Genetic and Cultural Factors Affecting Growth Performance of Slash Pine

G. L. Reighard, D. L. Rockwood, and C. W. Comer

Abstract.--Five- to seven-year growth performances of genetically select slash pine progenies planted at five northern Florida sites were evaluated for differences due to family, provenance, plantation site, competition (pure and maximum), plot design (block and Nelder), spacing (472-43,100 trees/ha), and age. Significant family differences were found for growth. Family x site interactions were important on poor sites. Intergenotypic competition and plot design did not affect family performance. Spacing influenced diameter and volume, but a family x spacing interaction was not apparent. Growth trends detected at age five continued at age seven, but variation among families decreased.

Additional Keywords: Pinus elliottii var. elliottii, genetic tests, genotype x environment interaction, spacing.

INTRODUCTION

Numerous genetic tests of slash pine (Pinus elliottii var. elliottii Engelm.) have been established in the southeastern United States during the past 25 years. Data from these tests have been used to select fast-growing, rust-resistant genotypes for clonal seed orchards. Recently, Franklin (1979, 1983) and Stonecypher and McCullough (1981) have advocated shortening the evaluation period in progeny tests by planting at high, non-conventional densities to create competition at earlier ages. Furthermore, factors such as plot design, age of measurement, and environment interactions require additional study to determine if present genetic evaluations are appropriate for wide geographic plantings of selected slash pine families. The objectives of this paper were to evaluate the effects of family, provenance, site, intergenotypic competition, plot design, spacing, and age on growth performance of slash pine progenies at five northern Florida sites.

Assistant in Forest Biomass, Associate Professor, and Assistant Research Scientist, respectively, Department of Forestry, University of Florida, Gainesville, FL. Research reported here was supported by the Cooperative Forest Genetics Research Program, Oak Ridge National Laboratory under subcontract No. 19X-09050C, and a cooperative program between the Institute of Food and Agricultural Sciences of the University of Florida and the Gas Research Institute entitled "Methane from Biomass and Waste."

MATERIALS AND METHODS

Nine slash pine progeny tests located at five northern Florida sites were measured in 1984 (Table 1). Height, diameter at breast height (DBH), and survival were recorded. Individual tree volume was calculated using an equation developed by Goddard and Strickland (1968) for five-year-old slash pine. Six tests had block plot designs with tree densities ranging from 1,121 to 10,000 trees/ha. The three remaining tests were Nelder designs with eight spacings. One Nelder test had densities ranging from 472 to 3,089 trees/ha, whereas the densities of the other two ranged from 4,800 to 43,100 trees/ha. Detailed descriptions of the tests and test sites are given by Rockwood (1983).

Analyses of variance were performed on data from either randomized complete block or split-plot designs in each study. Coefficients of variation were determined for height and DBH data from five tests. Spearman's rank correlation coefficients were calculated for volume data between common families of comparison tests. Rank correlations were also calculated between the volume data from each of the nine tests and the volume clonal evaluations assessed by the Cooperative Forest Genetics Research Program at the University of Florida.

RESULTS AND DISCUSSION

Family and Site Factors

Growth varied by progeny test (Table 1) and was influenced by site quality. Good growth occurred in tests 8-78-1, 8-78-2, and 0-58, which were planted on similar lower coastal plain sites. Tests 0-59 and 0-60 were planted on less fertile, flatwood sites and had only average growth. Growth differences due to site were also evident between the tests at Gainesville, FL (10-N, 10-P) and Trenton, FL (11-N, 11-P). Early survival, however, was not affected by site quality.

Growth differences due to family were statistically significant in every test except 10-P and 11-P. In tests that contained a commercial checklot (i.e., 0-58, 0-59, 0-60), selected slash pine families generally grew and survived better than the check; although an average of]9% of the selected families had less plot volume than the check for a given site. Since some families occasionally performed poorly on particular sites, family mixes would be preferred over family blocks for certain sites if no families have demonstrated superiority.

Family ranks for individual tree volume in each of the tests were not statistically correlated with the standardized clonal evaluations (Table 2), which are based on row-plot progeny tests planted at operational spacings. The low correlations for sites other than Cantonment suggested that genotype x environment interactions were present. Earlier comparisons of other families across various test sites also suggested such interactions (Goddard et al. 1976, Goddard et al. 1982) whenever site differences were large. Most highly-rated families were consistent, however, in these tests. Since fifth-year performance in

Table 1. Mean growth performance for all slash pine families in each progeny test.

