



Seed Source Variations in Growth and Ornamental Traits of Virginia Pine

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SEED SOURCE VARIATION IN GROWTH AND ORNAMENTAL TRAITS OF VIRGINIA PINE

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INTRODUCTION

The Christmas tree Industry in the South has grown rapidly due to a large demand for a freshly-cut product and increased costs for non-regional trees. Virginia pine (*Pinus virginiana* Mill.) has become the most popular species for Christmas tree production in the Southern United States. Before the rise in popularity of Virginia pine, few Christmas trees were produced in the South because no acceptable native species were recognized. Fast juvenile growth, multiple branching, and good response to shearing give Virginia pine excellent potential for Christmas tree production. Still, there are serious problems with the planting stock available to growers. To increase the long term market share, characteristics affecting growth and form of Virginia pines need to be improved.

This study is an investigation of phenotypic and genetic variation in Virginia pine. Investigation of variation is the first, and possibly the most, important step of any breeding program; without variation in a population, there can be no genetic improvement. Detection of any trends of variation early in the breeding process can prove to be very valuable.

As important as variation is, it is of little value if the traits measured are not pertinent to the objectives of the breeding program. The traits used must be assessed very carefully to achieve the desired improvement of critical characteristics. In the past, the Christmas tree industry used many criteria in the selection of traits for breeding. Most of these were based on subjective estimates of form characteristics. This study is an attempt to quantify form characteristics using a series of measured traits.

Genetic variation in Virginia pine is of primary interest in this study. In another study, Genys (5) established a range-

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wide provenance test that included 17 provenances from 10 states. His seventh-year results showed that southern seedlots from Alabama, Tennessee, South Carolina, and Virginia had high mortality when planted north of the species range on poor sites and that trees from the southernmost sources in Alabama had intermediate growth rates in comparison to trees from other sources. He also reported a 20 to 23 percent difference in height growth among all sources. In the fifteenth-year results of the same provenance test, Genys et al. (6) reported that in the most southerly plantations the northern sources grew less than average. In the northern plantations the southern sources grew at average or above average rates. Certain North Carolina and Tennessee sources proved to be superior in height growth throughout the study. The southern sources tended to have the longest needles but needle length was not correlated with height growth. Generally, across all traits studied there were 10 to 20 percent differences between the best and poorest geographic seed-sources. In addition, a north-south trend could be detected statistically if all data were considered.

Virginia pine is usually utilized only for pulp production because of its excessive number of knots. The branching characteristics of the species made it attractive for Christmas tree production. In an investigation of dry matter distribution, Matthews et al. (7) used 20 selected Virginia pine trees to show genetic control over some crown characteristics. The test population was established using trees selected for self pruning ability. They estimated heritability for height at age 8 to be 0.32, heritability for diameter to be 0.28, and heritability for branch weight to be 0.32.

Heritability estimates for young Virginia pine have proven to be quite variable. Evans and Thor (4) reported significant source differences in a test of material from Kentucky and Tennessee. Their heritability estimates for second-year heights varied from location to location of 0.16 to 0.48 and for diameters from 0.08 to 0.41. Meier and Goggans (8) reported heritabilities of 0.50 for first-year heights, 0.49 for second-year heights, 0.29 for fifth-year heights, and 0.59 for eighth-year heights. They also reported heritabilities of 0.33 for diameter after the eighth year and 0.31 for needle length.

Bailey et al. (1) reported strong genetic influence on some crown characteristics. Using a population synthesized from

paired poorly-pruned and well-pruned trees, they estimated heritability for branch angle as 0.75, for branch diameter as 0.29, for branch length as 0.42, for total number of branches as 0.21, and for number of nodes as 0.32. They found branch length to be the only crown characteristic showing significant differences between the progeny of the poorly pruned and the well pruned trees.

Belanger and Bramlett (2) used Virginia pine to devise a ranking system that they called the Christmas tree index. This index combined tree height with subjective rankings of tree density, tree symmetry, and stem straightness. This measurement was computed to assess the relative quality of unsharped trees for use in Christmas tree breeding.

