Early Selection is effective in 20-year-old Genetic Tests of Loblolly pine

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Summary

Five tests with open-pollinated loblolly pine families measured at ages 5, 10, 15 and 20 years were used to examine age trends in family and phenotypic variances, juvenile mature correlations and response to early selection.

Family and phenotypic variances increased with age in all tests for both height and volume per tree. The ratio of family variance over phenotypic variance was equivocal. In one test the ratio increased and in another it decreased with age while the other three tests showed no clear pattern.

Juvenile-mature correlations were generally very high even for measurements between ages 5 and 20 years. Genetic correlations were larger than correlations based on family means which were larger than within plot correlations.

Families and individuals were selected at young ages and tracked to age 20. Families selected at age five were only nominally lower in volume at age 20 years than selections at age 20. However, individuals selected at age five years were not nearly as large at age 20 as those selected at age 10. Individuals selected at age 10 were nearly as large at age 20 as individuals selected at age 20.

Key words: Early Selection, Juvenile-Mature Correlation, Correlated Response, *Pinus taeda.*

Zusammenfassung

Es wurden fünf Versuche mit frei abgeblühten *Pinus taeda* Familien im Alter von 5, 10, 15 und 20 Jahren gemessen, um Alterstrends bei familiären und phänotypischen Varianzen, Jugend-Alters-Korrelation und die Reaktion auf frühzeitige Selektion zu untersuchen.

In allen Experimenten nahmen mit zunehmendem Alter die Familienvarianzen und die phänotypischen Varianzen sowohl für die Einzelbaumhöhe als auch für das Volumen pro Baum zu. Das Verhältnis der Familienvarianz zur phänotypischen Varianz war nicht zu bestimmen. In einem Versuch nahm das Verhältnis zu, und in einem anderen nahm es mit zunehmendem Alter ab, während die drei übrigen Experimente kein klares Muster aufwiesen.

Jugend-Alters-Korrelationen waren gewöhnlich sehr hoch, selbst für Messungen zwischen dem Alter 5 und 20. Genetische Korrelationen waren größer als Korrelationen, die auf Familien-Mittelwerten basierten, welche wiederum größer waren als die Korrelationen zwischen Parzellen.

Familien und Einzelbäume wurden in früherem Alter selektiert und deren Wachstum bis zum Alter 20 verfolgt. Die im Alter von 5 Jahren selektierten Familien hatten im Alter 20 ein nur unbedeutend kleineres Volumen als diejenigen, die im Alter 20 selektiert worden waren. Im Gegensatz dazu waren jedoch im Alter von fünf Jahren selektierte Einzelbäume im Alter von 20 Jahren lange nicht so groß wie solche, die im Alter von 10 Jahren selektiert worden waren. Einzelbäume, die im Alter von 10 Jahren selektiert worden waren, waren im Alter von 20 Jahren fast genauso groß wie im Alter von 20 Jahren selektierte Einzelbäume.

Introduction

Selection in genetic tests is usually conducted before economic rotation age in the interest of speeding the breeding-testing-selection cycle turnover. The assumption is made that early performance is indicative of later performance of the selected tree or family.

Some have suggested that early performance of genotypes is not strongly related to later performance; therefore, early selection is ineffective. Cannell (1978) hypothesized that genotypes which perform well in an open grown situation, i.e., before crown closure, may not be well suited for competitive growth conditions. In that case, the genetic correlation between early performance and later performance may be zero or negative if the genotype suited to open grown conditions is unable to cope in the competitive environment. Franklin (1979) also suggested that heritability of growth-traits may be high and then decrease, possibly to zero, at about the time of crown closure and then increase as the stand reaches maturity. Such a model would agree well with Cannell's proposal if tree growth in noncompetitive and competitive environments are controlled by different genes.

Others (Lambeth 1980, Nanson 1967, Squillace and Gansel 1974) have suggested that the most efficient age for selection is between 5—10 years for some conifers. Efficiency in these studies was determined as the selection age which results in the greatest genetic gain per unit of time in continuous cycling of breeding, testing, and selection. Results have been inconclusive because of the scarcity of older genetic tests in which to track the performance of individuals or families over a period of time. Such tests are necessary to examine genetic correlations, heritability and genetic versus environmental variances over time.

