AN OCALA SAND PINE PROGENY TEST
COMPARED WITH A SEEDLING SEED ORCHARD

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Abstract.--Sixty-three half-sib families of Ocala sand pine were grown in a seedling seed orchard and a progeny test in Central Florida. At age 7, differences among families were significant for height, dbh, and survival in the seed orchard, for survival in the progeny test, and for dbh and survival in the combined analysis of variance of both locations. In the combined analysis the location X family interaction was only significant for survival. However, inspection of family means of each trait showed that some of the best and worst families changed rank dramatically between tests.

Additional keywords: Half-sib family, genotype X environment interaction, *Pinus clausa*, seedling seed orchard, progeny test.

Geneticists of the Region 8 Tree Improvement Program are assessing the performance of 120 half-sib families of sand pine (Pinus clausa (Chapm.) Vasey) in Central Florida on the Lake George Ranger District north of Silver Springs. In addition to the seed orchard, 106 of these families, plus three check lots, were also planted the same year (1978) in a progeny test on State Highway 19 about 20 miles from the orchard. Both the seedling seed orchard and the progeny test also serve as progeny tests for most of the ortets represented in a clonal seed orchard growing contiguous to the seedling seed orchard.

The purpose of the family assessments is to provide data on which to base thinnings and roguings in the seedling seed orchard. If family performance is uniform on the two sites, then genetic gain can be maximized by roguing a large number of the worst half-sib families from the seedling orchard. However, if there are strong genotype X environment interactions, then family selection must be decreased and heavy thinnings accomplished primarily by means of removal of the worst trees within each family.

METHODS

Both the seedling seed orchard and the progeny test were established in January and February 1978. In the seedling orchard 120 families were planted in 250 blocks as non-contiguous single-tree plots at a spacing of 5 feet. In the progeny test 106 families plus 3 check lots were established in 10-tree row plots in 7 replications in a randomized complete-block design.

The seed orchard has been thinned twice, once in 1981 and once in 1983. Of the 30,000 trees planted, 7,466 remain. Two more planned thinnings will reduce this number to less than 2,000. The progeny test has only been thinned by natural mortality, and survival is currently 45 percent. The progeny test was included in a RARE II Wilderness area soon after establishment, so that no competition control or cultural activity of any kind has been possible.

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Table 1. Degrees of freedom, mean squares and significances of differences for three traits among 63 sand pine half-sib families in a seedling seed orchard, a progeny test, and a combined analysis of variance of both tests.

SOURCE OF VARIATION	DEGREES of FREEDOM	MEAN SQUARES for: PERCENT SURVIVAL	HEIGHT	DBH
		SEEDLING SEED ORCHARD		
Replicate (R)	3	0.146	6.274	1.433
Family (F)	62	0.023 **	1.469 **	0.121 **
RF	186	0.005	0.458	0.030
		PROGENY TEST		
Replicate (R)	3	0.257	8.389	0.170
Family (F)	62	0.088 **	5.513 ns	0.177 ns
RF	186	0.045	6.189	0.186
		COMBINED ANALYSIS OF VARIANCE		
Location (L)	1	4.715 **	8,296.046 **	250.190 **
F	62	0.060 **	3.513 ns	0.169 **
R(L)	6	0.204	7.331	0.796
LF	62	0.051 **	3.469 ns	0.125 ns
RF(L)	372	0.025	3.324	0.108

* Difference is statistically significant at the .05 level.
** Difference is statistically significant at the .01 level.
ns Difference is not statistically significant.

Both the orchard and the test were measured in 1981 at age 3. The orchard was also measured in 1983 at age 5 and in 1984 at age 6. The progeny test was measured a second time in March, 1985 at age 7. Both height and dbh were included in the last measurements at each test, and it is this set of measurements which *we* will investigate.

We performed a combined analysis of variance for survival, height, and dbh from both the orchard and the progeny test. To adapt the seed orchard and the progeny test to compatible field designs, we had to modify the field design of each. A road system divides the seed orchard into three large blocks of roughly equal size. Each family plot in a block is represented by a number of non-contiguous single-tree plots. Hence, for the purpose of data analysis we treated each of these large blocks as a replication. In the progeny test we used data from only the first four of the seven replications. These were, in fact, the most complete replicates anyway.