Progeny Test No.	Florida Location	Age (yrs)	Ht. (m)	DBH (cm)	Vol. (m^3)	Surv. (%)
8-78-1	Cantonment	6	7.7	10.4	.0299	86
8-78-2	Cantonment	6	7.3	10.7	.0297	90
0-58	Cantonment	7	7.5	10.6	.0296	87
0-59	Perry	7	6.0	8.8	.0189	89
0-60	Yulee	7	5.9	8.6	.0182	89
10-N	Gainesville	5	3.1	3.3	.0064	96
10-P	Gainesville	5	3.6	3.9	.0074	95
11-N	Trenton	5	5.3	5.5	.0111	96
11-P	Trenton	5	5.8	5.8	.0121	94

Table 2. Spearman's rank correlation coefficients between progeny test performance and composite clonal evaluations.

Progeny Test No.	Florida Location	No. Common Families	Volume
			--r---
8-78-1	Cantonment	7	.32
8-78-2	Cantonment	7	.61
0-58	Cantonment	22	.40
0-59	Perry	22	.04
0-60	Yulee	19	.25
10-N	Gainesville	32	.08
10-P	Gainesville	21	-.08
11-N	Trenton	25	.19
11-P	Trenton	17	.06

conventionally spaced tests is not as well correlated with subsequent measurements as are 10th-year data, the higher correlations for the Cantonment sites may be due to the excellent growth which was equivalent to that of older trees.

Genotype x environment interactions were less apparent in the comparisons between common families in the nine tests (Table 3). Excluding comparisons involving test 10-P, rank correlations were positive (r=.16 - .73). Therefore, family rankings for growth performance within these tests did not change significantly. The failure of the standardized clonal evaluations to demonstrate genotypic stability for family performance across sites limits the usefulness of the evaluations for selecting superior families for planting. Further study of the methodology used in family evaluation is needed, since comparisons between the progeny tests (Table 3) indicated genotypic stability did occur at a modest level.

Test comparisons (Table 3) emphasizing site differences rather than plot designs generally had positive rank correlations (r=.33 - .57). Since plot designs and spacings were identical, the largely non-significant correlations from these paired tests suggested family **x** environment interactions were occurring. These interactions affected growth of some families on the poorest site, test 10-P. Correlations from the three paired tests involving 10-P were negative, and two were significant. Possibly the slash pine families that grew well on moderate to good sites may have been more sensitive to site quality and therefore, were physiologically predisposed to site and spacing interactions on poor sites.

Family performance was also linked to geographic origin in tests having commercial spacings (i.e., 0-58, 0-59, 0-60). Families from southeastern Georgia and northeastern Florida consistently grew the best. Volume growth of these families averaged 3% more than southern Alabama and Mississippi families and 9% more than north-central Florida families. However, these comparisons may **be** influenced by the unequal and limited sample sizes from the geographic regions. Slightly different geographic patterns were observed in the fifth-year data (Goddard **et** al. 1982).

In addition to family performance across sites, intergenotypic competition was investigated in test 8-78-1. Contrary to findings by Williams et al. (1983) for loblolly pine, no differences in growth were found between pure plots (one family) and mixed plots (nine families) which agreed with results reported by Franklin (1983) for studies on loblolly family competition. Survival, however, was significantly higher (+9%) in the mixed plots.

Plot Design and Spacing Factors

Comparisons of tests from the same site but having different plot designs, from different sites with the same plot design, and from different sites with different designs showed that, with the exception of the 10 tests, plot design affected family volume rankings less than did site differences (Table 3). Families in Cantonment tests 8-78-1

Table 3. Spearman's rank correlation coefficients for volume data of common families across different tests and plot designs.

Test Comparison	Plot Design Comparison	No. Common Families	Volume (m^3) --r---
8-78-1/8-78-2	Block/Nelder	9	.73*
10-P/10-N	Block/Nelder	20	-.46*
11-P/11-N	Block/Nelder	13	.57*
0-58/0-59	Block/Block	14	.57*
0-58/0-60	Block/Block	14	.47
0-59/0-60	Block/Block	14	.36
10-P/11-P	Block/Block	17	-.05
10-N/11-N	Nelder/Nelder	25	.33
10-P/11-N	Block/Nelder	18	-.48*
10-N/11-P	Nelder/Block	15	.16

*Significant at the 5% level.

and 8-78-2 were significantly correlated (r= .73) despite the differences in plot design and spacings between the two tests. The 11-P and 11-N test comparison gave similar results. The similarity of family volume production across two plot designs with different spacings suggested family x spacing interactions were not influencing family rankings. This was in contrast to Stonecypher and McCullough's (1981) observations from a eight-year-old Nelder test of Douglas-fir. They found family x density interactions at spacings (735 to 26,300 trees/ha) greater than those tested in the 10-N and 11-N tests. There were, however, significant spacing x family interactions for height in tests 8-78-2 and 10-N. Therefore, some slash pine families were affected differentially by spacing at ages five and six, although most family ranks changed little.