This study utilized data from 20-year-old Texas Forest Service loblolly pine *(Pinus taeda)* progeny tests. These are some of the oldest progeny tests for loblolly pine available anywhere. These tests have been used to determine the effectiveness of early selection by examining genetic versus phenotypic variances, juvenile-mature correlations, heritability as a function of age, and to track early selections to determine how they perform at later ages.

Materials and Methods

Field Testing:

The five genetic tests, used in this report, were planted between 1952 and 1959 *(Table 1).* All were planted in a randomized complete block design with open-pollinated families located at random within each replication. Families were usually represented by a 26-tree row plot in each replication. One test (6) had 100-tree square plots.

In one test (6) the open-pollinated families were obtained by collecting seeds from a phenotypically superior tree in

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Table 1. — Description of the five open- pollinated, loblolly pine genetic tests grown in east Texas by the Texas Forest Service.

Test Number	Number of Reps	Number of Families	Mother-Tree Type	Plot Type-Size	Ages Thinned	Means: Height (m) Age 5	Means: Height (m) Age 20	Means: Age 5 Survival
5	2	36	SPA	Row - 26	10, 19	4.7	17.6	93%
6	2	19	Selected for Growth and Form	Block - 100	13	4.2	17.6	87%
12	3	17	Selected for Specific Gravity	Row - 26	10, 16	4.0	16.4	91%
13	2	15	Selected for Specific Gravity	Row - 26	13	4.7	17.7	93%
15	3	48	SPA[1]	Row - 26	13	4.3	17.6	80%

[1]) Seed Production Area.

each of 19 natural stands. In two tests (12 and 13) the open-pollinated seeds were obtained from trees selected for extremes of wood specific gravity. The remaining two tests (5 and 15) consisted of open-pollinated families from a seed production area and are, therefore, likely to be related families since natural stands of loblolly pine are often seeded by a few mother trees.

All tests were measured for height and diameter at ages 5, 10, 15 and 20 years. Heights at older ages were measured with a Haga altimeter. A conic volume equation was used to calculate volume per tree. Silvicultural thinnings were conducted between age 10 and 15 in all tests. A second thinning was made between age 15 and 20 in tests and about 40 percent of the living trees were removed at each thinning and families were thinned to an equal basal area per plot in each test.

Analyses:

Each of the tests received the same analyses. There were no analyses across tests due to lack of family balance. Analyses of variance and covariance among traits provided tests of statistical significance. Variance and covariance components were obtained from the expected mean squares for a Randomized Complete Block design assuming all effects were random. Individual tree heights and volume were analyzed at each measurement age and in those years when thinning took place the analysis was based on the population before thinning.

Juvenile-mature correlations were calculated as follows:

$$\text{genetic correlation} = r_{G_{J,M}} = \frac{\text{Cov}\ (J,\ M)}{\sqrt{\sigma_J^2}\ \sqrt{\sigma_M^2}}$$

$$\text{family mean correlation} = r_{F_{J,M}} = \frac{MCP_{F_{J,M}}}{\sqrt{MS_{F_J}}\ \sqrt{MS_{F_M}}}$$

$$\text{within plot correlation} = r_{W_{J,M}} = \frac{MCP_{W_{J,M}}}{\sqrt{MS_{W_{J,M}}}\ \sqrt{MS_{W_{J,M}}}}$$

phenotypic correlation = $r_{P_{J,M}}$ = correlation based on individual trees across reps

Where:

J,M = subscripts for the youngest age (J) and the oldest age (M) in the correlation

σ_J^2, σ_M^2 = family variance components from separate analyses of variance for the juvenile and mature traits

Cov (J, M) = family covariance component for the juvenile and mature traits

MS, MCP = Mean squares and mean cross products from the analyses of variance and covariance

F, W = Subscripts denoting effects in the analyses of variance and covariance (family and within plot)