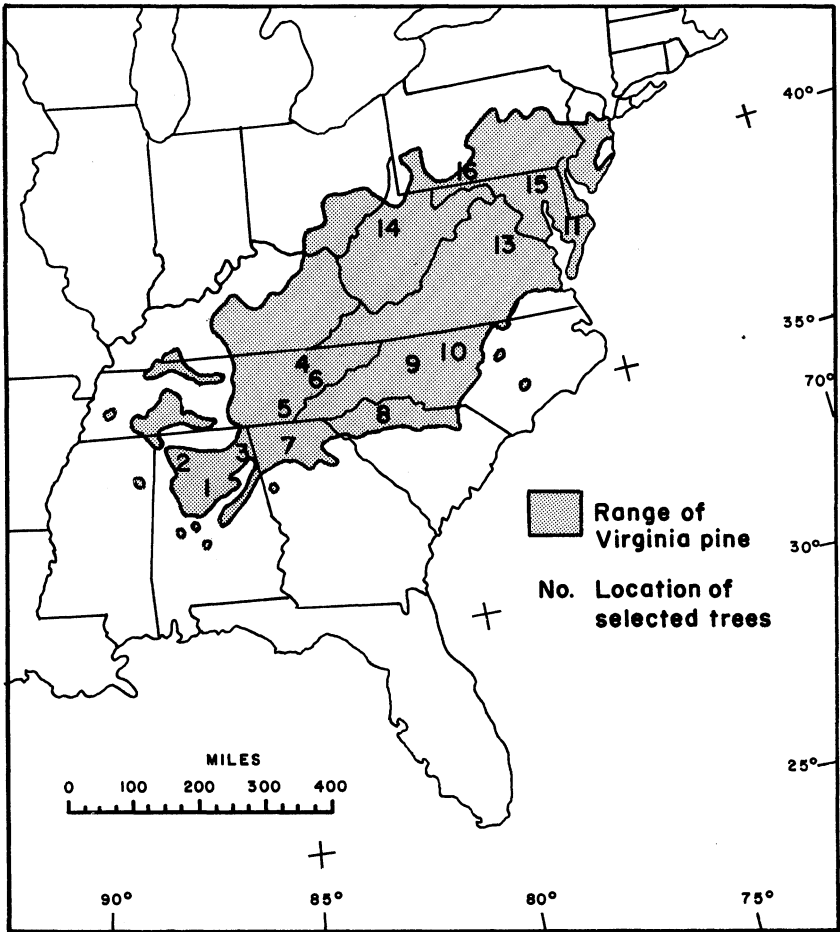
If a quantifiable index can be developed for evaluating tree quality, it could be utilized with heritability estimates to evaluate possible improvement through a breeding program.

MATERIALS AND METHODS

In 1975, studies were initiated at Auburn University and seeds collected for a seed-source progeny test of Virginia pine to evaluate ornamental traits. Cooperators were asked to collect cones from 10-12, average to good, mature trees in their areas. These trees were to be at least one-quarter mile apart. Cones were collected from 167 parent trees over the north-eastern and southern portions of the native range of the species, figure. All cones were kept separated by parent tree. These seeds were used to establish three seed-source progeny tests at different locations. The sites represented three physiographic regions in Alabama. Plantings were located in DeKalb County, representing the upland region; Lee County, representing the Piedmont region; and Escambia County, representing the Coastal Plain. Material in the Lee County location was utilized for this study. Identification of the source counties can be found in table 1.

Seeds from the 167 parent trees were planted in the spring of 1977 at Stauffer Nursery near Opelika, Alabama, in a randomized complete block design with five replications. The Lee County location of the seed-source progeny test was established in the winter of 1978. At the time of planting, the site was an old pasture that had been in recent use.

The seedlings were hand planted on an eight by eight-foot spacing in randomized complete block design with the seed-



Virginia pine seed selection sites.

lings kept in the same block as in the nursery. Families were randomized within blocks without consideration of the sources from which they originated and were represented in each block by a 10-tree row plot.

Measurements of all traits were made at the end of the third growing season. Six of 10 trees in the family plots were chosen for intensive measurement, while total heights were measured on all trees.

Ornamental Characteristics

Distances between nodes were determined by measuring total heights and distances down from the tip to the third,

TABLE I. ORIGINAL LOCATIONS OF SEED-SOURCES

Source number	Location
1	Jefferson County, Alabama
2	Lawrence County, Alabama
3	DeKalb County, Alabama
4	Anderson County, Tennessee
5	Polk County, Tennessee
6	Blount County, Tennessee
7	Lumpkin County, Georgia
8	Spartanburg County, South Carolina
9	Iredell County, North Carolina
10	Guilford County, North Carolina
11	Wicomico County, Maryland
13	Orange County, Virginia
14	Ritchie County, West Virginia
15	Carroll County, Maryland
16	Bedford County, Pennsylvania

fourth, and fifth nodes. The internodal distances were obtained by subtraction and were the means of two values.

The number of branches per node was determined by counting the branches on those same three nodes used in the internodal length determination. The mean of the number of branches on these nodes was used in subsequent calculations.

Crown width was measured in two directions. The first measurement was made where the width was maximum and the second was made 90 degrees from the first. These two measurements were then averaged and the mean was used to represent the crown width variable.

Angle and diameter of the limbs on the third and fourth nodes from the top were measured. Limb angles were measured with a large protractor that was positioned against the stem of the tree with the zero index pointed at the top of the tree. These limb angles were averaged for each tree. Diameter of one of the limbs at each of the two nodes was measured near the place of attachment to the stem. These two diameter measurements were then averaged.

Diameter outside bark at 6 inches from the ground was measured to the nearest centimeter and was called 'diameter' throughout the study.

Finally, taper was calculated as a function of crown width and height. This ratio of crown width divided by height is used as one criterion in sheared trees by the United States Department of Agriculture in assigning grades to Christmas trees.

All of the analyses of variance, covariance, and cross product analyses were based on the following linear model:

$$Y(ijk) = \mu + B(i) + S(k) + P(S)_{jk} + E(ijk)$$

where:

$Y(ijk)$ = the mean of the plot in the i th block of the j th parent nested within the k th source.

μ = the overall mean.