Spacing significantly affected family height and/or diameter (DBH) growth in all spacing tests except 8-78-1. DBH was influenced by spacing in tests 8-78-2, 0-58, 0-59, 0-60, 10-N, and 11-N. Height was affected in tests 10-N and 11-N. In the Nelder tests, spacing influenced height, DBH, and volume in a manner similar to that reported by Stonecypher and McCullough (1981) for Douglas-fir. DBH and volume increased with each subsequent decrease in density. Height also increased with decreasing density up to the two lowest densities where it decreased slightly. Therefore, growth differences between the progeny tests reflected spacing as well as site differences.

Age Factors

Spearman correlations between family height, DBH, and volume data for years three versus five, four versus six, and five versus seven were significant (r=.75 - .93) in all tests. Family performance rankings changed little over two years, irregardless of the different spacing treatments.

The coefficient of variation (CV) for growth data recorded in 1982 and 1984 from four tests planted at two operational spacings decreased over time (Table 4). The CV for height of trees planted at wide spacings varied from 0.9% less than to 1.5% more than the CV of narrow spacing trees. The CV for DBH was 1.5-1.7% larger at the narrow spacings in three of four tests. Similarly, the CV for DBH at five spacings (4800, 8400, 14,600, 25,100, and 43,300 trees/ha) in Nelder plots from test 11-N decreased from the densest to the widest spacing at both ages three (34% to 25%) and five (27% to 21%).

Table 4. Coefficients of variation (CV) for height and DBH of all families tested at two spacings and measured in 1982 and 1984.

Progeny Test (Planting Yr.)		CV for Height Wide/Narrow Spacings[a] 1982	1984	CV for DBH Wide/Narrow Spacings 1982	1984
		-----------	----------- (%)	-----------	-----------
8-78-1	(1978)	13.2/14.4	11.5/11.8	18.4/20.7	15.9/17.5
0-58	(1977)	13.6/13.2	11.9/11.9	18.1/18.3	14.8/16.5
0-59	(1977)	21.9/18.5	16.6/15.1	29.3/26.2	22.1/21.3
0-60	(1977)	21.2/22.5	16.5/17.4	29.3/31.5	20.5/22.0

[a] Spacings were 1,223 and 2,446 trees/ha, respectively.

Even though high **densities** appeared to encourage expression of intrafamily variation at three, five, and seven years of age, no family x spacing interactions for DBH were found in the Nelder tests (8-78-2, 10-N, 11-N) where high densities were tested. Furthermore, the Nelder data and the decreasing CV with time suggested that significant family x spacing interactions may not occur in these tests in the future. Thus the merits of using narrow spacings and alternate plot designs to evaluate the growth potential of slash pine families at young ages have yet to be demonstrated.

LITERATURE CITED

Franklin, E. C. 1979. Model relating levels of genetic variance to stand development of four North American conifers. Silvae Genetica 28(5-6):207-212.

Franklin, E. C. 1983. Patterns of genetic and environmental variance in a short-term progeny test of loblolly pine. Proc. 17th S. For. Tree Imp. Conf. pp. 332-343.

Goddard, R. E. and R. K. Strickland. 1968. Volume and weight tables for five-year-old plantation grown slash pine. Univ. Fla. Sch. For. Res. Conserv. Res. Rpt. No. 14. 7 pp.

Goddard, R. E., D. L. Rockwood, H. R. **Kok**, C. A. Hollis, and J. A. Hendrickson. 1976. Cooperative Forest Genetics Research Program 18th Progress Report. Univ. Fla. Sch. For. Res. Conserv. Res. Rpt. No. 25. 20 pp.

Goddard, R. E., D. L. Rockwood, and H. R. Kok. 1982. Cooperative Forest Genetic Research Program 24th Progress Report. Univ. Fla. Sch. For. Res. Conserv. Res. Rpt. No. 33. 25 pp.

Rockwood, D. L. 1983. Alternative designs for progeny testing slash pine. Proc. 17th S. For. Tree Imp. Conf. pp. 179-185.

Stonecypher, R., and R. McCullough, 1981. Evaluation of full-sib families of Douglas-fir in a Nelder design. Proc. 16th S. For. Tree Imp. Conf. pp. 55-76.

Williams, C. G., F. E. Bridgwater, and C. C. Lambeth. 1983. Performance of single family versus mixed family plantation blocks of loblolly pine. Proc. 17th S. For. Tree Impr. Conf. pp. 194-201.