SWEETGUM VARIATION CHANGES WITH TIME

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Abstract.--An 11-year-old progeny test of open-pollinated sweetgum (Liquidambar styraciflua L.) at two sites in Mississippi indicates that conclusions drawn from early results (ages 2 and 6) may not apply at later ages. Genotype-environment interactions became less important between ages 6 and 11. The choice of test sites greatly affects the usefulness of results.

Additional keywords: Forest tree improvement breeding, genotype-environment interactions, selection, planting site.

Commercial growers are starting to plant sweetgum (Liquidambar styraciflua L.), causing increased interest in genetic improvement. Most reports on genetic research on sweetgum have concerned juvenile growth characters (Wilcox 1970, Mohn and Schmitt 1973, Sprague and Weir 1973), juvenile cell and wood characters (Randel and Winstead 1976, Winstead 1972, Webb 1964) or phenological characters (Williams and McMillan 1971). Little has been reported on trees older than age 6.

This paper reports results through age 11 from an open-pollinated progeny test grown on two diverse sites in Mississippi. Two previous papers discussed results from this experiment (Wilcox 1970, Mohn and Schmitt 1973). However, over time, changes in genotype-environment interaction have provided new information of importance to tree breeders.

MATERIALS AND METHODS

Forty sweetgum trees were chosen from throughout southern Mississippi to represent a range of phenotypes and sites. Open-pollinated seeds were collected and grown in a non-replicated nursery in 1962. The seedlings were outplanted at each of two locations in February 1963, using 4-tree linear plots, 12 foot equidistant spacing, and a 5-replication randomized complete block design. One site was on the Harrison Experimental Forest (HEF) near Gulfport, Mississippi (30°35'N latitude, 89°05'W longitude). The other site was on the Delta Experimental Forest (DEF) near Greenville, Mississippi (33°25'N latitude, 90°95'W longitude), 200 miles north of Gulfport. The soil at the HEF site is a well drained, strongly acid, Orangeburg fine sandy loam with low natural fertility. The soil at the DEF site is a poorly drained, slightly acid, Sharkey clay soil with high clay content and high fertility.

Height was measured to the nearest 0.1 ft. at ages 2, 6, and 11. At ages 6 and 11 dbh was measured to the nearest 0.1 in. Plot means were computed and examined by analysis of variance (Table 1). Estimates of components of variance were computed from mean squares. Within-plot variances were computed from individual tree data on all plots.

Table 1.--Form of analysis of variance

Source of Variation	df	Expected Mean Squares
Within location		
Replication	r-1	
Family	f-1	$\frac{\sigma_w^2}{n} + \sigma_{rf}^2 + r(\sigma_{fp}^2 + \sigma_f^2)$
Replication x Family	(r-1)(f-1)	$\frac{\sigma_w^2}{n} + \sigma_{rf}^2$
. . . .		. . . .
Within Plot	rf(n-1)	$\frac{\sigma_w^2}{n}$
Over location		
Planting location	p-1	
Replication/Location	p(r-1)	
Family	f-1	$\frac{\sigma_w^2}{n} + \sigma_{rf(p)}^2 + r\sigma_{fp}^2 + rp\sigma_f^2$
Family x Location	(f-1)(p-1)	$\frac{\sigma_w^2}{n} + \sigma_{rf(p)}^2 + r\sigma_{fp}^2$
Rep x Family/Location	(r-1)(f-1)p	$\frac{\sigma_w^2}{n} + \sigma_{rf(p)}^2$
. . . .		. . . .
Within Plot	rfp(n-1)	$\frac{\sigma_w^2}{n}$

Where n = harmonic mean of number of trees per plot.

Families and sites were considered to be random. Parent trees were not chosen strictly at random and sites were purposely chosen to represent contrasting environments in order to magnify genotype-environment interaction, producing conservative estimates of genetic gain.

