GENETIC IMPROVEMENT OF VIRGINIA PINE CHRISTMAS TREES

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Abstract.-- Approximately 10 half-sib families of Virginia pine from 9 different sources located in Alabama, Mississippi, South Carolina and Tennessee were grown and evaluated after 3 years in a test in north Alabama. Characteristics measured pertinent to Christmas tree production were height, diameter, branches per whorl, needle color, stem straightness and an overall quality rating. There were significant differences among sources, however an extreme amount of variation due to families-within-sources and among trees within each plot was also observed. Estimates of narrow-sense heritabilities ranged from a low of h = 0.10 for branches per whorl to a high of h = 0.35 for needle color. Stem straightness and height were found to be the most important characteristics for an improvement program. Potential genetic gains are presented with selection emphasizing the above two characteristics. Results of this study were compared to the results obtained in 3 similar tests demonstrating the effect of site quality on estimates of heritabilities and genetic gains.

Additional keywords: Pinus virginiana, heritability, genetic gain, provenance test.

In the 1960's and 1970's Christmas tree growers from several southern states organized growers' associations, signifying the establishment of the industry in the South. The primary species being utilized was Virginia pine (Pinus virginiana) (Davis et al. 1981; Hu and Main 1980). Over 10 million Virginia pines were planted across the south in the 1982-83 planting season (Murray, 1983). It is evident that the Virginia pine has been accepted by consumers and growers and has become the foundation species for the Christmas tree industry in the South.

The key to a successful Christmas tree operation is the production of high-quality trees. The quality of the trees is largely dependent upon the cultural practices used by the grower and the genetic potential of the tree. While appropriate cultural practices were established early, little has been done to improve the genetic component. Seedlings being used to establish Christmas tree plantations are grown from seed collected from wild stands or from parents in seed orchards originally selected for pulpwood characteristics. To compound the problem, a large portion of the seedlings (possibly between 30 and 50 percent) planted throughout the South have originated from one orchard comprised of eight clones, all selected

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from one county in Alabama.

Estimates of heritabilities are necessary before an effective breeding program can be initiated. They also are used to predict the amount of genetic gain that can be anticipated from the improvement program. The purpose of this study is to give estimates of heritabilities ("narrow sense") and the potential genetic gains they indicate for several characteristics of importance in Virginia pine Christmas tree production.

METHODS

During the fall of 1980, members of the S-128 Regional Research Project collected open-pollinated seed from 16 sources of Virginia pine. Seedlings from 8 of these collections, 2 from Alabama, 3 from South Carolina, 2 from Tennessee and 1 from Mississippi along with 11 half-sib families from the Kimberly-Clark Corporation seed orchard were used to establish a progeny test at Alabama A&M University during the spring of 1983. The 85 half-sib families representing the above 9 sources were planted in a randomized complete block design with six-tree-row family plots and 6 replications. Trees were planted 4 feet apart within each row and 7 feet between rows. One border row was planted around the entire test.

The planting site was mold-board plowed and disked prior to planting. Weeds were controlled within each row by use of herbicides and between rows by mowing. Several insecticide sprayings were made to control the Nantucket pine tip-moth. The trees were allowed to grow naturally for 3 years and were not sheared.

Each tree was evaluated for total height, stem diameter, crookedness, needle color, branches per whorl, and an overall quality rating. The evaluation of crook and rating were based on a five-point scale with 5 as the highest score given to the straightest or best trees.

The estimate of variation for sources and families-within-sources were obtained using both the General Linear Model (GLM) and Variance Component procedures of Statitistical Analysis Systems (SAS) (SAS Institute 1979). Estimates of narrow-sense heritabilities were then calculated. Source differences were then compared to results obtained from the Alabama A&M planting of the S-128 seed source study. Heritability estimates of this study (A&M -FWS) were compared to the results obtained in 2 previous half-sib progeny tests conducted by the author at Alabama A&M (A&M) and at the University of Tennessee Highland Rim Field Station (HRFS) and a similar progeny test conducted at Auburn University (Aub) (Warlick et.al. 1985). The average of all estimates of heritabilities was used to calculate potential genetic gains. This resulted in an estimate of genetic gain based on at least 7,000 trees from 200 half-sib families.

RESULTS AND DISCUSSION

Seed Source Differences

Two of the most important characteristics evaluated were height and crookedness. The means for these characteristics for the 9 sources are presented in Table 1. The means for these characteristics obtained in the A&M planting of the S-128 seed source study are also presented for comparison purposes.

TABLE 1. -- Seed source means for height and crook of Virginia Pine at 3 years.