Juvenile-mature correlations are notworthy because the juvenile trait, measured at different ages, is part of the mature trait. For example, if height is measured at ages 10 and 20 years then height at age 20, is equal to age 10 height plus the increment of growth (I) between 10 and 20 years. The correlation between (J) and (M) can be broken into two contributing sources — the variance of (J) and the covariance between (J) and (I) as follows:

$$r_{J,M} = \frac{\text{cov}(J,M)}{\sigma_J\ \sigma_M} = \frac{\text{cov}(J,\ J+I)}{\sigma_J\ \sigma_M} = \frac{\sigma_J^2}{\sigma_J\sigma_M} + \frac{\text{Cov}\ (J,\ I)}{\sigma_J\sigma_M}$$

Thus, it is conceivable that a juvenile-mature correlation can exist purely because of the variance in the juvenile trait even when height at age 10 is uncorrelated with later growth. To avoid that phenomenon, we also calculated the correlation between juvenile (J) and subsequent performance (I) to maturity:

$$r_{J,I} = \frac{\text{Cov}\ (J,\ I)}{\sigma_J\sigma_I}.$$

The top one-third of the families were selected at each measurement age (referred to as the "selection trait"). The performance of these families was tracked to later measurement ages (referred to as the "response trait"). The performance of the families for the response trait was expressed in terms of superiority over the test mean of all families by division:

$$\%\ \text{superiority} = \left(\frac{\text{mean of top one-third families}}{\text{test mean of all families}} - 1\right) 100.$$

The purpose of the selection and tracking process was to determine the effectiveness of:

1. early family selection versus later selection on the same trait (for example, family selections at age five were tracked to age 20 and their performance was compared to the top one-third families at age 20) and
2. selection on one trait to achieve a correlated response in another. For example, selection was made on the

basis of height to determine the effect on later volume performance.

The best individuals in the best families were tracked over time by the same procedures used for families.

Results and Discussions

Means:

The five tests analyzed had excellent survival and represent a narrow range in mean height growth at early and later ages (*Table 1*). Growth rates were excellent but the results from these tests may not accurately reflect what would happen in environments with poor growth.

Variances:

The traits analyzed in each test will be referred to as H5, H10, H15, H20, V5, V10, V15 and V20. The H and V indicate height and volume/tree respectively. The numbers indicate the measurement age.

The analyses of variance indicated significant family differences (.05 probability level) for all eight traits in each test with two exceptions. For traits V5 in Test 15 and V20 in Test 6, family differences were significant at the .10 probability level.

There was a steady increase in phenotypic (family plus rep-by family plus within plot) and family variance components with age for height (*Fig. 1*). The same variances for volume also showed a consistent increase with age but the increase was more exponential with dramatic increases in variance between 15 and 20 years of age (Fig. 1).

The picture was unclear for age trends in the ratio of the family variance component divided by the phenotypic variance $\frac{\sigma_F^2}{\sigma_P^2}$ -- an indicator of heritability (*Fig. 1*). Since the families were open-pollinated, additive genetic variance could not be estimated reliably by multiplying σ_F^2 by a constant. For height, heritability increased with age for tests (5) and (15), decreased in test (12) and increased to age 15 then dropped at age 20 in tests (6) and (13). The results were similarly equivocal for volume. There was a tendency toward a slight (though statistically nonsignificant) increase in the $\frac{\sigma_F^2}{\sigma_P^2}$ ratio with age for both height and volume for the average of all five tests.

Juvenile-Mature Correlations:

Juvenile-mature correlations were always positive and, in most cases, reasonable high, especially genetic correlations (*Table 2*). Phenotypic juvenile-mature correlations for volume were more often, though not always, larger than those for height. Our results are consistent with those of PASCHKE (1979) and WAKELEY (1971) who found diameter juvenile-mature correlations to be generally higher than those for height. Diameter and tree volume in our study are more highly correlated than height and volume. Height

