PERFORMANCE OF SINGLE FAMILY VERSUS MIXED FAMILY PLANTATION BLOCKS OF LOBLOLLY PINE

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<u>Abstract.--Sixteen</u> loblolly pine (Pinus taeda L.) families were planted in single family and in mixed family (noncontiguous) plots in 1978. The original purpose of the study was to compare growth and straightness between the two stand types. Preliminary results from measurements at age four indicated that single family plots performed better than mixtures of the same families. Family by stand type interactions were not estimable for growth traits and were small for quality and disease resistance. Family performance correlated well with progeny test assessments.

<u>Additional keywords:</u> Intergenotypic competition effects, single family plantation blocks, <u>Pinus taeda.</u>

INTRODUCTION

Intergenotypic competitive effects can be manifested as a yield increase for all genetic entries in one stand composition type over another. For example mean grain yield from pure plots was greater than the mean of mixtures of tropical rice varieties (Jennings and Aquino, 1968). By contrast, mean yields did not differ by stand types for soybeans (Sumarno and Fehr, 1980; Hinson and Hanson, 1962).

Cereal yields in monoculture are inversely related to the competitive ability of the genotype (Hamblin and Donald, 1974; Donald and Hamblin, 1976). Rice varieties have shown this most consistently. The taller, leafier plant types tended to compete effectively but had low grain yields (Jennings and deJesus 1968). Strong competitive ability of this type has been a deterrent to advances in plant breeding programs because it distorts genetic variances and, consequently, selection (Hamblin and Rosielle, 1978).

Yield differences have been observed with loblolly pine families as well. Five Piedmont loblolly pine families were planted in single family and mixed family plots to increase the size and number of plantable seedlings. Single family plots had taller seedlings than the mixed plots after the first year (Dierauf, Virginia Division of Forestry, unpublished data). The germination rates among families accounted for the higher yields rather than inherent growth differences among families (N.C. State Cooperative Annual Report 1975).

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Several intergenotypic competition studies have been conducted with forest tree seedlings (Adams et al. 1973; Tauer, 1975; Adams 1980) but the results have shown no consistent relationship between yield and intergenotypic competition. Results from two recently measured field studies should address this question (Sam Land, Mississippi State University, pers. comm.; Lambeth, unpublished data).

The following study was used to answer two questions:

- Do yields from single family plantations approximate yields from a mixture of families?
- 2) How do families in pure blocks compare with the commercial check for straightness, rust resistance and growth?

METHODS

Procedure and Test Design

The seeds were stratified and sown in containers then later arranged in the field design to maintain the same competitive relationships from greenhouse to outplanting. The seedlings were outplanted at 3 m spacing in southeastern N.C. on a poorly drained sandy site. Seedlings received tip moth control the first year and weed control the second year.

Height (meters), diameter at breast height (centimeters), rust resistance and straightness!!! were tallied after four growing season⁻ in the field. Volume (cubic decimeters) was estimated from height * dbh². Mortality was low (2%) and the lowermost branches had not begun to prune off although crown closure had begun. Sixty-eight percent (4901 trees) of all test trees, includin borders, had some sign of fusiform rust <u>[Cronartium quercum (Berk.) Miyabe ex</u> Shirai f. sp. <u>fusiforme].</u>

Sixteen half-sib families that represented a wide range with respect to growth, straightness, and rust resistance (as evaluated from genetic tests) were selected. A commercial check collected from seed production areas in eastern North Carolina was also included; this is the same check used in Weyerhaeuser Company's first-generation High Wood Density progeny tests.

A sets-in-blocks design with three blocks was used. In each block, six seedlots were grouped in each of four sets. Four different single family plots (64 trees per plot) were assigned to a set within each block and were confounded with sets. The commercial check and a bulked mix of all sixteen families were included in each set.

Statistical Analyses

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The data analyses were performed with the assistance of the Statistical Analysis System package (SAS Institute 1979). Set and block * set interaction

N.C. State Industry Pine Cooperative straightness score 1-6.

terms were not significant at the 95% confidence level so the data was pooled over sets. !flocks and family terms were random. Stand composition type was a fixed term. The analyses were done on a plot mean basis.

The eight-year progeny test performance ranks were based on unitled measures that represented the number of standard deviations above or be low the mean of all families tested in the High Wood Density breeding program. This measure was used because of the family imbalance across tests and across two overlapping breeding regions that have now been combined.

Rust resistance was measured as the number of trees without stem galls in both the family yield trial and the progeny test data. An arcsin \checkmark Y transformation was used to approximate a normal distribution.