Source	Height (cm) A&M (FWS)	Height (cm) A&M (S-128)	Crook (5-pt. scale) A&M (FWS)	Crook (5-pt. scale) A&M (S-128)
K-C	170.4^{a}		3.54^{ab}	
Telico, TN.	161.1^{b}	189.7^{a}	3.39^{bc}	2.73^{a}
Green Mt., AL.	160.7^{b}	183.0^{abc}	3.53^{ab}	3.00^{a}
S.C. Up. Pied.	159.0^{b}	188.8^{ab}	3.32^{c}	2.69^{a}
Anderson Co., TN.	157.8^{b}	177.3^{abc}	3.09^{d}	2.91^{a}
S.C. Mid. Pied	157.0^{bc}	193.7^{a}	3.30^{c}	3.35^{a}
S.C. Low. Pied	155.4^{bcd}	170.8^{bc}	3.38^{bc}	2.71^{a}
Tish.Co., MS.	151.6^{cd}	168.0^{c}	3.31^{c}	2.54^{a}
Dekalb Co., AL.	149.8^{d}	191.1^{a}	3.69^{a}	3.29^{a}

Means within each column followed by the same letter do not differ at the 0.05 level of significance according to the Duncan's Multiple Range Test.

The Kimberly-Clark Corporation orchard seedlings were significantly taller and ranked second in stem straightness. These results are expected because of the comparison of select seed orchard material versus seed collected from natural stands. There was only an 11 cm difference in height from the next tallest source to the shortest source. Also, the Dekalb Co., AL. source which was the shortest in the FWS study was the tallest in the S-128 study. This source also had the best score on stem straightness. Although the source differences were highly significant, it never accounted for more than 2.5 percent of the total variation observed in any of the characteristics which were evaluated. For these reasons, seed source differences are not considered to be very important in a breeding program for the improvement of Virginia pines for Christmas tree production in north Alabama. However, it should be noted that none of the seed sources tested originated more than 200 miles north of the test location.

Heritabilities

The estimates of narrow-sense heritabilities are presented in Table 2 for the results of this study, two other studies completed by the author and one study completed at Auburn University. The highest heritability obtained in all studies was for needle color, while the lowest was generally for branches per whorl. The heritability estimates also varied according to study location. The HRFS location yielded the best growth and lowest heritability for height. The A&M location yielded the poorest growth and highest height heritability primarily because of a heavy compacted soil. This study (FWS) was located next to the A&M study, but was mold-board plowed prior to planting, yielding much better growth and a lower heritability estimate. A higher heritability can be the result of either or both of the following: (1) the denominator of the equation, primarily the component due to the environmental variance, may be smaller, and/or (2) the additive genetic component, families-within-source, is larger. In these studies the relative amount of environmental variance, primarily the within-plot variance component, was lowest at the HRFS location and highest at the A&M location. This suggests that the better site benefits the poorer trees relatively more than the better trees, resulting in less tree-to-tree variation within a plot.

TABLE 1. -- Estimates of heritabilities of three-year-old Virginia pine from 4 half-sib progeny tests.

	Progeny Test				
Variables	A&M	HRFS	A&M (FWS)	Auburn	Average
Height	0.28	0.13	0.19	0.16	0.19
Diameter	0.16	0.15	0.16	0.13	0.15
Crook	0.12	0.19	0.14		0.15
Color	0.39	0.38	0.35		0.37
Branches	0.16	0.11	0.10	0.12	0.12
Rating	0.15	0.15	0.19		0.16

The above heritability estimates are fairly low for most of the variables. This is due primarily to a large within-plot variance component which accounted for between 42 and 61 precent of the total phenotypic variance. The second largest source of variation in all cases was the component due to the interaction of replications and families-within-source. These two components accounted for between 73 and 90 percent of the total variance for all characteristics. The tremendous amount of tree-to-tree variation within a family presents a large obstacle to the genetic improvement of Virginia pine Christmas trees by lowering the estimates of heritabilities and potential genetic gains.

Selection strategy

As previously stated, the first level of selection - selection of the best seed sources - is not of primary of importance. The next level is selection of the best families within each source. Previous research by the author (Brown 1987) has shown that there are no significant interactions between families and locations in north Alabama and central Tennessee. The best families can be used in a breeding program for the areas tested negating the need to make separate selections and establish different seed orchards.

The next selection level is the selection of individuals within families. However, the selection of families and individuals within families brings up an important question: What characteristics should be emphasized in a breeding program? A quality Christmas tree is a combination of several characteristics, such as good growth, dense crown, straight stem, and dark needle color. To maximize one characteristics would likely be at the expense of other characteristics. This could result in an overall decrease in tree quality or performance.

Previous research has eliminated the characteristics of internodal distance, limb angle and crown form, because of extremely low heritabilities, lack of significant differences among families-within-sources or high correlations with other more important characteristics. For example, stem diameter can also be eliminated for similar reasons. The best Christmas tree would be the tallest with the smallest stem diameter. However, there is a positive correlation between height and diameter of 0.81. Selection for a smaller stem diameter may result in a negative effect on height.