Narrow-sense individual-tree heritabilities (h^2) were estimated as follows:

$$h^2 = \frac{4\sigma_f^2}{\sigma_w^2 + \sigma_{rf}^2 + \sigma_{fp}^2 + \sigma_f^2}$$

where components of variance are: σ_f^2 = family component

σ_{rf}^2 = replication by family interaction

σ_{fp}^2 = family by planting location interaction

σ_w^2 = within plot

Standard errors for estimates of the family component of variance were obtained using procedures modified from Comstock and Robinson (1951) and then used to compute standard errors for estimates of heritability as follows:

$$SEh^2 = \frac{4SE\sigma_f^2}{\sigma_w^2 + \sigma_{rf}^2 + \sigma_{fp}^2 + \sigma_f^2} \quad \text{(Becker 1967)}$$

Expected genetic gains (EGG) were computed for a hypothetical controlled crossing scheme involving the best tree from each of the eight best families. Procedures were modified from Namkoong et al. (1966). Standardized selection differentials (i) from Becker (1967) were used with pooled components of variance to estimate the expected genetic gains as follows:

Within location:

$$EGG_F = i_F \left[\frac{(\sigma_{fp}^2 + \sigma_f^2)}{\left(\frac{\sigma_w^2}{rn} + \frac{\sigma_{rf}^2}{r} + (\sigma_{fp}^2 + \sigma_f^2) \right)^{\frac{1}{2}}} \right]$$

$$EGG_{I/F} = i_{I/F} \left[\frac{3(\sigma_{fp}^2 + \sigma_f^2)}{(\sigma_w^2 + \sigma_{rf}^2)^{\frac{1}{2}}} \right]$$

Over Location:

$$EGG_F = i_F \left[\frac{\sigma_f^2}{\left(\frac{\sigma_w^2}{rnp} + \frac{\sigma_{rf}^2}{rp} + \frac{\sigma_{fp}^2}{p} + \sigma_f^2 \right)^{\frac{1}{2}}} \right]$$

$$EGG_{I/F} = i_{I/F} \left[\frac{3\sigma_f^2}{(\sigma_w^2 + \sigma_{rf}^2 + \sigma_{fp}^2)^{\frac{1}{2}}} \right]$$

Total Gain = $EGG_F + EGG_{I/F}$

Location means and combined means for height over years were subjected to polynomial regression using the methods outlined by Graybill (1961).

RESULTS AND DISCUSSION

Height means at age 11 (Table 2) seem to indicate that the locations have similar production potentials, with the HEF location (K = 25.9 ft.) having a slight advantage over the DEF location (Tc = 22.8 ft.). However, closer examination of growth trends shows that height growth was initially rapid at HEF and slowed down with time; the reverse was true at DEF (Fig. 1). Mean dbh at age 11 was 3.52 in. at HEF and 3.29 in. at DEF. Although early dbh data were not available, growth trends from ages 6 to 11 were the same for dbh as for height. During the same period, diameter growth at HEF averaged only 0.27 in. per year while DEF averaged 0.38 in. per year. Only part of this difference can be accounted for by the amount of growing space, since survival was 81 percent at DEF and 97 percent at HEF. If present growth trends continue, the trees at DEF will eventually be larger than those at HEF.

Table 2.--Means and expected genetic gains (as a percent of the mean) for sweetgum planted at the Harrison. Experimental Forest (HEF) the Delta Experimental Forest (DEF) and combined locations.

| Character Location | Mean | Family | Method of Selection[1] | | Combined |
			Individual Within Family	
			% Expected Genetic Gain	
2 Year Height (ft.)				
HEF	7.24	5.9	10.0	15.9
DEF	3.15	6.9	11.6	18.5
Over Locations	5.19	5.3	8.4	13.7
6 Year Height (ft.)				
HEF	17.45	5.7	8.5	14.2
DEF	11.53	2.7	4.0	4.7
Over Locations	14.49	1.2	1.4	2.6
11 Year Height (ft.)				
HEF	25.93	5.7	8.7	14.4
DEF	22.76	2.2	3.4	5.6
Over Locations	24.34	2.0	2.5	4.5
6 Year Dbh (in.)				
HEF	2.16	7.1	11.1	18.2
DEF	1.39	5.4	8.3	13.7
Over Locations	1.78	4.5	6.1	10.5
11 Year Dbh (in.)				
HEF	3.52	7.2	10.9	18.1
DEF	3.29	2.6	3.6	6.2
Over Locations	3.41	3.7	4.9	8.6

