VARIATION AND ESTIMATED GAINS IN HEIGHT, DIAMETER, AND VOLUME GROWTH FOR OPEN-POLLINATED PROGENY OF VIRGINIA PINE (*Pinus virginiana* Mill.)

David Todd and Eyvind Thor [1/]

Abstract.--Ten-year old open-pollinated progeny of random trees from 12 stands in Tennessee and Kentucky were analyzed for height, diameter, and volume growth. Approximately 20,000 individual progeny representing 128 half-sib families outplanted at three locations in Tennessee were measured. Variance componenets indicated that most of the variation in height, diameter, and volume growth was among half-sib progeny within families. However, the among family and among stand variance components made significant contributions to the total variation. Interaction variance components for locations with parent stands, and locations with families within stands were low for all variables; these components did not exceed 1.5% of the total variation. Two plantations were marked from conversion to seedling seed orchards. Gains in volume growth by selecting the best one third of the families and the best individuals within these families were estimated to be 18% and 30%.

METHODS

Twelve natural stands were selected from the Coastal Plain, Cumberland Plateau and Mountains, and the Great Valley physiographic regions of Tennessee and Kentucky (Figure 1). Stands were even-aged and of average or better than average quality. These stands ranged in age from 28 to 53 years and site indices varied from 60 to 87 feet (Thor, 1964). Only one stand (stand 10) had received any silvicultural treatment; this stand was a United States Forest Service seed production area which had been thinned heavily to remove undesirable trees.

From each stand 15 trees were selected as potential parent trees. Parent trees were healthy dominants or codominants with poor, average, or excellent phenotypic characteristics.

Originally, six open-pollinated progeny plantations were established. However, for this study only three plantations were used (Ames Plantation, Camp York, and Highland Rim) (Figure 1). Only 128 parent trees yielded enough seedlings to be included in the experiment and the number of progeny varied so much that only the Highland Rim plantation included all 128 families. Ninety families were represented at the other two locations.

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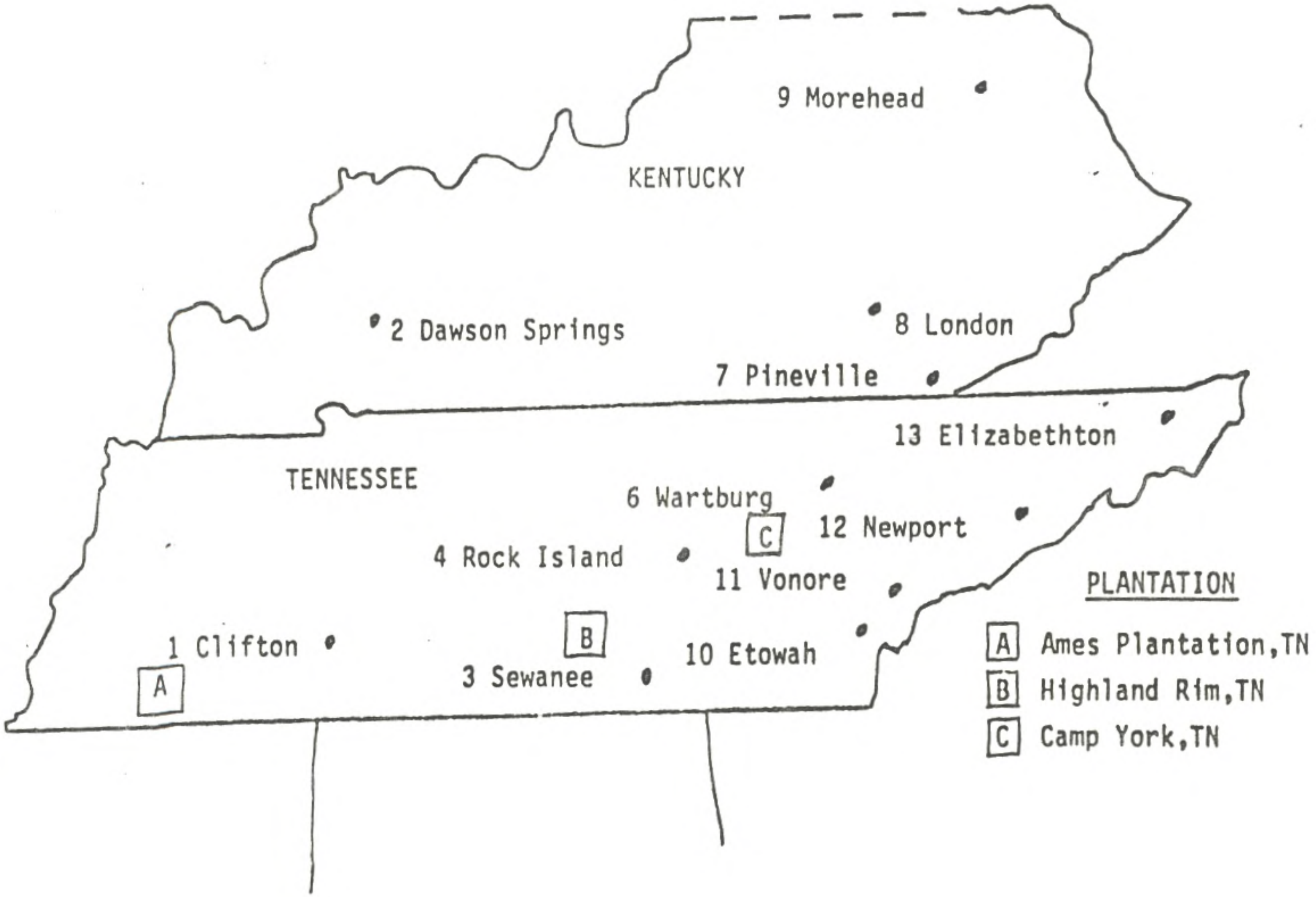