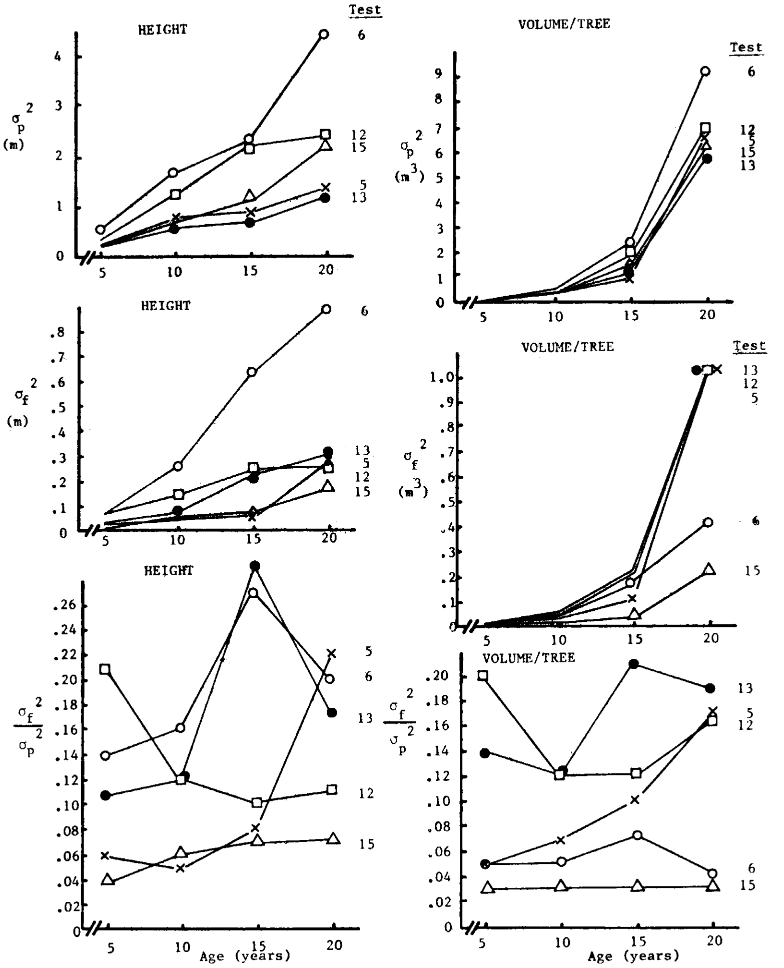

Figure 1. — Age trends in phenotypic (σ_p^2) and family (σ_f^2) variance components in five open-pollinated, loblolly pine tests in east Texas.

Table 2. — Genetic, family mean, within plot and phenotypic correlations for height and volume measurements at ages 5, 10, 15 and 20 in five loblolly pine tests in east Texas. The value in parentheses is the correlation between the juvenile trait and the increment of growth between the juvenile and mature measurements.

