

Age-Five Results from the Cooperative Forest Genetics Research Program Slash Pine Polymix Trials

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Abstract:--The Cooperative Forest Genetics Research Program (CFGRP) has completed polymix test installation for the second generation of slash pine (White, et al.) objective of this testing is to evaluate the general combining ability of advanced generation slash pine selections for rust resistance and individual tree volume. The eight tests comprising Polymix Series I were established in the winter of 1997-1998 and contain 139 polymix families. The field design for this test series was randomized complete block with twenty blocks of single-tree plots per location. Great care was taken in selection and silvicultural treatment of these sites. The resulting age-five single-tree heritabilities for rust resistance and individual tree volume were 0.26 and 0.30, respectively. These heritabilities are from twice to three times those realized from first generation tests at the same age. The differences between heritabilities across generations result from better silvicultural treatment which provided a more uniform environment and faster growth, and from a better field design which positioned the offspring more efficiently across the environment. Increases in the heritability of rust resistance are most probably due to the uniform environment for growth. The more uniform environment also affected the difference between filler and non-filler microsites making the types of microsite appear less different than was previously assumed.

Keywords: Heritability, rust resistance, volume, slash pine

INTRODUCTION

As part of a complementary mating and testing structure for the second cycle of slash pine, the CFGRP installed two series of polymix tests intended to evaluate the general combining ability of 359 advanced generation selections (van Buijtenen and Lowe 1979, White *et al.* 1993). The breeding population for the second cycle was divided into two superlines with approximately 30 elite selections and with 12 breeding groups per superline. Each breeding group, which contained about 40 individuals, was divided according to rust resistance and volume breeding values into three strata, classes. Class I contained the top one-third of the parents, while Class II was intermediate, and Class III was the bottom one-third composed primarily of infusions. Inclusion of an individual in the polymix breeding was based on the following criteria: (1) Elite selections; (2) Class I forward selections; (3) Class I backward selections tested at fewer than six locations; (4) Class II backward selections tested at fewer than two locations; (5) Class II forward selections whose parents were, on average, tested at fewer than two locations; and (6) Poorly tested parents present in seed orchards (White *et al.* 1993).

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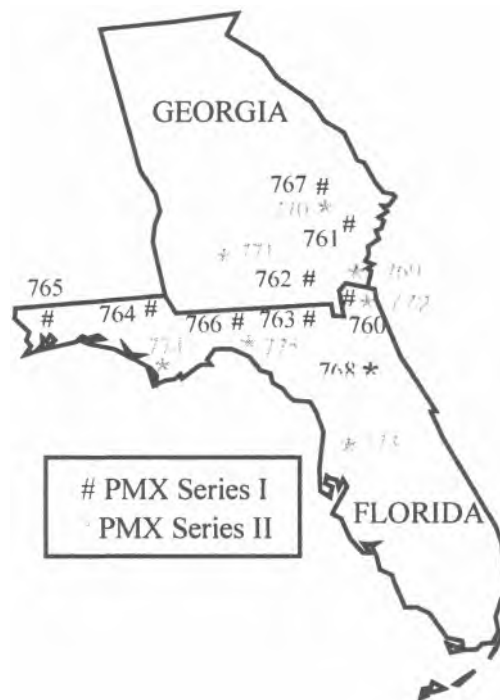


Figure 1. Locations of slash pine PMX tests in Series I and Series II, eight tests apiece.

Test sites were intended to be environments where slash pine would be planted operationally. They were reasonably uniform and were to be treated in a manner which enhanced seedling growth and site uniformity through reduced weed competition, nutrient amendment and soil preparation. The specific weed competition goals were no weed competition on the beds for the first three years and no woody competition in the test until the measurement schedule was completed. The general guidelines for fertilizer application were phosphorus application at planting, if needed, and a balanced fertilization at age three.

Analyses of the age-five data from the eight locations of Polymix Series I are reported here (Figure 1). The analyses were intended to (1) rank parents and predict breeding values for rust resistance and volume, (2) quantify the effect of stem-galled trees on the analysis of volume, and (3) quantify the effect of filler microsite on growth, rust resistance and survival.

