PARENTAL SELECTION VERSUS HALF-SIB FAMILY SELECTION OF LONGLEAF PINE

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Longleaf pine (*Pinus palustris* Mill.) differs from other southern pines in that it grows very slowly in height during the first few years. The speed with which longleaf seedlings come out of this grass stage will be important to any program for genetic improvement of the species. This study reports variation in open-pollinated progeny relative to parental ratings established by use of comparison trees. It indicates that both progeny-test selection and phenotypic selection for early height growth will be effective.

METHODS

In 1955, wind-pollinated seeds were collected from 100 randomly selected trees in Harrison and two adjacent counties in southern Mississippi. These trees and three comparison trees near each were measured. Comparison trees were on the same sites and were approximately equal to the parent trees in age, as determined from increment cores, and in diameter. Heights were measured to the nearest foot and diameters to the nearest 0.1 inch. Seeds were weighed.

In 1956, 21 seeds from each tree were sown in each of six nursery replications which were arranged in a 10 × 10 triple lattice design. In the spring of 1957, the seedlings were lifted and their average green weights determined.

Immediately prior to planting, a previously cleared 8.5-acre area was burned. The seedlings were planted on it at a 6- by 12-foot spacing. For outplanting, the number of seedlings per plot was reduced to eight. The plantation was periodically mowed and brown-spot infection was effectively controlled by spraying. The trees were measured after 5 years, when most of the seedlings were coming out of the grass stage. They were measured again after 8 years in the field,when they had assumed a more even growth pattern.

Since few or no trees survived in some of the plots, missing plots presented an analytical problem. This was solved by a computer program applicable to lattice designs which yields unbiased means and sums of squares for randomized complete blocks (Goulden 1952; Homeyer et al. 1947). Adjusted means, adjusted family mean squares, and average effective mean squares for error provided by the lattice design were used in the computations. Within-plot variances were derived from a 10 percent random sample of the plots. Tests of significance are at the 0.05 level.

RESULTS AND DISCUSSION

Seed and seedling weight.--It was assumed that large seeds would produce large nursery plants, which, when outplanted, would rapidly come out of the grass. Initial analyses disclosed that there were significant differences in green weight per lifted seedling ranging from 16 to 28 grams. Furthermore, the green weight depended in a positive and significant manner on seed weight, which varied from 66 to 132 g./1,000. The regression was:

$$\text{green weight} \qquad 14.49 + 0.084\ (\text{seed weight}).$$

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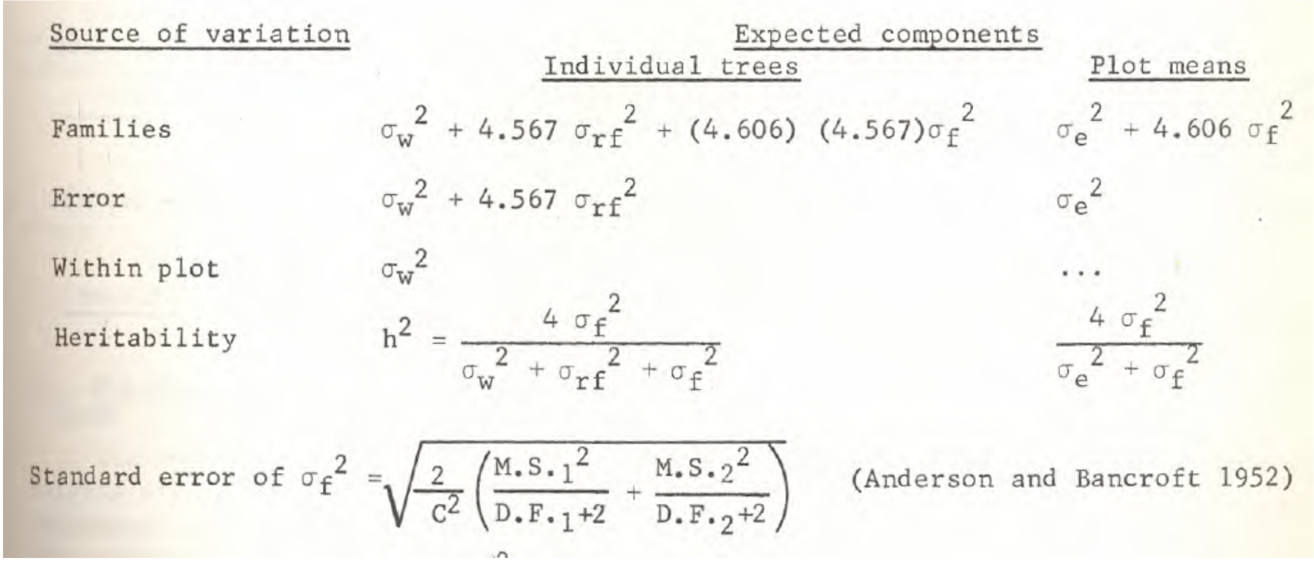
The regression coefficient is statistically significant; the standard error is 0.012 and R^2 is 0.26. The data indicate that green weights of nursery seedlings may be increased an average of 25 percent over the smallest seeded families by selecting the largest seeded families.