RESULTS AND DISCUSSION

Single Family Plots Versus a Mixture of Families

Due to the young age of the test and the fact that competition influences were not strong, no firm conclusions can be drawn regarding yield in pure block versus mixtures of families. However, the single family plots have a slight growth advantage over mixed plots which is statistically different at the 95% level (Table 1). The mean of single tree plots is 3.1% (.12 meters) greater than that for the mixed family plots; the volume increment was 9.0% (1.4 dm3).

Table 1.--Fourth-year results from the family yield: the values from the F-test of significance for family, stand type (mixed versus pure stand) and family-by stand interaction terms for height, volume straightness and rust resistance.

Source	df	Height (m) F-value	Volume (dm ³) F-value	Straightness Score F-value	Rust Resistance (% gall-free) F-value
Family	15	2.97*	2.64*	5.00**	4.64**
Stand Type	1	4.76*	5.75*	1.60	2.00
Family * Stand	15	1.89	1.60	1.13	1.67

* > 5%** > 1%*** > .1%

This growth advantage is an early indication of a consistent, positive relationship between growth and <u>intrafamily</u> competition. The phenomenon is previously unreported for forest trees.

Rust infection was as severe in the mixture (50% of the trees were rus resistant) as it was in the single family plots (48%). It is unlikely that stand types would differ in this respect. The fusiform rust fungus require

alternate hosts, pine and oak <u>(Quercus)</u> thus it did not spread from pine to pine once the stand became infected. Increased rust infection is not likely the consequence of a family block plantation system. Also, straightness was not affected by whether the families were grown in bulked plots or single plots (Table 1).

Family by stand type interaction was not significant at the 95% confidence level for all traits (Table 1). The lack of significance suggested a closer look at the relative efficiency of composite versus pure block plots to estimate the family means for growth traits. This was done to determine if the test was adequately designed to detect biologically important rank changes since this was not one of the objectives at the time of test establishment. Each stand type was then analyzed separately.

The single family (square block) plot design was inadequate to estimate family height means precisely and accurately at this early stage of stand development (Table 2).

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Single family plot	Mixed family plot
.0920	.0005
.04	.02
5.6%	3.5%
	Single family plot .0920 .04 5.6%

Table 2.--A comparison of the relative efficiency of the single family (block plot) design and the mixed family (noncontiguous) design for height within the family yield trial, at age four.

The block * family (error) term was higher, the family term was nonsignificant at the > 95% level and the coefficient of variation is higher when compared with the mixed family (noncontiguous) plot design which is highly efficient and requires fewer trees per family and fewer replications (Lambeth et al., in press).

The two plot designs represented the extremes for genetic test designs with multiple tree family plots. When replicated three times as in the yield trial the square block plots tend to encompass high levels of within-plot (environmental) error which is reflected in growth. After crown closure growth becomes more uniform and within-plot error tends to diminish. The coefficient of variation among plots generally drop as site capture progresses. Thus, large block plots do not provide accurate and precise estimates of family means by age four when planted at operational spacing unless a prohibitively large number of replications is used (williams and Lambeth, unpublished data). Quality traits did not show the same trends as growth traits did. Almost neither demonstrated the family * stand interaction term to be statistically important, family differences in straightness and in rust resistance were statistically significant for the separate analyses of both plot designs (Table 3). Bole straightness and rust infection apparently are not as affected by s' heterogeneity unaccounted for by the test design as growth traits are.

Table 3.--Analyses of each plot design for rust resistance and straightness 4-year results of the family yield trial.

	Mixed Family Plot	Single Family Plot
Straightness		
Pr > F Family term	.002	.044
Block * Family Varian (error)	.025	.030
Rust Resistance		
Pr > F Family term	.032	.044
Block * Family Variar (error)	.064	.072

The overall study design was not adequate to assess rank changes from one stand type to another (family * stand interaction) for growth traits. The ability of the two types of plot designs to estimate family means within an allowable margin of error was confounded with any biologically important rank changes.

The differences between plot design were very small for quality traits so the designs were comparable. However, family * stand interaction was not statistically important. Families do not appear to change rank from one stand type to another with respect to straightness and rust resistance.

Realized Genetic Gains

Family ranks correlated well with progeny test ranks (Table 4). The correlations indicated that the rust score had been an effective tool to disc differences among rust-resistant and rust-susceptible genotypes in field tests. It should be noted that the score was effective for loblolly pine progeny tests in North Carolina where rust infection and rust-associated mortality tended to be lower than other parts of the southeastern U.S. The gall/no gall trait may not have been as effective in an area where a large proportion of the trees readily succumbed to the disease. The trait discerned between live trees without rust and trees that survive with rust but does not take in account rust-infected trees that died as a result of the disease (R. J. Weir, N.C. State University, pers. comm.)