MATERIAL AND METHODS

Seedlings were grown in greenhouses by two cooperators, Rayonier and International Paper, during the summer of 1997. The growers along with the cooperators for whom the seedlings were being grown randomized the seedlings into planting order during mid-summer. Seedlings completed the growing season with the growers. From December of 1997 through February of 1998, eight tests were planted as one each by the following cooperators: Florida Division of Forestry, Foley Timber and Land, Plum Creek, Georgia Forestry Commission, International Paper, Smurfit-Stone, Rayonier and Packaging Corporation. All sites were well-tilled and weed-free. Tillage ranged from disking on old-field sites to single, double or triple bedding on wet sites. Soil types varied from a sand with a deep spodic horizon to a sandy clay loam.

The nominal spacing was six feet along the bed and 10 feet between beds. Family identification was maintained for all planting positions, although some positions were designated as fillers because of an atypical microsite. There was no specific limitation on the number of planting spots designated as filler within a block. Sites were mapped by row and column as well as block and tree within block.

Weeds were primarily spot treated along the beds after planting and were controlled by mowing or directed spray between the beds. Fertilization was applied during the third growing season in the form of 500 kg of 10-10-10 with micro-elements per hectare.

Polymix Series I was measured in the fall of 2002 after the fifth growing season. The variables measured were height (m), diameter at breast height (cm) and status. Within the status code are levels indicating rust infected or healthy and, if infected, the extent of the infection (branch or stem). Volume in dm³ was calculated from height and diameter as:

Volume=0.25B(10dbh)²(1.4+.33((height/10)-1.4)), which considers the stem a cylinder up to breast height and a cone thereafter (Lambeth *et al.* 1983).

Two traits were considered in the analyses, Volume and Rust (infected or not infected). For most volume analyses rust infected trees with stem galls were removed. Tests 762 and 765 were discarded from the rust analyses because of low incidence of the disease.

Analyses were run by site and then across sites for both traits with filler positions removed. Two additional analyses were performed: (1) stem rusted tree were included in the volume analyses and the results compared to those from volume with removal of stem rusted trees; and (2) the effect of filler microsite was assessed for height, survival, volume and rust by indicating filler and non-filler positions as a treatment. Mixed model analyses considering tests and block as fixed effects and family and its interactions as random effects were used throughout.

RESULTS AND DISCUSSION

Single Site Analyses

Least-square means for survival, volume and rust are given by test in Table 1. The age 5 survivals were excellent ranging from 84 to 97%. Test means for volume and rust proved more variable with values from 8.2 to 28.9 dm³ for volume per tree and 6 to 61% for rust incidence. Single-site heritabilities (Table 1) for volume were all quite good for age 5 data and ranged from 0.16 to 0.62. Among sites where the rust infection level was greater than 20%, the single-site heritabilities ranged from 0.16 to 0.41 on the binary scale. There is little doubt that the PMX I Series is a vast improvement in test quality over first-generation slash pine progeny tests. The mean volume across the eight PMX I tests is 19.3 dm³. This is the size equivalent in average volume of first-generation tests

between 7 and 8 years of age. The average single-site heritability for volume at age 5 is 0.37 compared to 0.11 for first generation tests (White *et al.* 1996). These results indicate the increased precision from the attention to detail implementing and caring for these tests.

Across Site Analyses

The enhancement in heritability is even more evident in the across-site analyses (Table 2). The across-site heritabilities for volume per tree without stem-galled trees were almost identical for the standardized and the non-standardized analyses (0.30), and the type B genetic correlations were 0.85 and 0.81, respectively. In the analysis of volume with stem-galled tree included, the heritability dropped to 0.22 and the type B genetic correlation dropped to 0.69. The across-site heritability estimate of 0.3 for volume per tree is almost three times that of average first-generation tests at any age (White *et al.* 1996). The removal of stem-galled trees from analyses raised the across-site heritability from 0.22 to 0.30 and the type B genetic correlation from 0.69 to 0.81. The heritability with stem-galled trees is three times that of the equivalent first-generation values.