$B(i)$ = the effect of the i th block measured as a deviation of the block mean from μ .

$S(k)$ = the effect of the k th source measured as a deviation of the source mean from μ .

$P(S)_{jk}$ = the effect of the j th parent nested within the k th source measured as a deviation on this effect mean from μ .

$E(ijk)$ = the random variable that is assumed to be normally distributed with mean of zero and variance of sigma squared.

The experimental error was composed of the interaction of the blocks, sources, and parents within sources. This error term was used in tests to measure the failure of the parent tree plots within seed-sources to be the same in all blocks. The degrees of freedom vary with the variable of interest but the design and model remain the same. In the cross-product analysis, a value was estimated for the missing plot to balance the design. Cross-product terms replaced expected mean squares in the estimation of the genetic correlations.

All analyses were based on plot means in order to reduce the size of the data matrix. As a result, the sampling component was included in the experimental error. The within-plot error was estimated by conducting a one-way analysis of variance on the plots and dividing the error term by the harmonic mean of the number of individuals measured for a particular trait in the plots.

Duncan's multiple range test was used to separate source means of all traits that were found to have significant F-values in the analysis of variance.

Heritabilities

Heritabilities were calculated using equations given by Namkoong (9).

Family Heritability:

$$Fh^2 = \frac{\text{Var } p(s)}{[\text{Var}(w)/hb] + [\text{Var}(e)/b] + \text{Var } p(s) + \text{Var}(s)}$$

Single Tree Heritability:

$$Sh^2 = \frac{4 \text{ Var } p(s)}{\text{Var}(w) + \text{Var}(e) + \text{Var } p(s) + \text{Var}(s)}$$

where:

Var p(s) = the variance component of the parent tree within seed-source.

Var (w) = the variance component of the plants within plot.

Var (e) = the variance component between plots.

Var (s) = the variance component between seed-sources

h = the harmonic mean of the number of plants per plot.

b = the number of blocks at the planting site.

The narrow sense heritability is a ratio of the additive or linear portion of the genetic variance to the total variation found in the population. These ratios are used in the calculation of expected gain from selection in a population. The methods of calculating these ratios change depending on the form of selection being used. These ratios are often used as a gauge of the amount of improvement that can be made for a given trait and also the rate at which the improvement can be made. Great care must be used when extrapolating these estimates beyond the experimental material. Formulae used in these calculations give generally smaller values than can be obtained with other formulae available for use.

Phenotypic and genetic correlations were used to evaluate the relationships among all traits. These can be used to interpret effects of indirect selection on traits that exhibit pleiotropy.

RESULTS AND DISCUSSION

Growth Characteristics

Height growth differences were statistically significant among seed-sources and among parents within seed-sources, table 2. When subjected to a Duncan's multiple range test, means of

sources were divided into 7 groups, table 3. Trees from Blount County, Tennessee, and from Spartanburg County, South Carolina, were significantly taller than 60 percent of the other seed-sources. Northernmost sources were grouped in the lower third of the means while the southern sources were in the middle third. These groupings exhibit trends that are not precisely clinal but do have a north-south relationship. These findings agree with Genys (5) who found that sources from North Carolina and Tennessee exhibited the best overall growth in a range-wide test in which the outplantings were considerably further north than in this study. If the trends were truly clinal, the southern sources would be expected to outperform the other sources.

Height is a very important characteristic in the improvement of Virginia pine for Christmas tree production. Most grading systems used to price Christmas trees rely heavily on height and many 'choose and cut' operations use height as a primary criterion for sales. Height seems to be the most profitable trait for improvement, if the pricing scheme is the only consideration. There are some problems with this approach. Increased height growth means increased shearing is required to control density. As Silen and Wilson (10) pointed out in their work with Douglas-fir, faster growing families sometimes were rated low because of gaps in the foliage whorls. Thus, distance between the whorls of branches must also be considered in the development of an improved variety.

Heritability of height was estimated to be 0.19 for family selection and 0.16 for individual tree selection. This is not very high, but it does give an indication that improvement of the trait is possible. This estimate is lower than those found by other investigators, but no estimates were available for comparison using a population similar to that sampled in this study.

TABLE 2. ANALYSIS OF VARIANCE AND VARIANCE COMPONENT ESTIMATES FOR THE TRAIT OF TOTAL HEIGHT

Source of variation	Degrees of freedom	Mean square	Variance component estimate
Blocks	4	42,970.8	
Sources	14	8,593.6**	142.7
Parent (Sources)	152	723.4**	55.0
Experimental Error	658	450.1	325.1
Within Plot Error	5,795	887.9	887.9

**significant at alpha = 0.01

TABLE 3. SOURCE MEANS FOR THE TRAIT OF TOTAL HEIGHT

Source	Total height ¹
	(cm)
Blount County, Tenn.	173.2 a
Spartanburg County, S.C.	169.5 a
Iredell County, N.C.	165.5 a b
Lumpkin County, Ga.	163.9 a b
Polk County, Tenn.	163.8 a b
Anderson County, Tenn.	161.8 a b c
DeKalb County, Ala.	156.5 b c d
Lawrence County, Ala.	155.8 b c d
Jefferson County, Ala.	154.8 b c d
Guilford County, N.C.	154.5 b c d
Orange County, Va.	150.8 c d e
Wicomico County, Md.	148.4 d e
Ritchie County, W. Va.	140.9 e f
Carroll County, Md.	134.7 f g
Bedford County, Pa.	125.1 g

¹Means followed by the same letter do not differ at the 0.05 level of significance, Duncan's Multiple Range Test.