A subset of 63 families was then chosen because those families contained no missing plots in the four replications at each location. Because the orchard contained no check lots, none were included in the analysis. In summary the combined analysis of variance comprised two locations, each containing four replications and 63 half-sib families.

There are some important differences between the seed orchard and the progeny test. First, the seed orchard is mostly on a longleaf (_Pinus palustris_ Mill.) island, but the progeny test is on a deep sand, a typical sand pine site. In the orchard each family plot is a number of noncontiguous single-tree plots randomly scattered throughout each replication, whereas in the progeny test each family plot is a single 10-tree row plot in each replicate.

The anlyses of variance were performed by means of program P8V of the Biomedical Data Processing Statistical Software system (Jennrich and Sampson 1983). Also, Duncan's multiple range tests were performed by hand.

RESULTS

In table 1 there were significant differences among families in the orchard for survival, height, and dbh. But survival was the only trait showing significant family differences in the progeny test. In the combined analysis of variance, survival and dbh showed significant differences.

The analyses considered here were based on measurements taken at ages 6 and 7 on the seed orchard and progeny test respectively. However, height at age 3 in the progeny test, with essentially the same subset of families considered, showed significant differences among families. The family rankin for height at age 6 differ little from those at age 3. Lack of competition control probably has allowed environmental noise (replicate X family interactions and variation among trees within plots) to mask family height growth differences. In table 1 only survival shows significant location X family interactions. However, we believe that an examination of the data will show some strong location X family interactions for height and diameter as well.

Table 2. Rank comparisons of the best and worst sand pine half-sib families for three traits in a seedling seed orchard and a progeny test.

FAMILY I.D.	SEEDLING SEED ORCHARD			PROGENY TEST		
			SURVIVAL			
	Percent	Rank	p = .05	Percent	Rank	p = .05
8	25.7	22	de-ij a/	77.5	1	a
7	43.5	1	a	32.5	47	de-gh
101	41.5	3	a	75.0	2	ab
116	11.5	63	1	15.0	63	h
			HEIGHT			
	Feet	Rank	p = .05	Feet	Rank	p = .05
12	20.7	2	ab	14.0	1	a
67	20.8	1	a	11.4	33	abc
97	17.6	63	f	11.9	21	abc
118	19.7	18	ab-ef	8.9	63	c
120	18.5	58	ef	8.9	63	c
			D B H			
	Inches	Rank	p = .05	Inches	Rank	p = .05
67	3.4	1	a	1.6	14	ab
39	2.9	25	bcde	2.0	1	a
40	3.0	9	bcd	2.0	1	a
97	2.5	63	f	1.6	14	ab
118	3.0	9	bcd	1.1	63	b
11	2.7	59	def	1.1	63	b

a/ Means not followed by the same letter are significantly different at the .05 level

In table 2 we have listed some of the rank changes of certain families for best and worst performance in all three traits. Some families maintain their rank as best or worst very well in both the orchard and the progeny test. Two examples are: (1) family 12 ranked 2 and 1 for height in the seed ochard and progeny test respectively; (2) family 120 ranked 58 and 63 for height in the orchard and the progeny test respectively. However, other families made dramatic shifts. Two examples are: (1) family 97 ranked 63 for height in the seed orchard but 21 for height in the progeny test; (2) family 118 ranked 9 for dbh in the orchard, but 63 for dbh in the progeny test.

Family 97 typifies a short term roguing problem. If the seed orchard were our only source of information, we would rogue this family. But in the progeny test on a site representative of the kind of site on which it will probably be planted, it grows well. Family 118 represents a long term problem. Without the progeny test we would select its best trees for further breeding, based on its rank of 9 in the seed orchard, but its rank of 63 in the progeny test should persuade us to exclude it from most sites on which we are likely to be planting sand pine.

CONCLUSIONS

The results in the combined analysis seem to bear a warning. Since the progeny test site is representative of the sites on which we intend to re-establish sand pine, we should probably pay heed to the progeny test results in our selection and roguing of families. If we should plan to put any operational plantings on longleaf islands, then we have some families, which seem to be better adapted to those sites also. Other families may be planted on either site without risk.

LITERATURE CITED

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