Figure 1. Location of parent stands and plantation sites.

Plantations consisted of seedlings planted in ten-tree family row plots arranged in a randomized complete block design. Each block was replicated ten times at each plantation. Spacing was four feet within family-row plots and eight feet between rows.

Measurements were made between late summer 1977 and spring 1978. Ten-year measurements included total height to the nearest foot and stem diameter (D.B.H.) to the nearest 0.1 inch. Individual tree volumes were computed from height and diameter measurements using a volume prediciton equation for young Virginia pine (Goebel and Mathews, 1966).

Analysis of variance was performed on an individual tree basis for each characteristic at each location and across all locations. All effects were assumed to be random. The analysis of variance was computed using the General Linear Model (GLM) procedures of the Statistical Analysis System (SAS 76) program (Barr et. al, 1976). The individual location and the combine(location analyses, with some exceptions, followed those used by Rink and Thor (1976).

RESULTS AND DISCUSSION

Individual Locations

Mean squares, degrees of freedom, and levels of significance for volume, height, and diameter are presented in Table 1. At all locations the effects of stands and families-within-stands were significant for all variables.

Estimates of variance components, heritabilities, and standard errors are presented in Table 2. The variance components and heritability estimates for the Ames and Highland Rim plantations were similar. At Camp York, however, larger estimates for the interaction of replication by family-within-stand and smaller estimates for the family-within-stand variance components for all variables were obtained. This resulted in lower heritability estimates at Camp York.

Standard errors for the family-within-stand variance components and for the heritability estimates were in most cases small. The average standard error for both estimates was about 20% of the estimate. Since all families are not represented at all locations, differences in variances among test sites are partially attributed to variance of uncommon families.

Combined Locations

Mean squares, degrees of freedom, and levels of significance for volume, height, and diameter are presented in Table 3. Sensitivity of the experimental design is evident by the predominance of significance for almost all sources of variation and variables.

Table 1. Sources of variation, degrees of freedom, mean square, and levels of significance for Ames, Camp York, and Highland Rim locations.

