Volume Gains of Rooted Loblolly Pine Clones at Age 10 in Florida and Alabama

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Abstract:--An estimate of the growth potential of clonal lines produced from elite crosses compared to trees grown from seed is needed to justify clonal forestry programs. A series of age 10 loblolly pine (*Pinus taeda* L.) rooted cutting tests planted in Nassau County, Florida and Monroe County, Alabama are some of the oldest clonally replicated studies in existence. A 3 X 3 factorial produced 9 cross families from which 4-6 clones were produced as rooted cuttings from seedling hedges. Clones and seedlings were planted in a randomized complete block design with split-plots for seedlings and rooted cuttings. Clone genetic values were estimated by Best Linear Unbiased Prediction method and genetic gains were estimated for various clone selection scenarios. Average volume gain over the family mean estimate by choosing the best clones from each family was 12.6%. The top clone of the 45 tested clones yielded 39.8% more volume than the grand mean. The top five and the top 10 clones had 30% and 23% more volume gain than the grand mean, respectively.

INTRODUCTION

Clonal forestry is becoming reality with recent successes in rooted cutting and somatic embryogenesis (SE) research. The economic returns of clonal forestry depend heavily upon identification and replication of individuals within a crossed family exhibiting superior growth and tree quality improvements. With SE technology, an unending supply of elite genetically clonal lines can be produced from one seed. The ability to cryogenically store lines to be reproduced later is the primary advantage over clonal production using clonal hedges and rooted cuttings. As might be expected, SE technology is expensive and it is important to determine how much more growth can be expected from choosing among the best clonal lines with the added benefit of starting with seed from crosses of the best available parents.

Before the development of SE technology, clonal forestry was investigated using rooted cuttings (Foster et al., 1987). To generate a clonal line using rooted cuttings, one seedling from a cross was hedged to produce cuttings for several other hedges. After production of a number of genetically identical hedges, cuttings were rooted for clonal testing. Hedged trees may be biologically limited to about 3-4 years of useful life before maturity causes a decline in rooting success although the exact number of years of useful

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life for southern pines is yet to be determined[1].

One of the oldest series of well-designed rooted cutting/seedling tests (Frampton, 1989) has completed the tenth growing season. Results after six growing seasons were published (Frampton, et al. 2000; Isik, et al. 2003). Clones selected from older rooted cutting tests cannot be rejuvenated and reproduced for operational planting, however rooted cutting clonal tests can provide an estimate of the growth gain from clonal forestry.

METHODS

A 3x3 factorial mating design was used to produce nine full-sib families of loblolly pine (*Pinus taeda* L.). Seedlings of full-sib families were used to establish clonal hedges. One year after hedge establishment, up to six clonal lines of cuttings were rooted from each of the nine crossed families. Seedlings from the same full-sib families and rooted clonal lines were established in a split-plot field design. There were a total of 45 clones tested in addition to the nine families established from seed. The two field studies were established on a bedded flatwoods site in Nassau County, Florida and on an old-field Upper Coastal Plain site in Monroe County, Alabama. Clones and seedling were randomly allocated to main plots and replicated 6 times at each site.

Both sites were measured for height and diameter at age ten and were analyzed for volume. Clone genetic values were predicted by the Best Linear Unbiased Prediction method and fitting a linear mixed model. Given the large differences in growth between the two sites, volume per tree was transformed for combined analysis by dividing the individual tree volumes by the standard deviation of each site. Variance components were estimated by SAS Mixed procedure and using REML method.

RESULTS

There were no significant differences in volume between from rooted cuttings vs. seedlings for either the Florida or the Alabama tests at age 10 although trees at the Alabama location grew about twice as fast as those at the Florida location (Figure 1).

This indicated that the rooted cuttings were growing as well as trees originating from seed. Cloning a family for genetic testing did not show slower or faster growth, but may yield greater within family genetic gains compared to the seedling based testing and selection (Isik et al. 2002).

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[1] Personal communication with Dr. Barry Goldfarb. NC State University College of Natural Resources
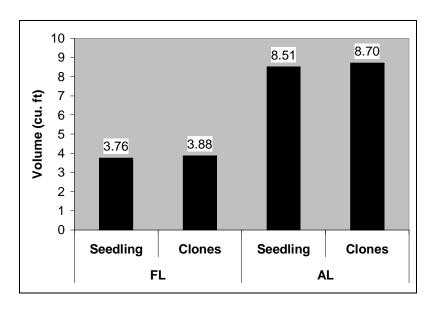
Figure 1. Volume from seedlings and clones of the same families at two sites at age 10.