	Height Juvenile-Mature Correlations				Volume Juvenile-Mature Correlations			
Measurement Ages Correlated	Genetic	Family Mean	Within Plot	Phenotypic	Genetic	Family Mean	Within Plot	Phenotypic
			TEST NUMBER 5					
5, 10	1.04(1.0)	.71(.04)	.67(.09)	.65	1.06(1.1)	.85(.77)	.78(.68)	.78
5, 15	.99(.95)	.72(.33)	.43(-.08)	.49	.99(.99)	.73(.68)	.65(.58)	.64
5, 20	1.13(1.2)	.83(.65)	.42(.02)	.48	1.44(1.4)	.74(.72)	.51(.48)	.52
10, 15	.78(.0)	.68(-.01)	.65(-.05)	.65	.98(.93)	.96(.86)	.93(.77)	.93
10, 20	.98(.94)	.80(.47)	.60(.04)	.64	.98(.97)	.95(.93)	.86(.79)	.87
15, 20	1.10(2.3)	.91(.47)	.69(-.10)	.72	1.00(1.0)	.98(.95)	.92(.77)	.93
			TEST NUMBER 6					
5, 10	.85(.54)	.80(.41)	.71(.22)	.74	.94(.92)	.73(.65)	.66(.58)	.67
5, 15	.78(.58)	.74(.50)	.51(.08)	.62	1.08(1.1)	.63(.60)	.41(.36)	.46
5, 20	.68(.49)	.63(.41)	.44(.14)	.54	.82(.81)	.44(.42)	.35(.32)	.39
10, 15	.99(.91)	.96(.73)	.73(.06)	.84	.98(.94)	.94(.83)	.90(.74)	.91
10, 20	.84(.53)	.90(.66)	.64(.20)	.76	.91(.86)	.86(.78)	.84(.76)	.85
15, 20	.94(.28)	.90(.20)	.75(.08)	.83	1.00(1.0)	.94(.78)	.94(.79)	.94
			TEST NUMBER 12					
5, 10	.99(.85)	.92(.47)	.68(.19)	.74	1.06(1.1)	.93(.90)	.73(.66)	.77
5, 15	1.03(1.0)	.85(.57)	.52(.15)	.63	1.12(1.1)	.88(.87)	.54(.50)	.61
5, 20	1.06(1.4)	.82(.59)	.48(.14)	.59	1.01(1.0)	.81(.80)	.57(.55)	.61
10, 15	1.03(1.0)	.96(.56)	.77(.20)	.85	.98(.93)	.97(.91)	.83(.60)	.88
10, 20	1.08(1.9)	.90(.54)	.68(.15)	.76	.99(.98)	.95(.92)	.87(.80)	.89
15, 20	.97(.70)	.92(.29)	.74(.07)	.82	.97(.91)	.93(.79)	.79(.39)	.84
			TEST NUMBER 13					
5, 10	1.00(1.0)	.87(.51)	.59(-.15)	.63	.94(.90)	.89(.83)	.70(.57)	.74
5, 15	.96(.91)	.78(.58)	.36(-.26)	.44	.95(.94)	.86(.83)	.52(.44)	.59
5, 20	.89(.81)	.73(.57)	.36(.01)	.43	.86(.85)	.80(.78)	.45(.42)	.52
10, 15	1.13(1.4)	.91(.67)	.62(-.20)	.70	1.02(1.0)	.98(.94)	.93(.78)	.94
10, 20	.99(.98)	.89(.69)	.62(.22)	.70	1.01(1.1)	.95(.93)	.87(.81)	.88
15, 20	.94(.31)	.89(.17)	.68(.14)	.74	.99(.97)	.98(.94)	.94(.84)	.95
			TEST NUMBER 15					
5, 10	1.05(1.0)	.72(.16)	.58(.0)	.64	.80(.74)	.66(.55)	.71(.52)	.68
5, 15	.67(.35)	.60(.17)	.55(.11)	.56	.59(.54)	.53(.48)	.64(.60)	.62
5, 20	.79(.66)	.52(.22)	.50(.21)	.38	.59(.57)	.45(.63)	.57(.55)	.52
10, 15	1.02(1.0)	.88(.24)	.66(-.17)	.75	.96(.86)	.94(.80)	.92(.77)	.93
10, 20	.99(.96)	.84(.48)	.63(.13)	.61	.86(.79)	.87(.80)	.87(.80)	.86
15, 20	.96(.74)	.86(.28)	.77(.15)	.76	.97(.91)	.96(.87)	.95(.83)	.95

correlations over time may be lower than those for diameter due to difficulty in accurately measuring heights at older ages.

When the correlations are based on family means, measurement errors tend to average out and the difference between volume and height juvenile-mature correlations are smaller than within plot correlations. Genetic correlations were larger than family mean correlations which were larger than within plot correlations.

The genetic correlation is an estimate based on genetic effects. Thus, there is a progression in the magnitude of the correlation which corresponds to the degree of genetic control of trait expression. This trend was also noticeable in correlations reported by LaFarge 1972, Squillace and Gansel 1974, Steinhoff 1974, and Wilkinson 1973. Ying and Morgenstern (1978) found little difference between family mean and within plot correlations. Others have suggested the reverse (Namkoong, *et al.* 1972; Namkoong and Conkle, 1976), i.e., that genetic correlations may be low or even negative while phenotypic correlations are high. However, it is invalid to look at genetic juvenile-mature correlations if there is no statistical difference among families because no meaningful genetic covariance with other traits can exist. In such a case the phenotypic juvenile-mature correlations must be due to environmental effects or autocorrelations.

