ESTIMATES OF HERITABILITIES AND GENETIC GAINS FOR POPULATIONS OF VIRGINIA PINE 1/

Richard M. Evans 2/ and Eyvind Thor 3/

In 1962, the Kentucky-Tennessee Section of the Society of American Foresters sponsored a study to determine the natural variation in Virginia pine (Pinus virginiana Mill.). There were two main objectives in the proposed study: to determine the natural variation in wood properties and to determine the genetic variation in open-pollinated progenies in the natural populations of Virginia pine found in Kentucky and Tennessee. Thor (1964) has reported information relating to the first objective. This paper presents some results of studies concerned with the second objective.

METHODS

In September and October of 1963, 1964, and 1965 open-pollinated *seed* were collected from 7 to 13 parent trees in 12 natural stands in Kentucky and Tennessee. The stands were located in seven physiographic regions and were considered to be representative of the natural populations (Figure 1). Only even-aged stands of average or better than average quality were used. Parent trees were healthy dominants or codominants with poor, average or excellent phenotypic characteristics. Stands varied in age from 28 to 58 years old and were on site indexes from 60 to 87 feet (Table 1).

One-year-old seedlings, grown in unreplicated family plots at the Tennessee Valley Authority's nursery at Norris, Tennessee were lifted for planting in the spring of 1967. From 57 to 127 families were planted in 10-tree-row family plots at a 5 by 8 foot spacing in 6 test locations. A randomized complete block design was used with 9 or 10 replication at each test site.

Test sites were widely scattered with 80 or more miles between each site (Figure 1). Two sites, Ames Plantation and Vina, were in the Coastal Plain geographical region of western Tennessee and northwestern Alabama, respectively. The Highland

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1/ This work is based on the senior author's *MS* Thesis at The University of Tennessee.

2/ Formerly, Graduate Research Assistant, The University of Tennessee. Presently, Assistant Geneticist, Western Gulf Forest Tree Improvement Program, College Station, Texas.

3/ Associate Professor of Forestry, The University of Tennessee, Knoxville, Tennessee.

Table 1. Location of sample plots, site indexes, and average values for D.B.H. and age. Averages are based on 15 trees per stand

Stand No.	Physiographic Region	Location	Co-operator	Site Index (ft. at 50 yrs)	D.B.H. (inches)	Total Age (years)
1	West Tennessee	Clifton, Tenn.	Univ. of Tenn.	75	9.0	28
2	West Kentucky	Dawson Springs, Kentucky	Ky. State Div. Forestry	69	11.6	52
3	Cumberland Plateau	Sewanee, Tenn.	USFS, Sewanee	73	9.7	34
4	Eastern Highland Rim	Rock Island, Tenn.	Univ. of Tenn.	74	10.2	42
6	Cumberland Mountains	Wartburg, Tenn.	Univ. of Tenn.	87	8.9	35
7	Eastern Ridge	Pineville, Ky.	Ky. State Div. Forestry	82	9.5	42
8	Cumberland Plateau	London, Ky.	USFS, Berea	83	10.9	47
9	Cumberland Plateau	Morehead, Ky.	Cumberland National Forest	69	8.8	32
10	Great Valley	Etowah, Tenn.	Cherokee National Forest	81	9.0	34
11	Great Valley	Vonore, Tenn.	Hiwasse Land Co.	60	9.8	53
12	Great Valley	Newport, Tenn.	Univ. of Tenn.	75	9.7	42
13	Great Valley	Elizabethton, Tenn.	Cherokee National Forest	64	11.1	43

