72% of FS2 trees were culls in the wide spacing treatment. Clone C2 had the greatest percentage of cull trees across all genotypes in the tightly-spaced treatment, while C3 had the most cull trees in the widely-spaced treatment. Across genotypes, the most variable were clones, not the seed orchard mix, regardless of spacing or growth trait. Consequently, the clonal genetic type was almost always the most variable type for total height, possibly due to environmental effects overwhelming genetic uniformity.

Generating stand values by applying age 6 stand data to LobDSS and integrating both empirical harvest data and sawtimber potential data for each family, resulted in a range of adjustments across all families. The exception was the SOM, which did have harvest data applied to merchantable tonnage, but did not have adjustments for sawtimber scores applied as it was used as a baseline for comparison for the other eight families. Adjustments were two-fold, one being a price increase for sawlog tonnage and the other being an increase or decrease in non-merchantable wood. Compared to SOM, several families had an increase in sawtimber potential and received a premium increase of 25% of the current sawlog price to account for the higher quality sawlogs. Families C2, C3, FS1, FS2, and FS3 all received sawlog price increases when planted at 1.5 m spacing. In order, their increase in percent high-quality sawtimber (score of 1) over SOM was 9.22, 7.67, 8.26, 13.08, and 1.43%. When these same families were planted in the wider spacing, differences in sawtimber quality were not as pronounced. In fact, the overall proportion of trees that were scored as 1 for sawtimber potential decreased.. Only three families were given a price increase for premium sawlogs, C2, C3 and FS1. While C2 and FS1 had a slightly better sawtimber potential than SOM (2.22%, 1.33), C3 had a large increase, producing nearly 7% more premium sawtimber.

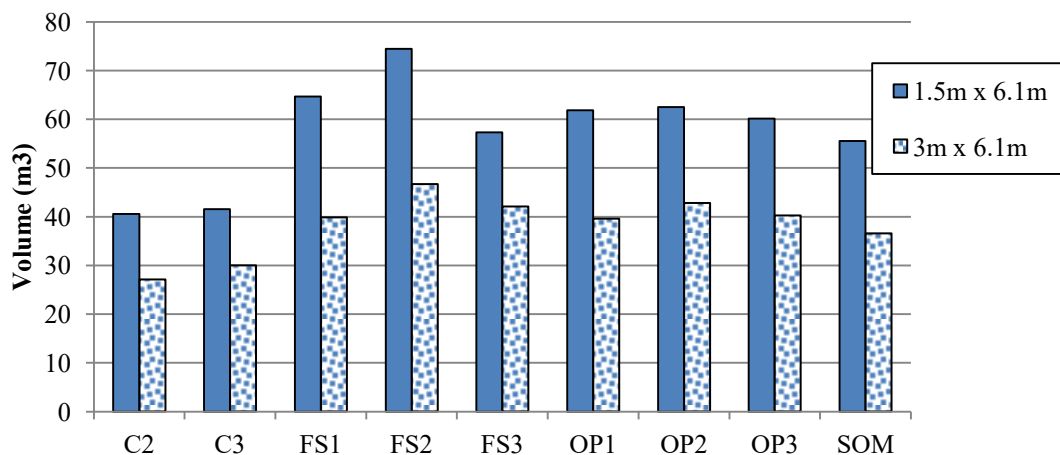


Figure 1. Mean volume per hectare of all 9 genotypes, at both the 1.5m x 6m and 3m x 6m spacing. Volume based on age 6 measurements.