Test	Survival %	Volume dm ³	h ² _b Volume	Rust	h ² _b Rust
760	93.1	15.3	0.29	44.6	0.31
761	90.4	16.4	0.16	28.8	0.27
762	97.0	21.8	0.38	6.0	0.03
763	84.1	16.7	0.47	47.7	0.38
764	88.0	20.4	0.23	60.6	0.36
765	97.3	25.8	0.49	8.2	0.04
766	88.7	28.9	0.62	49.5	0.41
767	91.8	8.2	0.30	23.5	0.16
Average	91.3	19.3	0.37	33.6	0.24

Table 1. Least-square means and single-site heritabilities for survival, volume per tree (dm³) and rust by test for age 5 data from slash pine PMX Series I. Rusted trees with stem galls were removed from volume calculations.

Analysis	h ² _i	r _B
Non-standardized, no stem galls	0.30	0.81
Standardized, no stem galls	0.30	0.85
Non-standardized, stem galls	0.22	0.69

Table 2. Individual tree heritabilities (h²_i) and type B genetic correlations (r_B) from three across-site analyses for volume (dm³) in the eight slash pine PMX Series I trials. The three analyses are non-standardized and standardized volume without stem-galled tree and non-standardized volume with stem-galled trees. For standardized volume, the volume of each tree was divided by the volume phenotypic standard deviation for that site.

Trait	Filler	Non-filler
Height (m)	5.5	5.6
Volume (dm ³)	18.7*	19.3
Survival (%)	87.01	91.44
Rust Incidence (%)	30.09	37.82

*significant at $\alpha=0.05$.

Table 3. Least-square means and significance levels for analyses of the effect of filler microsite versus non-filler microsite adjusted for genetic entry for height, volume, survival and rust incidence across the eight sites of PMX Series I. Site by microsite type interaction was never significant.

So, for across-site heritability for volume, better testing techniques tripled the first generation heritability and the elimination of stem-galled trees caused the value to quadruple. The primary reason that the removal of stem-galled trees raised the type B correlation and thus the heritability is that differential infection rates for families across sites were caused by different rust resistance levels for the parents and different rust hazards for sites. These differential rust infection levels for families affected the average growth rate for the family by site causing apparent genotype-by-environment interaction for growth rate. When stem-galled trees were removed from the analysis, GxE for growth rate virtually disappeared. The increases in heritability for this test series also apply to fusiform rust incidence. All of these single-site rust heritabilities are more than twice the average values reported by rust incidence level for the first-generation slash pine tests (White *et al.* 1996).

Filler Microsite Analyses

In the analysis for the effect of filler microsites, four variables were analyzed: height, volume, survival and rust incidence. Of these four variables only volume was significantly affected by filler microsite, Table 3. The trends for the effect of filler microsite were generally in the direction expected. When adjusted for genetic entry, the trees in filler microsites were shorter (5.5 vs 5.6 m), had lower survival (87% vs 91%) and less volume per tree (18.7 vs 19.3 dm³) than non-filler microsite trees. The effect of filler versus non-filler microsites was only statistically significant for volume. While the filler effect apparently exists, the magnitudes of the differences in growth and survival between microsite types is not sufficient to discourage implementation of spacial statistical designs for which the designation of planting spots as fillers is extremely problematic.

LITERATURE CITED

- Lambeth, C. C., W. T. Gladstone and R. W. Stonecypher. 1983. Statistical efficiency of row and noncontiguous family plots in genetic tests of loblolly pine. *Silvae Genet.* 32: 24-28.

- van Buijtenen, J. P. and W. J. Lowe. 1979. The use of breeding groups in advanced generation breeding. Proc. 15th South. For. Tree Improve. Conf., Miss State, June 19-21, P. 59-65.
- White, T. L., G. R. Hodge and G. L. Powell. 1993. An advanced-generation tree improvement plan for slash pine in the southeastern United States. *Silvae Genet.* 42:359-371.
- White, T. L., G. L. Powell and G. R. Hodge. 1996. Genetics of slash pine: Parameter estimates and breeding value predictions. CFGRP Confidential Document, University of Florida pp. 166.