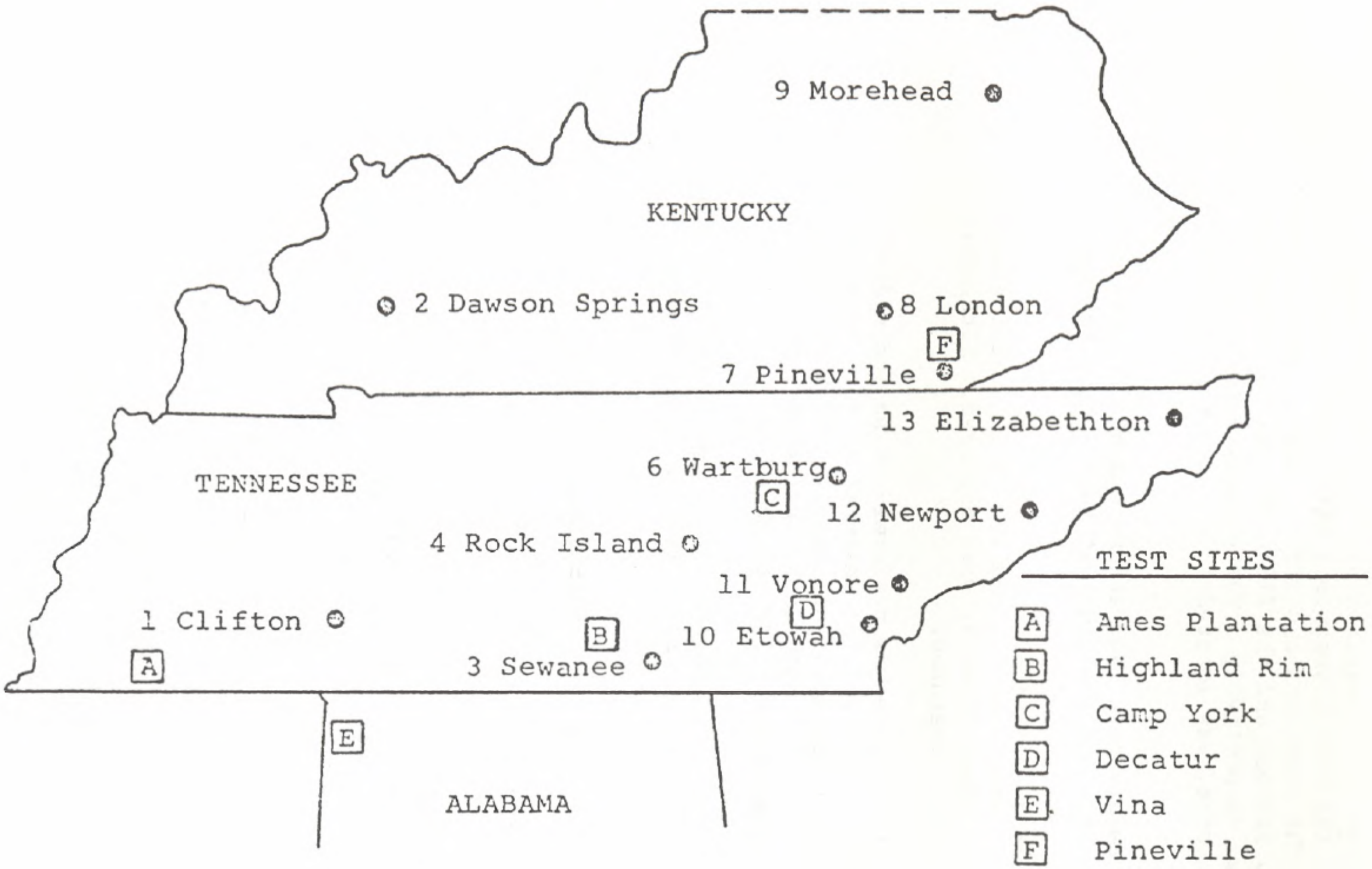

Figure 1. Locations of stands and test sites.

Rim site was located in the eastern highland rim of central Tennessee and had the most homogeneous site conditions of all test locations. The Camp York and Decatur sites were located on the Cumberland Plateau and the Ridge and Valley regions of eastern Tennessee, respectively. The Pineville test site, the most northern site, was located in eastern Kentucky on strip mine spoil.

Field measurements were made at the end of the 1967 and 1968 growing seasons. The seedlings at that time were two- and three-years old, respectively. In 1967, one growing season after planting, seedling height was measured. In 1968, after the second growing season, seedling height, stem diameter, branch length, and branch diameter were measured. Altogether about 52,000 trees were measured.

An analysis of variance was performed on an individual tree basis for each characteristic measured at each location. Effects due to stands, replications, families within stands, and trees within plots were assumed to be random. All analyses were calculated on an IBM 360 Model 65.