The correlations between the juvenile trait and the subsequent increment of growth to mature trait measurement (*Table 2*) were not generally as large as the overall juvenile-mature correlations, suggesting that variance in the juvenile trait contributed significantly to the overall correlation. This was especially true for tthe within plot correlations and more so for height than volume. The volume and height correlations were of similar magnitude even though the makeup of the correlations is considerably different.

The phenotypic and family variances for volume increased dramatically with age (*Figure 1*) such that the contribution of variance in the juvenile trait to the overall juvenile-mature correlation was small. The correlation between juvenile growth and subsequent growth to maturity was relatively large and the primary source of high juvenile-mature correlations. The reverse was true for height for within plot correlations and, to some extent, for family mean correlations. The genetic correlations between juvenile and subsequent growth were usually high for both height and volume.

The within plot correlations between juvenile and subsequent growth were dismally low for height. It appears that there is little or no relationship between early height growth and later growth. The main reason for the observed high within plot, juvenile-mature correlations is the variation in size at younger ages which is maintained as the stand ages. For volume, high within plot juvenile-mature correlations are a result of big trees at young ages tending to also growth faster in subsequent years.

Selection Response:

It is apparent that genetic gain potential for height is much lower than that for volume per tree (*Table 3*). The top one-third families at age 20 had an average of only 4.4 % height superiority over the test mean. The top one-third families for volume had 20.6 % superiority over the test mean. In spite of the low height variance among families, the correlation with family volume was high and early family selection based on height was nearly as effective at picking the best volume families at age 20 as was early selection based on volume.

Early selection was very effective in picking the best families at age 20. From these data, there is no apparent advantage to delay selection beyond age five if generations are cycled more rapidly with early selection. Selecting the best individuals in the best families resulted in some trends similar to those for family selection *(Table 4)*. Some excepttions were that individual selection should possibly be made at age 10 rather than age five (or somewhere between ages five and 10) since average volume superiority at age 20 was much larger for tenth year selections (54 % versus 102 %) and selection should be based on volume rather than height (58 % versus 102 %). However, within plot heritabilities are usually low and only a small portion of the individual volume superiority could be captured through breeding and selection.

Genetic gain estimates at age 5 (and sometimes at age 10) will likely overestimate gains at maturity for two reasons:

1. imperfect juvenile-mature correlations, and
2. family and individual variances, relative to the mean, are larger — especially for height *(Tables 3* and *4)*. For example, percent superiority over the mean in age five tests average 29 % while the value for age 20 tests was only 15 % *(Table 4)*.

In drawing the latter conclusion we have assumed that genetic gain will behave similarly to superiority over the mean figures employed in *Tables 3* and *4*. We were unable to make clean estimates of genetic gain because precise estimates of additive genetic variance and heritability were impossible with open-pollinated families.

Tests (5) and (15) showed lower superiority over check values with family selection for both height and volume than the other tests *(Table 3)*. The families in these tests have lower variance relative to the mean because they are probably interrelated because they originated from seed production areas *(Table 1)*. It is likely that only a few mother trees seeded the natural stand from which the seed production area was constructed. The same pattern was not observed for within family selection *(Table 4)*, probably because within family genetic variation is less reduced from interrelatedness than between family genetic variation.

Table 3. — Percent superiority over the test mean for the response trait of the top one third of the families based on the selection trait in five open-pollinated loblolly pine tests. For example, the top one-third families for height at age 5 had a volume superiority of 9% at age 20 in Test 5.

* = Height, V = Volume 5, 10, 15 and 20 = Measurement Ages

Selection Trait*	-	Response Trait	% Superiority Over the Test Mean					
			Test 5	Test 6	Test 12	Test 13	Test 15	Average
H5	-	H5	4	9	9	5	5	6.4
H10	-	H10	3	7	5	3	3	4.2
H15	-	H15	3	8	5	4	3	4.6
H5	-	H20	1	5	5	3	2	3.2
H10	-	H20	1	7	4	2	3	3.4
H15	-	H20	2	7	5	3	2	3.8
H20	-	H20	3	8	5	3	3	4.4
H5	-	V20	9	16	30	20	8	16.6
H10	-	V20	8	20	25	9	11	14.6
H15	-	V20	12	20	30	18	10	18.0
H20	-	V20	12	20	30	17	9	17.6
V5	-	V5	16	20	32	20	18	21.2
V10	-	V10	12	15	23	14	13	15.4
V15	-	V15	12	19	28	18	13	18.0
V5	-	V20	5	14	30	20	6	16.2
V10	-	V20	11	20	30	20	12	18.6
V15	-	V20	17	20	30	18	12	19.4
V20	-	V20	17	22	31	20	13	20.6