After 8 years in the field, however, neither seed weights nor seedling weights at planting time were related to height. Perhaps the nursery advantages were, in part, lost in transplanting.

Sib analyses and heritabilities.--Analyses of variance showed that family differences in survival and height growth were statistically significant. Mean field survival at 5 years was only 59 percent. Survival of the best 75 families ranged from 48 to 83 percent and did not differ significantly according to Duncan's range test. The lowest family survival was 22 percent. The mean 8-year heights of the best 20 families varied from 7.1 to 10.2 feet; differences among these families were not statistically significant. Heights of the three best families, however, averaged 10.2 feet at 8 years, compared to 5.8 feet for the population mean and 0.7 foot for the poorest entry.

Components of variance and heritabilities based on individuals and plot means were estimated from mean square components:



Source of variation	Expected components	
	Individual trees	Plot means
Families	$\sigma_w^2 + 4.567\,\sigma_{rf}^2 + (4.606)\,(4.567)\sigma_f^2$	$\sigma_e^2 + 4.606\,\sigma_f^2$
Error	$\sigma_w^2 + 4.567\,\sigma_{rf}^2$	σ_e^2
Within plot	σ_w^2	...
Heritability	$h^2 = \dfrac{4\,\sigma_f^2}{\sigma_w^2 + \sigma_{rf}^2 + \sigma_f^2}$	$\dfrac{4\,\sigma_f^2}{\sigma_e^2 + \sigma_f^2}$

$$\text{Standard error of } \sigma_f^2 = \sqrt{\frac{2}{C^2}\left(\frac{\text{M.S.}_1{}^2}{\text{D.F.}_1+2} + \frac{\text{M.S.}_2{}^2}{\text{D.F.}_2+2}\right)}$$

(Anderson and Bancroft 1952)

C is the coefficient of the σ_f^2 component, and M.S. and D.F. are the mean squares involved in calculating the component along with their degrees of freedom. In calculating mean square components of heights for individual trees, the plot mean squares were first multiplied by 4.567, the harmonic mean number of plants per plot. The coefficient 4.606 is an approximation, calculated by Federer's (1951) method, to account for missing plots. Heritability estimates are shown in table 1.

Parent-progeny analyses and heritabilities.--Adjustments for age and site were applied to both parental diameters and heights prior to correlation with progeny height (table 2). Adjustments for age were made by dividing diameter and height by the age of the tree and expressing the results as mean annual diameter or mean annual height growth. Adjustments for environment were made

Table 1.--Sib analyses components of variance and heritabilities for 5-year survival and height and for 8-year height

Character	Components				Reliability ratio 1/	Individual heritability	Plot heritability
	σ_w^2	σ_{rf}^2	σ_f^2	σ_e^2			
5-year survival	...	...	18.40	189.73	0.33	...	0.35
5-year height	1.880	0.218	.065	...	.45	0.12	.40
8-year height	12.47	2.02	2.22	...	.17	.53	1.27

1/ In the absence of a satisfactory formula for the standard error of the heritability, the ratio $\frac{S.E.\ (\sigma_f^2)}{\sigma_f^2}$ is used. If this ratio is greater than 0.50, reliability of the heritability value is low.

Table 2.--Correlations of progeny heights with parental diameters and heights before and after environment and age adjustments

Adjustments	Parental diameters	Parental heights
None	-0.28 (significant)	-0.04
Age	+ .02	+ .24 (significant)
Environment (via comparison trees)	- .06	+ .12
Age and environment	- .02	+ .17 (significant)

by subtracting the mean for trees on a particular site from the mean of the selected tree. The difference was entered in correlation computations. When both adjustments were applied, the age adjustments were applied first.

The highest positive parent-progeny correlation was r = 0.24 for parental annual height growth and mean family height (table 2). This indicates that the age adjustment alone was best. It is thus advisable to convert parental total height to annual height growth when calculating parent-progeny regressions. Using the r value of 0.24 in the formula

$$h^2 = 2b\,\frac{\sigma_x}{\sigma_y} = 2r$$

the heritability is 0.48 ± 0.21. The standard error was calculated from

$$S.E._{h^2} = \frac{2\,\sigma_x}{\sigma_y}\sqrt{\frac{1}{N-2}\left(\frac{\sigma_y^2}{\sigma_x^2} - b^2\right)}$$

where N is number of pairs (adapted from Falconer 1960).

While mean annual height growth of parent is useful in selection, other measures such as the periodic annual height growth (Squillace et al. 1967) should be tested in the future.

The failure of comparison trees to increase parent-progeny correlations was disappointing (table 2). Perhaps peculiarities of site and the relative lack of competition among these open-grown longleaf pines made the technique ineffective. The failure suggests a need for reassessment of the use of comparison trees in selection.