Components of variance and heritabilities calculated on an individual tree basis were estimated from the mean square components:

Source of variation	Expected components
Families in stands	$\sigma_w^2 + w\sigma_{f(s)r}^2 + wr\sigma_{f(s)}^2$
Families in stands x replications	$\sigma_w^2 + w\sigma_{f(s)r}^2$
Within plot	σ_w^2
Heritability	$h^2 = \dfrac{4\,\sigma_{f(s)}^2}{\sigma_w^2 + \sigma_{f(s)r}^2 + \sigma_{f(s)}^2}$

RESULTS AND DISCUSSIONS

Mean Values. All families were not represented at every test site. Therefore, differences in mean values among sites must partially be contributed to families not common among compared test sites and are not a valid indication of environmental differences. To facilitate a comparison of means among test sites, mean stand values of second-year height for families common to all test sites are summarized in Table 2. The Highland Rim site (B) has the overall

Table 2. Second year mean stand height for families common to all test sites

Stand	Test Sites A	B	C	D	E	F
2	2.36	3.19	1.82	2.47	3.18	1.24
3	2.32	3.33	1.95	2.34	3.13	1.37
4	2.40	3.48	2.21	2.78	3.31	1.28
6	2.36	3.36	1.94	2.74	3.13	1.29
7	2.38	3.41	2.04	2.72	3.22	1.47
8	2.41	3.26	1.93	2.56	3.16	1.25
9	2.39	3.47	2.20	3.18	3.22	1.34
10	2.61	3.64	2.23	2.86	3.51	1.40
11	2.51	3.47	2.04	2.80	3.42	1.56
13	2.54	3.56	2.00	2.85	3.45	1.34
Average	2.42	3.42	2.04	2.73	3.27	1.35

Table 3. Ranking of stands within each test site based on second-year mean height[a]

Ranking	Test Sites A	B	C	D	E	F
1	10	10	10	9	10	11
2	11	13	4	10	13	7
3	13	4	9	13	11	10
4	8	9	7	11	4	3
5	4	11	11	4	7	9
6	9	7	13	6	8	13
7	7	6	3	7	2	6
8	2	3	6	8	8	4
9	6	8	8	2	3	8
10	3	2	2	3	6	2

[a] Stands ranked in descending order by stand mean heights presented in Table 2.

largest second-year mean height (3.42 feet) and each stand mean value is larger than that observed for any other test site. Likewise, the smallest test site mean height (1.35 feet) was found at Pineville (F); consistently this strip mine site had the smallest mean stand heights.

Table 3 presents a ranking at each test site of the mean second-year stand heights. Some stands tend consistently to be ranked relatively high or low. For example, Stand 10 is ranked among the best three at all test sites, and Stand 2 is consistently ranked lower than seventh. Furthermore, common among the stands ranked relatively high or low is a tendency for them to be from the same physiographic region. Stands 10, 11, and 13 of the Great Valley physiographic source (Table 1) rank in the upper 30 percent 13 times, out of the possible 18 (72 percent). If the stands of this physiographic source were ranked randomly one would expect only 5 out of the possible 18 in the upper 30 percent of all stands. A chi-square test indicated that the ranking of physiographic sources was different from the results of random distribution. The F-test indicates significant difference in second-year height among stands at all test sites.

Components of variance and heritabilities. Estimates of variance components and heritabilities are presented in Table 4 for second-year height and second-year stem diameter. Since all families were not represented at all locations, differences in variances among test sites are partially attributed to variances among uncommon families. However, general comparisons will be made on the assumption that variances and means of uncommon families are the same as among common families.

In comparing the variances of Table 4 to the means of Table 2 the effects of scale (Falconer, 1967) are apparent. For example, Highland Rim which has the largest mean second-year height also has the larger variances. In contrast, the Pineville site has the smallest mean height and variances.

The standard errors of the family within-stand variance, as calculated by Snyder (1969), were in general small. Average standard errors were 20 to 25 percent of the family within-stand variance.

Heritability estimates were highly variable among test sites. Estimates for first-year heights range between the Highland Rim (h =0.44) and Ames Plantation (0.17) test sites. Estimates of second year height heritability ranged from 0.48 to 0.17 at the Highland Rim and Ames sites, respectively.