Differences in crown widths were found to be highly significant among seed-sources and among parent trees within seed-sources, table 4. When subjected to a Duncan's multiple range test, the means of the sources were divided into five groups, table 5. The Blount County, Tennessee, source had the largest mean and the means of the northern sources were grouped in the lower one-third of the array.

Crown width in unsheared trees is a measure of growth potential of lateral branches and could be used to project a tree's ability to cover flaws in the crown. When laterals have

TABLE 4. ANALYSIS OF VARIANCE AND VARIANCE COMPONENT ESTIMATES FOR THE TRAIT OF CROWN WIDTH

Source of variation	Degrees of freedom	Mean square	Variance component estimate
Blocks	4	28,643.0	
Sources	14	4,830.9**	77.2
Parent (Sources)	152	573.3**	44.1
Experimental Error	658	353.2	246.7
Within Plot Error	3,906	587.2	587.2

**significant at alpha = 0.01

a good growth rate, shearing response and density should be good. However, selection of extremely large crown widths will cause an increase in shearing expense.

For family selection, the heritability estimate was 0.23 and for individual tree selection it was 0.19. These values are about the same as for height, and the rate of improvement of the trait could be somewhat slow.

Taper differences were found to be significant among both seed-sources and parents within seed-sources, table 6. A Duncan's multiple range test divided the means into five groups,

TABLE 5. SOURCE MEANS FOR THE TRAIT OF CROWN WIDTH

Source	Crown width ¹
	(cm)
Spartanburg County, S.C.	134.7 a
Blount County, Tenn.	133.5 a
Jefferson County, Ala.	132.1 a b
Anderson County, Tenn.	131.8 a b
Iredell County, N.C.	129.1 a b c
DeKalb County, Ala.	128.4 a b c
Lumpkin County, Ga.	127.5 a b c
Polk County, Tenn.	125.8 a b c d
Lawrence County, Ala.	124.4 b c d
Orange County, Va.	122.5 b c d
Wicomico County, N.C.	119.8 c d
Guilford County, N.C.	119.3 c d
Ritchie County, W. Va.	116.9 d
Carroll County, Md.	107.3 e
Bedford County, Pa.	99.9 e

¹Means followed by the same letter do not differ at the 0.05 level of significance, Duncan's Multiple Range Test.

TABLE 6. ANALYSIS OF VARIANCE AND VARIANCE COMPONENT ESTIMATES FOR THE TRAIT OF TAPER

Source of variation	Degrees of freedom	Mean square	Variance component estimate
Blocks	4	0.0036	
Sources	14	0.0306**	.0004
Parent (Sources)	152	0.0085**	.0010
Experimental Error	58	0.0037	.0037
Within Plot Error	3,905	0.0110	.0110

**significant at alpha = 0.01

TABLE 7. SOURCE MEANS FOR THE TRAIT OF TAPER

Source	Taper ¹
Jefferson County, Ala.	0.830 a
Ritchie County, W. Va.	0.814 a b
Anderson County, Tenn.	0.801 a b c
DeKalb County, Ala.	0.799 a b c d
Orange County, Va.	0.796 a b c d
Wicomico County, Md.	0.788 b c d
Spartanburg County, S.C.	0.786 b c d
Lawrence County, Ala.	0.786 b c d
Carroll County, Md.	0.781 b c d
Iredell County, N.C.	0.773 b c d e
Bedford County, Pa.	0.771 c d e
Lumpkin County, Ga.	0.760 c d e
Guilford County, N.C.	0.759 d e
Blount County, Tenn.	0.758 d e
Polk County, Tenn.	0.738 e

¹Means followed by the same letter do not differ at the 0.05 level of significance, Duncan's Multiple Range Test.

table 7. The ranking of the means was unlike any of the other growth traits measured because this variable compared the lateral branch growth to the primary leader growth. The pattern of taper differences in the seed-sources did not exhibit the same north-south trends associated with the other growth related traits.

Heritability of taper was estimated to be 0.46 for family selection and 0.29 for individual tree selection. This high family heritability suggests that improvement of this trait may be rapid in early generations if acceptable selection intensity is used. In unshaired trees, a very high taper indicates that the source exhibited a bush-like characteristic, while a low taper indicates the source has a candlestick-like appearance. The value and direction of improvement of this trait is still in question.