Source	d.f.	Volume	Height	Diameter
Ames				
Replication	9	.5507**	197.1803**	1.3880NS
Stands	10	2.6814**	204.9419**	17.0351**
Replication x Stands	90	.0802NS	9.2225NS	.7008NS
Family within Stands	79	.3797**	42.7205**	2.7327**
Replication x Family within Stands	689	.0807**	9.6240**	.6722**
Within Plot	5551	.0697	5.3691	.6429
Camp York				
Replication	9	1.6418NS	348.6930**	3.9068**
Stands	9	3.8621**	88.0778**	17.0990**
Replication x Stands	81	.2268NS	16.0305NS	.9713NS
Family within Stands	80	.7085**	32.2690*	2.7416**
Replication x Family within Stands	685	.2356NS	24.9829**	1.0711**
Within Plot	4008	.2132	6.0741	1.0327
Highland Rim				
Replication	9	1.4775**	273.5270**	3.4109**
Stands	11	6.9285**	191.8290**	26.5132**
Replication x Stands	99	.2503**	11.7065**	.9095NS
Family within Stands	124	.9062**	36.7236**	3.4662**
Replication x Family within Stands	993	.1648NS	8.0030**	.6801NS
Within Plot	8995	.1848	4.9925	.8019

* Significant at the .05 level.
** Significant at the .01 level.
NS Nonsignificant at the .05 level.

Table 2. Variance components, heritability estimates, and standard errors for volume, height, and diameter growth for three locations. Numbers in parentheses indicate percentage contribution to the total variation.

	s^2_W	$s^2_{RxF/S}$	$s^2_{F/S}$	S.E.$_{F/S}$ [a]	s^2_{RxS}	s^2_S	s^2_R	h^2 [b]	S.E.(h^2)[c]
Volume									
Ames Plantation	.0697	.0014	.0041	.0008	NC [d]	.0039	.0007	.2189	.0425
	(87.3)	(1.7)	(5.1)			(4.9)	(0.9)		
Camp York	.2132	.0041	.0087	.0020	NC	.0066	.0029	.1539	.0354
	(90.5)	(1.7)	(3.7)			(2.8)	(1.2)		
Highland Rim	.1848	NC	.0098	.0015	.0010	.0071	.0021	.2014	.0308
	(90.2)		(4.8)		(0.5)	(3.5)	(1.0)		
Mean	.1559	.0018	.0075		.0010	.0072	.0019		
Height									
Ames Plantation	5.3691	.5868	.4561	.0927	NC	.2740	.2879	.2845	.0578
	(77.0)	(8.4)	(6.5)			(3.9)	(4.1)		
Camp York	6.0741	3.4887	.1345	.0962	NC	.1327	.6816	.0555	.0397
	(57.8)	(33.2)	(1.3)			(1.3)	(6.5)		
Highland Rim	4.9925	.3993	.3809	.0615	.0433	.1772	.2554	.2639	.0426
	(79.9)	(6.4	(6.1)		(0.7)	(2.8)	(4.1)		
Mean	5.4786	1.4916	.3238		.0433	.1882	.4083		
Diameter									
Ames Plantation	.6429	.0040	.0284	.0059	.0005	.0240	.0010	.1682	.0349
	(91.7)	(0.6)	(4.1)		(0.1)	(3.4)	(0.1)		
Camp York	1.0327	.0071	.0308	.0080	NC	.0296	.0060	.1151	.0299
	(93.4)	(0.6)	(2.8)			(2.7)	(0.5)		
Highland Rim	.8019	NC	.0369	.0058	.0027	.0267	.0024	.1760	.0276
	(92.1)		(4.2)		(0.3)	(3.1)	(0.3)		
Mean	.8258	.0040	.0320		.0011	.0268	.0031		

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[a] Standard error of the family-within-stand variance component.

[b] Heritability = $\frac{4s^2_{F/S}}{s^2_W+s^2_{RxF/S}+s^2_{F/S}}$

[c] Standard error of the heritability estimate.

[d] NC=negative estimate of component.

Table 3. Sources of variation, degrees of freedom, mean squares, and levels of significance for volume, height, and diameter growth for combined locations.