Table 4, -- Spearman's rank correlation coefficients between 8-year progeny test assessments and 4-year family performance in the yield trial.

	Progeny Test				
Yield Trial	Rust Resistance	Straightness	Height	Volume	
Rust Resistance	.621**				
Straightness		.604**			
Height <mark>a/</mark>			.737***	.667**	
Volume ^{a/}				.607**	

are based on mixed raming proc performance only.

***.1% significance level **1%

Correlations for growth traits reflect the degree to which family ranks from mixed family plots and progeny tests vary together. Since single family plots did not have significant family differences ranks were misleading.

The correlations are high in spite of the fact that family performance for the yield trial was assessed from a single test site at age four and compared with 8-year progeny test data. This attests to the test quality and rapid growth rate of the yield trial.

One other striking consistency emerged from the single family plots. The commercial check (excluded from all other previously reported analyses) was compared with the performance of the sixteen families. Seedlot differences were statistically significant for the single family plot design when the check was included. The check ranked 17 out of 17 for growth and straightness and 11 out of 17 for rust resistance. The differences between the check and the mean of the improved families is 7.3%, 25.3%, 6.9%, and 9.1% for height, volume, straightness and rust resistance respectively (Table 5).

The maternal parent of each of three families included in this test have since been rogued out of the seed orchard so this suggests improvement over the check for planting stock in current use was conservative. These estimates of gain may not reflect what would happen on a range of site types.

Table 5.--A comparison between the commercial check and stand type means.

	Stand Type Means		Commercial Check
	Mixed	Pure	
Height (m)	3.86 + .15	3.98 + .21	3.71
Volume (dm ³)	17.86 + 2.3	19.34 + 3.1	15.44

SUMMARY AND CONCLUSIONS

Single family plots had a slight overall growth advantage over mixture which indicated a positive relationship between intrafamily competition and growth. However this conclusion is preliminary since competition influences were not strong in this 4-year-old planting. Rust infection was as severe in the family plots as it was in a mixture of the same families. Straightness assessments were also the same in both stand types.

The test was not suited to estimate family * stand interactions so no evidence of rank changes from mixed stands to pure stands could be detected for growth traits. No family * stand interactions were detected for quality traits.

Progeny test ranks (age 8 years) for growth, rust resistance and straightness correlated highly with family performance in the trial. All families showed improvement over the commercial check for growth and straightness.

LITERATURE CITED

- Adams, W. T. J. H. Roberds and B. J. Zobel. 1973. Intergenotypic interactions among families of loblolly pine <u>(Pinus taeda L.)</u>. Theor. Appl. Gen. 43:319-322.
- Adams, W. T. 1980. Intergenotypic competition in forest trees. Proc. 6th N. Amer. For. Bio. Wkshop, Edmonton, Alberta.
- Donald, C. M. and J. Hamblin. 1976. The biological yield and harvest cereals as agronomic and plant breeding criteria. Adv. Agron. 28:361-405.

Hamblin, J. and C. M. Donald. 1974. The relationship between plant form, competitive ability and grain yield in a barley cross. Euphytica (23):535-542.

Hamblin, J. and A. A. Rosielle. 1978. Effect of intergenotypic competition on genetic parameter estimation. Crop Sci. 18(1):51-55.

Hinson, K. and W. D. Hanson. 1962. Competition studies in soybeans. Crop Sci. (2):117-123.

- Jennings, P. R. and R. C. Aquino. 1968. Studies on competition in rice. III. The mechanism of competition among phenotypes. Evol. (22):529-543.
- Jennings, P. R. and J. deJesus. 1968. Studies on competition in rice. I. Competition in mixtures of varieties. Evol. (22):119-124.
- Lambeth, C. C., w. T. Gladstone and R. W. Stonecypher. Statistical efficiency of row and noncontiguous family plots in genetic tests of loblolly pine. Silv. Gen. (in press).
- North Carolina State-Industry Cooperative. 1975. Annual Report.
- SAS Institute. 1979. SAS User's Guide. Statistical Analysis System Institute, Inc. 494 p.
- Sumarno and w. R. Fehr. 1980. Intergenotypic competition between determinate and undeterminate soybean cultivars in blends and alternate rows. Crop Sci. (20):251-254.
- Taner, C. G. 1975. Competition between selected cottonwood genotypes. Silv. Gen. 24:44-49.