Table 4. — Percent superiority over the test mean for the response trait of the top three individuals in each of the top one-third families based on the selection trait in five open-pollinated loblolly pine tests. For example, the top three individuals in the top one-third families for height at age 5 had a volume superiority of 39% at age 20 in Test 5.

* H = Height, V = Volume 5, 10, 15 and 20 = Measurement Ages

Selection Trait*	-	Response Trait	% Superiority Over the Test Mean					
			Test 5	Test 6	Test 12	Test 13	Test 15	Average
H5	-	H5	19	36	35	17	38	29
H10	-	H10	14	27	25	16	18	20
H15	-	H15	12	25	23	10	15	17
H5	-	H20	4	15	13	6	6	9
H10	-	H20	5	17	15	5	9	10
H15	-	H20	7	18	17	7	9	12
H20	-	H20	8	25	17	10	13	15
H5	-	V20	39	78	95	49	45	61
H10	-	V20	37	82	60	44	66	58
H15	-	V20	47	70	98	43	62	64
H20	-	V20	38	81	100	67	62	70
V5	-	V5	106	168	171	89	147	136
V10	-	V10	90	150	139	78	109	113
V15	-	V15	72	147	138	72	105	107
V5	-	V20	38	55	95	36	48	54
V10	-	V20	62	140	130	73	104	102
V15	-	V20	57	173	101	71	103	101
V20	-	V20	58	178	126	83	103	110

The phenotypic, juvenile-mature correlations were similar in magnitude to those used by LAMBETH (1980) who suggested that selections could be made as early as age six with an economic rotation age of 30 years. However, genetic correlations were much higher, suggesting that selections could be made earlier than age six. The first measurement age in these tests (age five) seems to be the most efficient selection age in terms of gain/year in a recurrent breeding program. Family selections at age 5 were quite accurate, whereas individual selections at age 5 were less effective than those at later ages but individual tree heritabilities are usually low and genetic gain from selection of families is greater than that for individuals. The results also support the conclusions of NANSON (1969) and SQUILLACE and GANSEL (1974).

A major assumption made by LAMBETH (1980) was that heritabilities do not change significantly with age. This assumption seems safe for the average of the five tests but not for any test individually.

The trends in population statistical parameters in these tests (family to phenotypic variance ratio, additive genetic variance and genetic juvenile-mature correlations) do not behave according to the model proposed by FRANKLIN (1979). Heritability did not decrease to zero and there were no negative correlations between measurements of growth at any two ages. Franklin's model was based on the effects of competition which may not have been as severe in these thinned tests. Furthermore, measurement may not have been frequent enough to pick up the trend hypothesized for young ages.

Conclusions

Conclusions drawn from the examination of age trends in population statistics involving variances, juvenile-mature correlations and response to early selection in the five open-pollinated tests are:

1. Family, within-plot and phenotypic variances increased with age for both height and volume. The height variances increased in a linear fashion while those for volume increased exponentially.
2. There was no detectable pattern in the ratio of family variance over phenotypic variance over time. The ratio changed considerably from one measurement age to another within any test but no significant trends were detectable.
3. Juvenile-mature correlations were generally high, especially genetic correlations which were often near one (1). Within-plot correlations were smaller than family mean correlations which were smaller than genetic correlations.
4. Height and volume juvenile-mature correlations were generally of similar magnitude even though the volume correlations tended to be larger than those for height.
5. Early family selection was very effective. Selections at age five were only nominally lower in volume at age 20 than selections at age 20. However, individual tree selection could perhaps be postponed until a later age.
6. Early family selections based on height were as effective at predicting ultimate volume as early selections based on volume.

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Efforts of the Texas Forest Service in installing, measuring and maintaining the genetic tests are sincerely appreciated.

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