Source	d.f.	Volume	Height	Diameter
Locations	2	281.1293**	75,820.0927**	432.2160**
Replication within Location	27	1.2234**	273.1334**	2.9019**
Stands	11	9.8113**	352.2290**	45.6821**
Location x Stands	19	.8145**	39.2409NS	3.3085**
Stand x Replication within Location	270	.1865**	12.1757**	.8585
Families within Stands	125	1.3372**	67.6670**	5.6565
Location x Families within Stands	159	.2536**	13.7791**	1.1271**
Replication within Location x Families within Stands	2367	.1608**	10.2223**	.7909NS
Within Plot	18554	.1565	5.3388	.8044

** Significant at the .01 level.
NS Nonsignificant at the .05 level.

Estimates of variance components, heritabilities, and standard errors are presented in Table 4. Although not directly comparable, the estimates obtained from the combined analysis and the mean of the estimates obtained from the individual locations are of the same magnitude.

The analysis indicates that for all variables the within-plot variance components accounted for the largest portion of the phenotypic variance, representing 91.7% for volume, 77.8% for height, and 93.1% for diameter. Location components of interaction (location by stand, and location by family within stand) are very small; together these accounted for only 1.0% for volume, 1.5% for height, and 1.1% for diameter of the phenotypic variation. Heritability estimates were .17 for volume, .20 for height, and .4 for diameter.

When tenth-year results are compared to the fifth-year results obtained by

Table 4. Variance components, heritability estimates, and standard errors of the family-within-stand variance components and heritability estimates for volume, height, and diameter for combined locations. Numbers in parentheses represent the percentage contribution to the phenotypic variation.

Variance Components	Variables		
	Volume	Height	Diameter
s^2_S	.0050(2.93)	.1494(2.18)	.0210(2.43)
s^2_{LxS}	NC [a]	.0391(0.57)	.0035(0.41)
$s^2_{F/S}$	.0067(3.92)	.3417(4.98)	.0287(3.32)
S.E.$(s^2_{F/S}) \pm$ [b]	.0011	.0538	.0045
$s^2_{LxF/S}$	.0017(1.00)	.0676(0.98)	.0064(0.74)
$s^2_{R/LxF/S}$	.0008(0.47)	.9279(13.52)	NC
s^2_W	.1565(91.68)	5.3388(77.77)	.8044(93.10)
h^2 [c]	.1664	.2048	.1379
S.E.$(h^2) \pm$ [d]	.0265	.0322	.0214

[a] NC = negative estimate of component.

[b] Standard error of the family-within-stand variance component.

[c] $$h^2 = \frac{4(s^2_{F/S})}{s^2_W + s^2_{R/LxF/S} + s^2_{LxF/S} + s^2_{F/S}}$$

[d] Standard error of the heritability estimate.

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Variance Components	Variables Volume	 Height	 Diameter
s_S^2	.0050(2.93)	.1494(2.18)	.0210(2.43)
s_{LxS}^2	NC [a]	.0391(0.57)	.0035(0.41)
$s_{F/S}^2$	.0067(3.92)	.3417(4.98)	.0287(3.32)
S.E.$(s_{F/S}^2)\pm$ [b]	.0011	.0538	.0045
$s_{LxF/S}^2$	.0017(1.00)	.0676(0.98)	.0064(0.74)
$s_{R/LxF/S}^2$	.0008(0.47)	.9279(13.52)	NC
s_W^2	.1565(91.68)	5.3388(77.77)	.8044(93.10)
h^2 [c]	.1664	.2048	.1379
S.E.$(h^2)\pm$ [d]	.0265	.0322	.0214

[a] NC = negative estimate of component.

[b] Standard error of the family-within-stand variance component.

[c] $$h^2 = \frac{4(s_{F/S}^2)}{s_W^2 + s_{R/LxF/S}^2 + s_{LxF/S}^2 + s_{F/S}^2}$$

[d] Standard error of the heritability estimate.

Rink and Thor (1976) there is considerable similarity. The only consistent difference is the slightly lower proportion of the phenotypic variation accounted for by the stand variance component at ten years than at five years.