Likewise, the negative correlation between diameter of parents and height of progeny was surprising. Parental diameter was not a helpful guide in selection. Since the traits in the parent generation were measured on mature trees, while in the progeny generation they were measured on young trees, an increase in these correlations can be expected in time. Therefore, the heritability of some characters estimated from parent-progeny correlations can be expected to increase as the progeny grow older. Whether this increase will be economically significant is not known.

Selection and gain.--When the best 25 percent of the parents were selected on the basis of annual height increment, percentage gain in progeny height was estimated by:

$$\frac{ish^2}{2\bar{x}} \times 100$$

where $i = 1.27$ (selection intensity)
$s = .3422$ (phenotypic standard deviation of parents)
$h^2 = .48$ (based on parent-progeny regression)
$\bar{x} = 1.84$ ft./yr. (parental mean)

This computed gain was 6 percent.

Realized gain was 12 percent. It is diagrammed in figure 1, where progeny heights are arrayed within parent tree height/age quartile classes. The mean heights of the progeny from parental quartile classes have the ratio 100:94:81:84. The corresponding ratio of the parents was 100:85:74:62. These results contrast with those of Rohmeder (1961) who stated (translation) that, "The fact that the expected ratio has not been found in any of the cases with various growth conditions and at various ages of progenies has meant disappointment for the plant breeders." He concluded that parental selection had little value, but in our investigation progenies from phenotypically selected parents were on the average 12 percent taller than the population average.

Considerable additional gain appeared to be possible from progeny-test selection. Selection of the 25 percent of the families with best mean plot heights results in 35 percent gain--an increase of 23 percent over parental selection. Because plot heritability was near 1.0 at 8 years (table 1), it is reasonable to expect that much of this gain would be genetic. Thus, it appears that at this intensity of selection, progeny testing was almost three times as effective as individual-tree selection for height growth in longleaf pine.

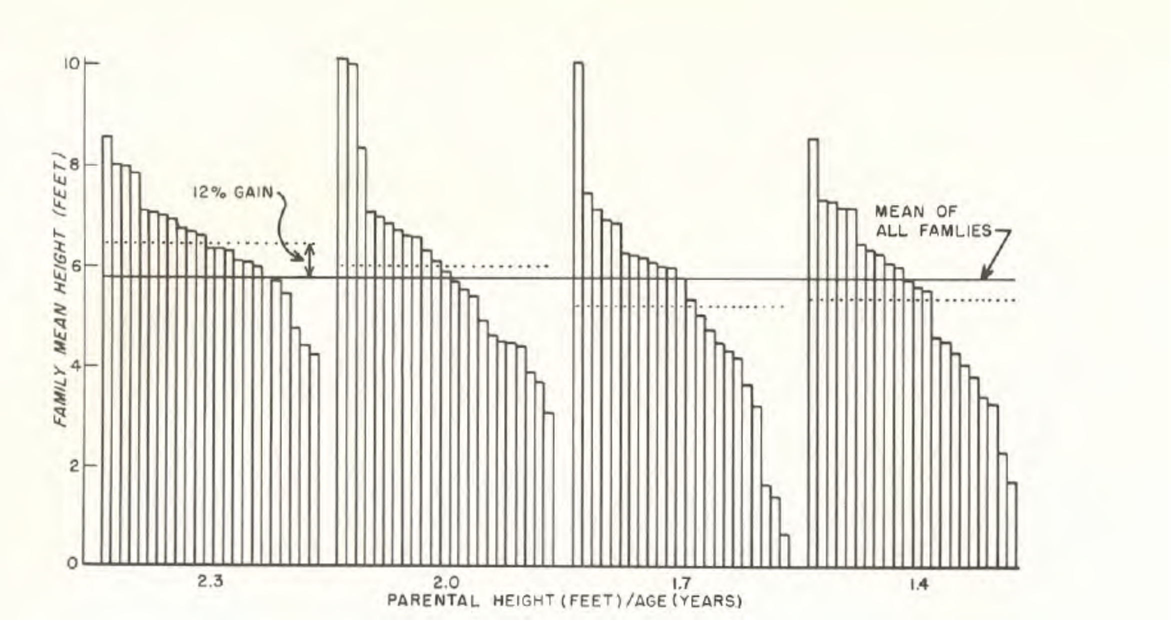


Figure 1.--Mean 8-year heights of families, by height/age quartile class of parent. Dotted line is mean of group. Each bar represents an average of 28 trees.

Another gain from progeny-test selection could be even more important. If the three best families are true genetic deviates, as seems likely from observation, their parents would be prime candidates in starting a new breeding program or seed orchard. Without progeny testing, the three most exceptional parents would have been lost to future breeding, because they were phenotypically unimpressive. Only about 30 percent of the parent trees could have been omitted from the progeny test with reasonable assurance of not missing these three parents.

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