[1] Selection of the best tree from each of the best eight out of forty families.
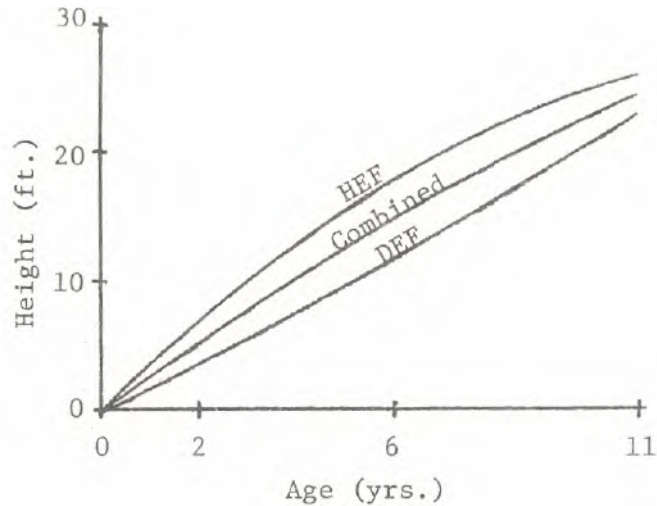
Figure 1.--The relationship of sweetgum height to age for
the Harrison Experimental Forest (HEF), the Delta
Experimental Forest (DEF), and combined locations

Differences in growth trends at the two sites were presumably due to soil characteristics. The well drained, acid, low fertility, fine sandy loam at HEF contrasts with the poorly drained, more nearly neutral, high fertility Sharkey clay at DEF. Despite these differences, both sites have similar problems which severely limit sweetgum growth. Good early growth at HEF probably occurred because the roots could penetrate the soil quickly. Later, as nutrient and moisture levels became limiting at HEF, growth rate decreased. Poor early growth at DEF was probably caused by the difficulty roots encountered in penetrating the soil, and the unavailability of moisture during the latter part of the growing season. As the roots finally penetrated the dense Sharkey clay at DEF, and were able to extract moisture from greater depths, growth rate surpassed that at HEF.

At age 2, the genotype-environment component of variance for height was less than half that of the genetic component of variance, but by age 6 it was five times as large. This trend reversed and by age 11 the genotype-environment component of variance for height dropped to less than twice the size of the genetic component of variance (Table 3). It remains to be seen whether genotype-environment interaction will continue to become less important or whether it will increase if the mean performance at DEF surpasses that at HEF.

Heritabilities were higher at HEF than at DEF (Table 3). They decreased through age 6 at both locations and then leveled off with the exception of dbh at the DEF location which dropped from 0.24 at age 6 to 0.16 at age 11. This decrease in heritability may have been a result of lower survival, giving extra growing space to many of the DEF trees and causing an increased non-genetic component in the denominator of the heritability formula. Heritabilities were rather low for data combined over locations because of high genotype-environment interactions.

Predicted gains based upon selection of the best eight of forty families were much lower at DEF than at HEF (Table 2) and were very low for data combined over locations. Predicted height gains for family selection over location were

5.3, 1.2, and 2.0 percent for ages 2, 6, and 11 respectively. Predicted gains for family selection for dbh at ages 6 and 11 were 4.5 and 3.7 percent. When gains for selecting the best individual within family were also considered, opportunities for gain were greatly increased. Predicted gains for combined selection for age 11 ht. were 14.4 percent at REF and 5.6 at DEF. For age 11 dbh, predicted gains for combined selection were 18.1 percent at REF and 6.2 percent at DEF.