Ranking the stands by volume growth revealed that three stands (stand 10, Etowah, Tennessee; stand 1, Clifton, Tennessee; and stand 11, Vonore, Tennessee) consistently ranked first, second and third at all locations. Although stand 12, Newport, Tennessee, ranked second at the Highland Rim location, it was only represented in this location.

APPLICATION OF RESULTS

Two of the progeny plantations, Ames and Camp York, were marked for conversion to seedling seed orchards. This was accomplished by selecting the best families and the best individual within a selected family row plot. Selected families were based on their performance across all locations. Although volume growth was the main selection criterion, individuals with poor stem form were not accepted, thereby possible sacrificing some volume gain.

Individual tree heritabilities are appropriate in the estimation of genetic gains only when individuals are selected based on individual performance, as in mass selection. When entire families are selected and rejected based on the mean of the family individuals and when individuals are selected or rejected based on their deviation from the family mean, then individual tree heritability estimates cannot be applied to these separate stages of selection to estimate gains. Falconer (1960) presented a method for computing gains resulting from family and within-family selection. This method computes heritability for family means (h^2_F) and heritability for individuals within family (h^2_W) in terms of individual heritability (h^2_I).

$$h^2_F = h^2_I \cdot \left[\frac{1+(n-1)r}{1+(n-1)t}\right]$$

$$h^2_W = h^2_I \cdot \left[\frac{1-r}{1-t}\right]$$

where: n = family size
r = .25 for half-sibs
t = intraclass correlation of family members.

Expected gains from both plantations are presented in Table 5. The selection differential (SD_F) between the mean of selected families and the location mean was multiplied by the family mean heritability (q) to obtain an estimate of gain (G_F) from family selection.

$$G_F = SD_F h^2_F$$

Table 5. Expected gains in volume growth (ft.^{3}) from selecting the best individual within a given family at Ames and Camp York. Numbers in parentheses indicate percentage contribution at each stage of selection.

Item	Ames	Camp York
1. Location Mean Volume (ft.^{3})	.5492	.9505
2. Mean Tree Volume (ft.^{3}) of the Selected Families	.6600	1.0900
3. Mean Tree Volume of the Selected Trees Within the Selected Families	1.0747	1.6907
4. Selection Differential for Selected Families	.1108	.1395
5. Selection Differential for Selected Trees Within Families	.4147	.6007
6. Number of Families Selected	27 of 90	28 of 90
7. Volume (ft.^{3}) Gain for Family Selection	.0921 (16.77%)	.0995 (10.47%)
8. Volume (ft.^{3}) Gain for Within Family Selection	.0721 (13.12%)	.0721 (7.58%)
9. Total Volume (ft.^{3}) Gain	.1642 (29.9%)	.1716 (18.05%)

Likewise, the selection differential (SD_W) between the mean of the individuals selected within selected families and the mean of the selected families was multiplied by the within family heritability (h_W^2) to obtain an estimate of gain (G_W) from within-family selection.

$$G_W = SD_W h_W^2$$

Since these gains are additive, the total gain is the sum of the gain obtained from each stage of selection. Expected volume growth gains from Ames and Camp York plantations by selecting 27 or 28 of 90 families at each location and the best individual within each of these families was .1642 ft.^{3} and .1716 ft.^{3}, respectively. The volume gain was 29.9% at Ames and 18.0% at Camp York above the population mean at each location.

Estimates of volume growth gain based on a hypothetical roguing of the Highland Rim location were also made using the method described by Falconer (1960). By selecting 30% of the families and the best individual within those families, the total volume growth gain was estimated to be 25.8% above the location mean. Similar results, 25.1% above the location mean, were obtained by using the variance component method of multistage selection described by Namkoong et al. (1966) as adapted by Evans and Thor (1971).

Based on ten-year data, the most promising seed sources appear to be those from the central part of the Great Valley of Tennessee. In addition, substantial improvement in volume, height, and diameter growth can be obtained through a selection breeding program in Tennessee for Virginia pine. Volume gains from seedling seed orchards compare favorably with those reported from grafted orchards of other southern pines.

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