Genetic factors including female and male general combining ability (GCA) effects, specific combining ability (SCA) and clonal differences explained about 33% of the total phenotypic variance (Figure 1). Genetic differences among females explained about 2.6% of the total variation in volume. Differences among males accounted for 6.5%, whereas SCA of females and males explained 7.4%. However, genetic differences among clones explained a greater percentage (12.7%) of the total phenotypic variation than GCA and SCA effects.
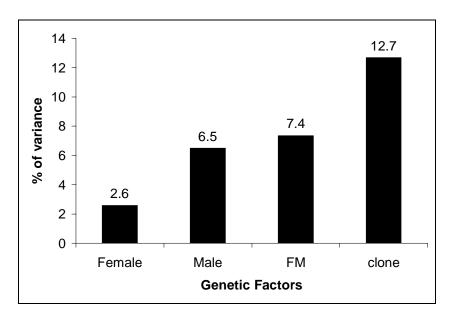

Figure 2. Percentages of the total phenotypic variance for volume explained by the genetic effects at age 10

Studies at NCSU using six-year results of these tests have shown the advantages of cloned family testing for within-family selection compared to the within-family selection from seedling testing option (Isik, et al. 2002). Therefore in this study we compared the best clone genetic values to its family breeding values instead of the seedlings (Figure 3). The best clone within a particular full-sib family had 3.9% (family 64) to 24.9% greater genetic gain (family 21) than their family breeding values. The average of the best clones provided 12.3% additional volume gain compared to their corresponding family mean. This would be the gain expected from using the clone in a vegetative propagation program. For use in an orchard program, selection of the same clones for their breeding values yielded 2.9% to 16.5% genetic gains over their family breeding values.

The low gains for family 64 are mostly because the means of clones within that family are tightly grouped with low variation between them. High gains are most likely to be realized with a clonal program by choosing very good families such as family 65 and family 35 with a high degree of variation among clones and then choosing the top performing clones to propagate.
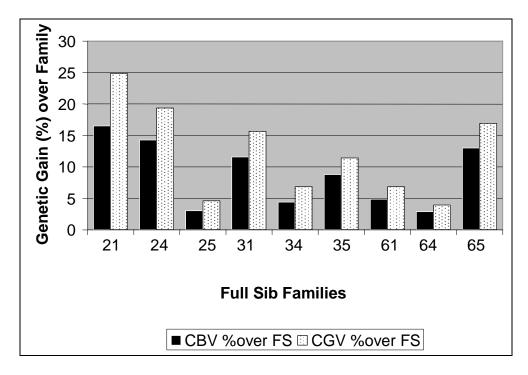

Figure 3. Genetic gains of the best clone breeding values (black bars) and clone genetic values over the respective family breeding values for volume at age 10.

The choice of the best clone per family was the same in the Florida and Alabama tests in six of the nine crossed families. In the three cases where the best clone was not the same, the top performing clones in one test was very close to the top in the other test. This is notable considering the distance between the two test locations and the obvious difference in site quality. The fact that clones ranked the same at both locations demonstrates the precision of clonal replication, which can sample several different microsites with the exact same genotype (Isik et al. 2002).

The volume increase of the best clone for each full-sib family can be important to estimate the gains achievable within a family. However many of the best clones may come from just a few of the best families. The best clone across both tests came from full-sib family 65 and had 39.8% more volume compared to the mean of all 45 clones (Figure 4). Each clone was represented by an average of 20 trees between the Florida and the Alabama tests. The top five clones, collectively represented by 106 trees, had 30 % more volume than the average. All five of these clones came from either full-sib family 65 or family 35. All of the top 10 clones came from either family 65 or family 35 except for one. Even choosing the top 10 clones yielded over 23.3% more volume gain than the test average.

Although no rust incidence was taken at age ten, Frampton, et al. (2000) reported significantly different rust incidence between seedlings vs. cuttings at age six for both sites. Rust incidence for the Nassau site at 22.3% for the seedlings and 15.6 for the cuttings. At the Alabama site, rust incidence was considerably higher at 51% for seedlings and 46% for cuttings. Clones had lower rust incidence than the seedling of the same families.
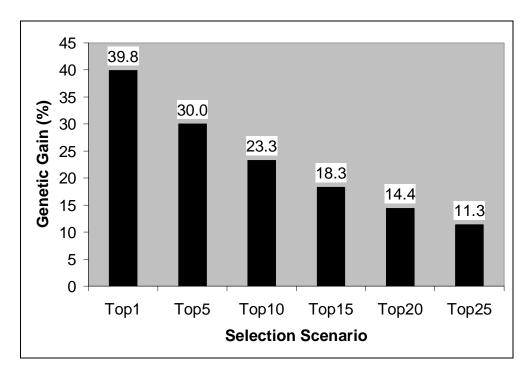

Figure 4. Percentage volume gain expected over the grand mean (averages of all 45 clones) by choosing the top clones out of 45 clones regardless of families. Each clone genetic value prediction was based about 20 ramets tested at two sites.

SUMMARY

The average volume gain from choosing the best nine clones (the top clone of each family) was 12.3% compared the mean of all of the rooted cutting families. Choosing the top five clones out of the 45 clones tested no matter what cross they came from yielded 30% more volume at age 10. All of these came from two crosses, however it may be less risky to accept less gain and choose good clones from some of the other full-sib families for operational deployment.

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