Differences in ground line diameter were found to be highly significant among seed-sources and among parent trees within seed-sources, table 8. The means were ranked into six groups by a Duncan's multiple range test, table 9. These means exhibited the same distributional trends found with height and crown width. Northern sources had the lowest means

TABLE 8. ANALYSIS OF VARIANCE AND VARIANCE COMPONENT ESTIMATES FOR THE TRAIT OF GROUND LINE DIAMETER

Source of variation	Degrees of freedom	Mean square	Variance component estimate
Blocks	4	36.62	
Sources	14	3.28**	0.05
Parent (Sources)	152	0.61**	0.03
Experimental Error	664	0.44	0.33
Within Plot Error	3,906	0.62	0.62

**significant at alpha = 0.01.

TABLE 9. SOURCE MEANS FOR THE TRAIT OF GROUND LINE DIAMETER

Source	Ground line diameter ¹
	(cm)
Spartanburg County, S.C.	4.23 a
Blount County, Tenn.	4.16 a b
Iredell County, N.C.	4.03 a b c
Lumpkin County, Ga.	4.01 a b c
Jefferson County, Ala.	3.97 a b c d
DeKalb County, Ala.	3.96 a b c d
Anderson County, Tenn.	3.94 a b c d
Orange County, Va.	3.91 a b c d
Polk County, Tenn.	3.88 a b c d
Lawrence County, Ala.	3.83 b c d
Guilford County, N.C.	3.78 c d e
Wicomico County, Md.	3.66 d e
Ritchie County, W. Va.	3.66 d e
Carroll County, Md.	3.50 e f
Bedford County, Pa.	3.28 e f

¹Means followed by the same letter do not differ at the 0.05 level of significance, Duncan's Multiple Range Test.

while central sources had the largest means. Again, southern sources fell into the middle of the rankings. The seed-source from Spartanburg County, South Carolina, had a mean significantly larger than 47 percent of the other sources. Estimates of heritability were 0.19 for family selection and 0.13 for individual tree selection.

Form Characteristics

Differences between internodal lengths were found to be highly significant both among seed-sources and among parents

within seed-sources, table 10. The means were subjected to a Duncan's multiple range test, table 11 and separated into six groups. The internodal length trait showed a north-south relationship similar to that of the height trait. The seed-source from Blount County, Tennessee, had a mean internodal length significantly longer than 80 percent of all other seed-sources.

No artificial means of controlling the internode length were used in this experiment. Therefore, the lengths measured give an average length of a growth flush. Like other southern pines, Virginia pine puts on more than one growth flush per season. This is very desirable in the Christmas tree industry,

TABLE 10. ANALYSIS OF VARIANCE AND VARIANCE COMPONENT ESTIMATES FOR THE TRAIT OF INTERNODAL LENGTH

Source of variation	Degrees of freedom	Mean square	Variance component estimate
Blocks	4	319.76	
Sources	14	40.29**	0.59
Parent (Sources)	152	7.54**	0.63
Experimental Error	658	4.41	1.57
Within Plot Error	3,906	15.52	15.52

**significant at alpha = 0.01

TABLE 11. SOURCE MEANS FOR THE TRAIT OF INTERNODAL LENGTH

Source	Internodal length ¹
	(cm)
Blount County, Tenn.	18.8 a
Iredell County, N.C.	17.7 a b
Polk County, Tenn.	17.4 b c
Spartanburg County, S.C.	17.2 b c d
Lawrence County, Ala.	17.2 b c d
Anderson County, Tenn.	17.1 b c d
Lumpkin County, Ga.	17.0 b c d
Jefferson County, Ala.	17.0 b c d
DeKalb County, Ala.	16.9 b c d
Guilford County, N.C.	16.7 b c d e
Ritchie County, W. Va.	16.3 c d e
Wicomico County, Md.	16.3 c d e
Orange County, Va.	16.1 d e f
Carroll County, Md.	15.6 e f
Bedford County, Pa.	15.0 f

¹Means followed by the same letter do not differ at the 0.05 level of significance, Duncan's Multiple Range Test.

but has made interpretation of this internode trait difficult. It is not known if the longer internode length of some seed-sources resulted from having fewer nodes. The high correlation of this trait with height could mean that faster growing trees had longer internode lengths. In Christmas tree production, this trait would be controlled by shearing the tree. This forces the tree to put on whorls of branches and controls internode length. It is very desirable to have many growth flushes because it will result in denser foliage and in average or below average internode lengths.

Heritability of the internodal length was estimated to be 0.31 for family selection and 0.14 for individual tree selection. Compared with the other traits investigated, this characteristic showed good potential for improvement. However, if the distance between the nodes is maximized and the additional shearing needed is not carried out, the resulting product may not have the desired density.

Differences in limb angle were found to be highly significant among seed sources and among parents within seed-sources, table 12. Means of the seed-sources were separated into five groups, table 13. The seed-source from Bedford County, Pennsylvania, had a greater limb angle than 80 percent of the other sources. The means of the sources showed a trend that was opposite to the north-south relationship found in many of the other traits. This is because as the limb approached a perpendicular position to the stem, the limb angle increased in magnitude. The slower growing trees exhibited larger limb angles.