Estimates of genetic gains. Estimates of phenotypic and genetic variance are of little practical value by themselves. The ultimate use of the estimates is to predict the amount of improvement, i.e., genetic gain, possible for a particular breeding program.

Table 4. Estimates of components of variance, standard error of family within-stand variance, and heritability for second-year seedling height and stem diameter

	σ_w^2	$\sigma_{f(s)r}^2$	$\sigma_{f(s)}^2$	$s\left[\sigma_{f(s)}^2\right]$[a]	h^2
Height					
Ames	33.52[b]	6.01	1.66	0.41	0.16
Highland Rim	43.02	4.66	6.58	0.99	0.48
Camp York	43.63	6.26	3.78	0.89	0.28
Decatur	47.72	8.82	3.29	0.79	0.22
Vina	43.64	7.46	4.70	0.97	0.34
Pineville	17.16	3.67	1.28	0.41	0.23
Diameter					
Ames	0.777[b]	0.136	0.018	0.006	0.08
Highland Rim	0.961	0.088	0.119	0.017	0.41
Camp York	1.016	0.142	0.066	0.015	0.21
Decatur	0.874	0.186	0.044	0.013	0.16
Vina	1.310	0.157	0.076	0.018	0.20
Pineville	2.111	0.561	0.108	0.042	0.16

[a] $s\left[\sigma_{f(s)}^2\right]$ = Standard error of family within stand variance.

[b] Components of variances are presented as $\sigma^2 \times 10^{+2}$.

Genetic gains for selection of the best stands and the best families and individuals within families was calculated for second-year heights at the Highland Rim. It was assumed that no genetic gain was made in the initial selection of parent trees. The formula used for predicting the genetic gain (G), for family and within family selection is represented as:

$$G = i_1 \frac{\sigma^2_{f(s)}}{\sigma_1} + i_2 \frac{3\,\sigma^2_{f(s)}}{\sigma_2} \quad \text{(Namkoong, \underline{et}.\underline{al}., 1965)}$$

Where:

i_1 = family selection intensity

i_2 = within family selection intensity

$$\sigma_1^2 = \frac{\sigma_w^2}{nr} + \frac{\sigma^2_{f(s)r}}{r} + \sigma^2_{f(s)}$$

$$\sigma_2^2 = \sigma_w^2 + \sigma^2_{f(s)r}$$

Genetic gains were calculated for two selection schemes. The two schemes differ only in that in Scheme I the tallest families were chosen from families of all stands, while in Scheme II the tallest families were chosen from families of the seven stands with greatest mean height. Table 5 gives the number of stands, families, and individuals involved in each selection scheme. There was an average of 9.2 individuals per family, therefore, when one individual per family is selected the selection intensity is 1.70 or 11 percent.

Table 5. Number of stands, families, and individuals selected and selection intensity for among and within families using Scheme I and II at the Highland Rim

Selection Scheme[a]	Number of Stands	Number of Families	Number Families and Individuals Selected	Selection Intensity	
				Family	Within Family
I	12	127	45	1.04	1.70
II	7	72	45	0.60	1.70

[a] Scheme I - selection of tallest individuals of the tallest 45 families of all stands.
Scheme II - selection of tallest individuals of the tallest 45 families of the best seven stands.

Components of variance used for the gain estimates of Scheme I were derived from an analysis of variance using all the families, but only families of the selected seven stands were used for Scheme II. The most striking difference among estimates of variance components for these two methods is the larger (27 percent) among family within stand variance for the selected seven tallest stands. Estimated genetic gains from the two proposed selection schemes are presented in Table 6. Both selection schemes give essentially the same gains. Gains from selection Scheme I and II were 0.74 and 0.77 feet, respectively, or 21 and 25 percent. This result compares well with the five percent estimated gain obtained fram mass selection.

Table 6. Gains from family and within family selection and estimated mean heights of two-year-old progenies at the Highland Rim test site

Selection Schemes	Gains (feet) Family	Within Family	Total	Estimated Population Mean Height (feet)
I	0.25	0.49	0.74	4.27
II	0.16	0.61	0.77	4.43

[a] Estimated second-year mean height of a population derived from random mating of selected trees.

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