Table 3.--Components of variance, heritabilities, and standard errors of heritabilites for the Harrison Experimental Forest (HEF), the Delta Experimental Forest (DEF) and combined locations.

| Character | Variance Component | | | | h^2 | SEh^2 |
Location	σ^2_w	σ^2_{rf}	σ^2_f	σ^2_{fp}		
2 Year Ht						
HEF	1.3398	.1446	.1577	-----	.384	±.067
DEF	.4128	.1440	.0519	-----	.341	±.162
Combined	.9241	.1182	.0718	.0330	.250	±.106
6 Year Ht						
HEF	12.5231	.7666	.9694	-----	.272	±.112
DEF	2.3160	.7917	.1543	-----	.189	±.134
Combined	8.0320	.4780	.0994	.4610	.044	±.077
11 Year Ht						
HEF	26.9782	3.4861	2.2413	-----	.274	±.121
DEF	5.0453	2.3834	.3975	-----	.203	±.145
Combined	17.4618	2.1742	.4411	.8742	.084	±.021
6 Year Dbh						
HEF	.2991	.0543	.0256	-----	.271	±.125
DEF	.0919	.0271	.0076	-----	.240	±.139
Combined	.2070	.0349	.0086	.0080	.133	±.088
11 Year Dbh						
HEF	.8111	.0773	.0646	-----	.271	±.116
DEF	.2419	.0581	.0124	-----	.159	±.121
Combined	.5641	.0476	.0208	.0176	.128	±.081

Sweetgum does well on a wide range of sites, but this does not mean that a particular family or genotype will do well on an equally wide range of sites. Breeders need to know the amount of genotype-environment interaction present in their breeding populations. But the importance of genotype-environment inter- action may change over time and may be influenced by the choice of sites. Genotype-environment interactions in this study were sufficiently high to suggest that much more progress can be made by breeding for a narrow range of environ- ments than for a wide range of environments.

LITERATURE CITED

Becker, W.A. 1967. Manual of procedures in quantitative genetics. 2nd ed.
    Pullman: Wash. State Univ. Press. 130 p.

Comstock, R.E. and Robinson, H.F. 1951. Consistency of estimates of variance
    components. Biometrics 7: 75-82.

Graybill, F.A. 1961. An introduction to linear statistical models. Vol. 1.
    N.Y.: McGraw-Hill Book Co., Inc.

Mohn, Carl A. and Schmitt, Dan. 1973. Early development of open-pollinated
    sweetgum progenies. 12th South. For. Tree Improv. Conf. Proc. p. 228-232.

Namkoong, G., Snyder, E.B. and Stonecypher, R.W. 1966. Heritability and gain
    concepts for evaluating breeding systems such as seedling orchards.
    Silvae Genet. 15: 76-84.

Randel, William R. and Winstead, Joe E. 1976. Environmental influence on cell
    and wood characters of _Liquidambar styraciflua_ L. Bot. Gaz. 137: 45-51.

Sprague, Jerry and Weir, R.J. 1973. Geographic variation of sweetgum. 12th
    South. For. Tree Improv. Conf. Proc. p. 169-180.

Webb, C.D. 1964. Natural variation in specific gravity, fiber length, and
    interlocked grain of sweetgum (_Liquidambar styraciflua_ L.) in the South
    Atlantic states. Ph.D. Thesis. Raleigh: N.C. State Univ. Sch. of For.
    138 p.

Wilcox, J.R. 1970. Inherent variation in south Mississippi sweetgum.
    Silvae Genet. 19: 91-94.

Williams, G.J. III and McMillan, C. 1971. Phenology of six United States
    provenances of _Liquidambar styraciflua_ under controlled conditions.
    Am. J. Bot. 58: 24-31.

Winstead, J.E. 1972. Fiber tracheid length and wood specific gravity of
    seedlings as ecotypic characters in _Liquidambar styraciflua_ L. Ecology
    53: 165-172.