The value of limb angle in Christmas trees is not in question. It has been recognized for many years that this is an important trait. The important question is the degree of angle that is desirable. Limbs with acute angles to the bole of the tree tend to hide flaws well, while limbs with large angles can be trimmed

TABLE 12. ANALYSIS OF VARIANCE AND VARIANCE COMPONENT ESTIMATES FOR THE TRAIT OF LIMB ANGLE

Source of variation	Degrees of freedom	Mean square	Variance component estimate
Blocks	4	263.4	
Sources	14	369.8**	5.4
Parent (Sources)	152	74.5**	8.4
Experimental Error	658	33.0	13.1
Within Plot Error	3,906	108.3	108.3

**significant at alpha = 0.01

at any time without leaving large gaps in the foliage. Heritability estimates for limb angle were 0.26 for family selection and 0.12 for individual tree selection.

Differences in the length of needles were found to be highly significant among seed sources and among parents within seed-sources, table 14. Using Duncan's multiple range test, table 15 the means were separated into seven groups, with the sources having the longest needle lengths being significantly different than 80 percent of the other sources. This trait exhibited a precise clinal relationship.

Heritability of needle length was the highest of any of the

TABLE 13. SOURCE MEANS FOR THE TRAIT OF LIMB ANGLE

Source	Limb angle ¹
	(degrees)
Bedford County, Pa.	66.0 a
Carroll County, Md.	64.9 a b
Jefferson County, Ala.	62.3 b c
Orange County, Va.	62.1 b c d
Anderson County, Tenn.	62.1 b c d
Ritchie County, W. Va.	60.9 c d e
Wicomico County, Md.	59.7 c d e
Lawrence County, Ala.	58.9 c d e
Guilford County, N.C.	58.9 c d e
DeKalb County, Ala.	58.6 c d e
Polk County, Tenn.	58.3 d e
Spartanburg County, S.C.	58.2 e
Blount County, Tenn.	57.9 e
Iredell County, N.C.	57.7 e
Lumpkin County, Ga.	57.3 e

¹Means followed by the same letter do not differ at the 0.05 level of significance, Duncan's Multiple Range Test.

TABLE 14. ANALYSIS OF VARIANCE AND VARIANCE COMPONENT ESTIMATES FOR THE TRAIT OF NEEDLE LENGTH

Source of variation	Degrees of freedom	Mean square	Variance component estimate
Blocks	4	3.6	
Sources	14	8.2**	0.12
Parent (Sources)	152	1.5**	0.22
Experimental Error	658	0.4	0.23
Within Plot Error	3,906	1.07	1.07

**significant at alpha = 0.01

TABLE 15. SOURCE MEANS FOR THE TRAIT OF NEEDLE LENGTH

Source	Needle length ¹
	(cm)
Jefferson County, Ala.	7.50 a
Lawrence County, Ala.	7.26 a b
Polk County, Tenn.	7.15 a b c
Ritchie County, W. Va.	6.96 b c d
DeKalb County, Ala.	7.00 b c d
Spartanburg County, S.C.	6.88 b c d e
Iredell County, N.C.	6.83 b c d e
Blount County, Tenn.	6.68 c d e f
Lumpkin County, Ga.	6.63 c d e f g
Wicomico County, Md.	6.60 d e f g
Anderson County, Tenn.	6.60 d e f g
Orange County, Va.	6.51 d e f g
Guilford County, N.C.	6.42 e f g
Carroll County, Md.	6.22 f g
Bedford County, Pa.	6.14 g

¹Means followed by the same letter do not differ at the 0.05 level of significance, Duncan's Multiple Range Test.

traits measured. Estimates were 0.53 for family selection and 0.56 for individual tree selection. These findings disagree with those reported by Meier and Goggans (8), who found no source differences and estimated heritability to be 0.31. These differences can be explained by differences in the material used to conduct the different experiments. The variation over such a wide area as sampled in this study should be greater than that of Meier's study which involved a much smaller geographical area.

Differences between limb diameters were not significant among seed-sources, but were highly significant among parents within seed sources, table 16. No multiple range test was conducted because of the lack of significant differences among seed-sources.

Heritability of limb diameter was estimated to be 0.41 for family selection and 0.16 for individual tree selection. Limb diameter has been shown to be highly correlated with the number of buds and new shoots stimulated by shearing (3).

Differences in number of branches per node were highly significant among seed-sources and among parent trees within

seed-sources, table 17. A Duncan's multiple range test separated the means into four groups, table 18.

Heritability of the number of branches per node was esti-

TABLE 16. ANALYSIS OF VARIANCE AND VARIANCE COMPONENT ESTIMATES FOR THE TRAIT OF LIMB DIAMETER

Source of variation	Degrees of freedom	Mean square	Variance component estimate
Blocks	4	4.2	
Sources	14	1.8	0.01
Parent (Sources)	152	1.1**	0.09
Experimental Error	658	0.7	0.28
Within Plot Error	3,906	2.01	2.01

**significant at alpha = 0.01

TABLE 17. ANALYSIS OF VARIANCE AND VARIANCE COMPONENT ESTIMATES FOR THE TRAIT OF NUMBER OF BRANCHES PER NODE

Source of variation	Degrees of freedom	Mean square	Variance component estimate
Blocks	4	4.19	
Sources	14	0.52**	0.01
Parent (Sources)	152	0.24**	0.02
Experimental Error	658	0.12	0.03
Within Plot Error	3,906	0.52	0.52

**significant at alpha = 0.01

TABLE 18. SOURCE MEANS FOR THE TRAIT OF NUMBER OF BRANCHES PER NODE

Source	Number of branches per node ¹
Blount County, Tenn.	3.9 a
Guilford County, N.C.	3.9 a b
Iredell County, N.C.	3.8 a b c
Lumpkin County, Ga.	3.8 a b c
Jefferson County, Ala.	3.8 a b c
Spartanburg County, S.C.	3.8 a b c
Polk County, Tenn.	3.8 a b c d
Anderson County, Tenn.	3.7 a b c d
Wicomico County, Md.	3.7 a b c d
Lawrence County, Ala.	3.7 b c d
Bedford County, Pa.	3.7 b c d
Ritchie County, W. Va.	3.6 c d
Orange County, Va.	3.6 c d
DeKalb County, Ala.	3.6 c d
Carroll County, Md.	3.5 d

¹Means followed by the same letter do not differ significantly at the 0.05 level of significance, Duncan's Multiple Range Test.

mated to be 0.26 for family selection and 0.12 for individual tree selection. These estimates are in agreement with those of Bailey et al (1) for number of branches of 0.21. The characteristic has potential for improvement and is very important in Christmas tree crown form and foliage density. Since the trait is statistically different among sources, great care must be used in the selection of seed-sources and families.

Correlations

Correlations among traits are important in indirect selection. Improving a single trait that is highly correlated with many other desirable traits is one of the fastest ways to improve a variety. To examine the relationship of all measured traits, both simple and genetic correlations were calculated, tables 19 and 20.

Phenotypic correlations between height and all other characteristics except taper, in the growth characteristics group, were positive. All of these positively correlated traits had correlation coefficients greater than 0.80 and were highly significant. Genetic correlations tended to be lower and had values of 0.54 for crown width, 0.53 for ground line diameter, and -0.32 for taper. These high correlations with crown width and ground line diameter seem to suggest that genes controlling these traits are related in some manner. In fact, these traits may be controlled by the same block of genetic material. There is the possibility of linkage or pleiotrophy, but often it is hard to distinguish these relationships in complex traits with open-pollinated material. Taper had a reverse trend that may have been caused by the same reasons.

Among crown form characteristics, the internodal distance trait had high positive phenotypic correlations with all growth characteristics except taper. These high correlations suggest that increased growth rate, expressed through height growth, is caused by increasing the length of the growth flush. This makes internode distance increase as total height increases. This increased growth rate also caused high positive correlations with diameter and crown width. Genetic correlations were not as strong as phenotypic correlations. A large amount of environmental and source influence could account for the differences between genetic and phenotypic correlations.

The number of branches per node had phenotypic correlations with growth characteristics that ranged from 0.23 for

TABLE 19. SIMPLE CORRELATIONS BETWEEN ALL CHARACTERISTICS

	Height	Distance between nodes	Number of branches	Limb angle	Limb diameter	Crown width	Needle length	Diameter
Height								
Distance between nodes	0.52							
Number of branches ...	0.23	0.50						
Limb angle ..	-0.14	-0.10	-0.01*					
Limb diameter ...	0.25	0.24	0.12	-0.24				
Crown width	0.83	0.43	0.18	-0.03	0.26			
Needle length	0.22	0.17	0.04	-0.05	0.24	0.20		
Diameter	0.81	0.40	0.20	-0.09	0.28	0.84	0.19	
Taper	-0.03	-0.03*	-0.02*	0.13	0.09	0.50	0.04	0.25

Numbers followed by * are not significant at alpha = 0.05.

TABLE 20. GENETIC CORRELATIONS BETWEEN ALL CHARACTERISTICS

	Height	Distance between nodes	Number of branches	Limb angle	Limb diameter ..	Crown width	Needle length .	Diameter
Height								
Distance between nodes	0.64							
Number of branches ...	0.21	0.04						
Limb angle ..	-0.34	-0.31	-0.18					
Limb diameter ...	0.17	0.39	0.41	0.03				
Crown width	0.54	0.18	-0.02	0.07	0.04			
Needle length	0.02	0.35	0.15	0.06	0.40	-0.23		
Diameter	0.53	0.14	0.24	-0.30	0.36	0.62	-0.05	
Taper	-0.27	-0.55	-0.30	0.47	-0.19	0.54	-0.45	0.22

height to -0.03 for taper. The genetic correlations were lower and suggest that only minor improvement could be expected in this trait through indirect selection. A genetic correlation between the number of branches per node and limb diameter of 0.41 was found. This showed relatively strong relationships between branching characteristics.

The limb characteristics had quite different trends in their correlations. Limb diameter had positive phenotypic correlations with other traits ranging from 0.28 to 0.09. Only limb angle gave a negative correlation with diameter. Limb diameter had even larger genetic correlations. The limb angle trait was negatively correlated with all other traits except taper in simple phenotypic correlations. In genetic correlations, all coefficients, except taper, were negative or very small. This inverse relationship could be beneficial in trees that need to hide flaws through control of limb angle.

CONCLUSIONS

Height growth could be the most important trait investigated in this study. The benefit of increased height growth is a more vigorous and responsive tree to cultural practices. Height was significantly different among seed-sources, so by choosing the correct source initial improvement of present stock can be made. Increased height growth could also increase internode length and lateral branch development. If height maximization is chosen for a selection scheme, more intensive shearing of the tree must follow, but it is likely that a more dense tree would result. If the additional shearing were not done, it is possible that the tree will not have sufficient density for a good quality Christmas tree. Height is highly correlated with all other growth characteristics, so improvement can be made in these traits if height is used as a criterion for selection. Although the heritability is low for height, selection within seed-sources could yield good gains early in a breeding program. The high correlation of height with some of the crown characteristics may be used for indirect selection of these traits and production of a more dense tree.

Number of branches per node is one of the most important traits affecting the density of the tree and must be selected for improvement. Its weak correlations with other important traits make it necessary to include it in the general scheme of selection.

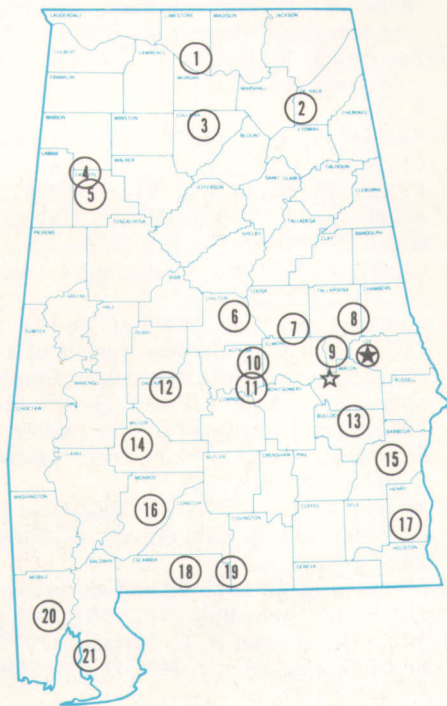
Significant differences among seed-sources indicated improvement could be made if appropriate sources were chosen for breeding. Significant differences within sources indicated additional improvement could be realized if selection beyond the seed-source level to the half-sib family and individual level was practiced. To preserve variation in the population, a percentage of several sources could be incorporated into a breeding program.

LITERATURE CITED

- (1) BAILEY, J. K., P. P. FERET, AND D. L. BRAMLETT. 1974. Crown character differences between well-pruned and poorly-pruned Virginia pine trees and their progeny. *Silvae Genetica* 23:181-185.
- (2) BELANGER, R. P., and D. L. BRAMLETT. 1975. Virginia pine (*Pinus virginiana*) as a Christmas tree. U.S.D.A. For. Serv. Res. Note SE 222. 8 pp.
- (3) BROWN JR., G. F. 1979. Shearing response of Virginia pine. *Amer. Christmas Tree J.* 23:49-51.
- (4) EVANS, R. M., and E. THOR. 1971. Estimates of heritabilities and genetic gains for populations of Virginia pine. *Proc. Eleventh Conf. South. For. Tree Impr.* p. 133-142.
- (5) GENYS, J. B. 1966. Georgraphic variation in Virginia pine. *Silvae Genetica* 15:72-76.
- (6) GENYS, J. B., J. W. WRIGHT, and D. C. FORBES. 1974. Intraspecific variation in Virginia pine, results of a provenance trial in Maryland, Michigan and Tennessee. *Silvae Genetica* 23:99-104.
- (7) MATHEWS, J. A., P. P. FERET, H. A. I. MADGWICK, and D. L. BRAMLETT. 1975. Genetic control of dry matter distribution in twenty half-sib families of Virginia pine. *Proc. Thirteenth South. For. Tree Impr. Conf.* p. 234-242.
- (8) MEIER, R. J., and J. F. GOGGANS. 1977. Heritabilities of height, diameter, and specific gravity of young Virginia pine. *Forest Science* 23:450-456.
- (9) NAMKOONG, G. 1979. Introduction to quantitative genetics in forestry. U.S.D.A., Tech. Bull. No. 1588. 342 pp.
- (10) SILEN, R. R., and B. C. WILSON. 1977. Genetically proven Douglas-fir Christmas trees. *J. For.* 75:255-259.

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2. Sand Mountain Substation, Crossville.
3. North Alabama Horticulture Substation, Cullman.
4. Upper Coastal Plain Substation, Winfield.
5. Forestry Unit, Fayette County.
6. Chilton Area Horticulture Substation, Clanton.
7. Forestry Unit, Coosa County.
8. Piedmont Substation, Camp Hill.
9. Plant Breeding Unit, Tallassee.
10. Forestry Unit, Autauga County.
11. Prattville Experiment Field, Prattville.
12. Black Belt Substation, Marion Junction.
13. The Turnipseed-Ikenberry Place, Union Springs.
14. Lower Coastal Plain Substation, Camden.
15. Forestry Unit, Barbour County.
16. Monroeville Experiment Field, Monroeville.
17. Wiregrass Substation, Headland.
18. Brewton Experiment Field, Brewton.
19. Solon Dixon Forestry Education Center, Covington and Escambia counties.
20. Ornamental Horticulture Substation, Spring Hill.
21. Gulf Coast Substation, Fairhope.