In an attempt to determine which characteristics have the greatest influence on overall tree quality, a multiple regression analysis was performed using the rating as the dependent variable being predicted by the other characteristics. The most signifiant characteristic accounting for more than 37 times the amount of variation of the second factor, was the crook value. To verify the magnitude of importance of this characteristic, 5 experienced Christmas tree growers and field workers remeasured and evaluated one replication. The result of the regression analysis of this data was similar, in that crook was the predominant predictor of overall tree quality. A shorter or "open" tree can still be a merchantable product, whereas a crooked tree, regardless of its height or density is commonly not salable. Based on these results and several other factors, it appears that the selection of superior trees should be most heavily weighted by the "quality rating" characteristic and stem straightness, followed by height growth with the least emphasis being placed on branches per whorl and needle color.

A commonly used method of selecting families for more than one trait is to remove all families not significantly better than the family with the worst performance. However, because of the large amount of variation in the error term for families-within-sources, using this method on the three most important characteristics eliminates over 90 percent of all families.

This culling is too drastic to maintain the genetic diversity needed for a breeding program.

The method utilized in this study was based on the calculation of the standard error of the means for each characteristic. Those families which were more than one standard error below the overall mean for two or more characteristics were culled. All families more than two standard errors less than the overall mean for any one characteristic were also culled. From the remaining families, the 20 best individuals were selected according to the following critieria:

a. A score of 4 or 5 for both the crook rating and overall rating.

b. Maximum height growth.

c. When two or more trees had approximately the same height, then the tree with the higher number of branches per whorl or darker needle color was favored.

d. No more than one tree from each family was selected.

The difference between the means of the 20 select trees and the overall mean for each characteristic was computed, resulting in the selection differential. Expected genetic gains were then computed and are presented in Table 3. For comparison the maximum expected gains were also computed for each characteristic. Between 84 and 96 percent of the maximum gain can be realized for the combined selection of crook, rating and height. Needle color should show some improvement with a very modest increase in the number of branches per whorl.

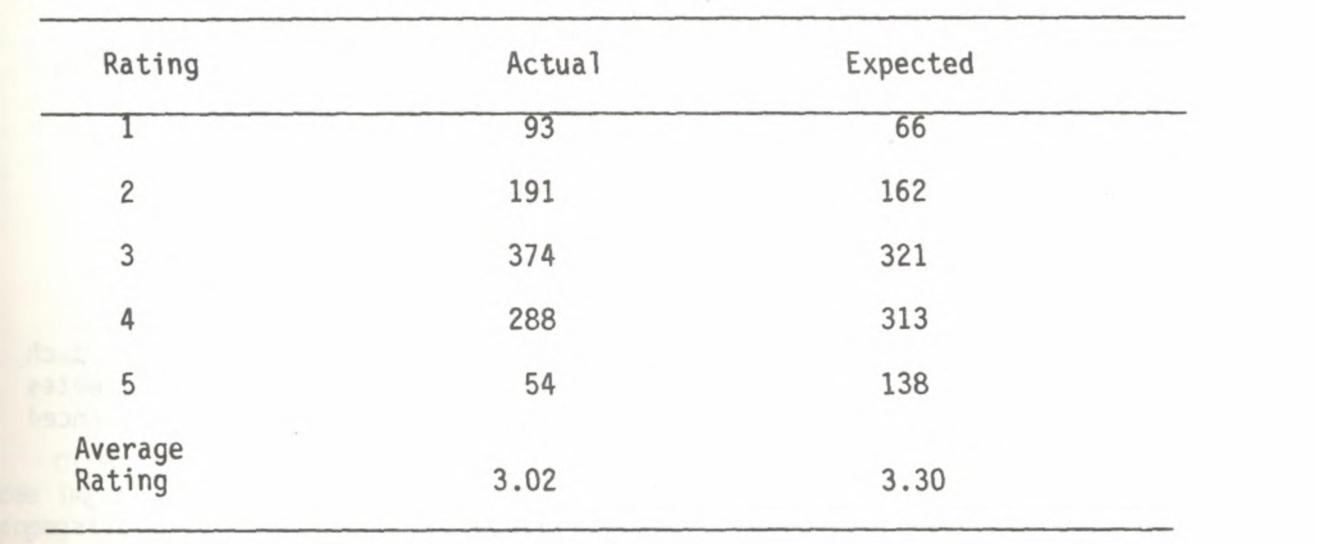
Table 3. Expected gains for selection for each characteristic individually and in combinatin with other characteristics.

Variable	Maximum gain	Select trees
Height	16.03 cm	13.51 cm
Crook	0.25	0.24
Color	0.56	0.21
Branches/whorl	0.20	0.06
Rating	0.33	0.28

The expected gain for most characteristics, such as height, has a definite clear meaning. The progeny from the select trees should exhibit an increase in height of 13.51 cm at age three. However, the expected gain in "quality rating" of 0.28 does not have a clear meaning. One method for obtaining a better understanding of the meaning and impact of this gain is to study the rating frequencies which produced the observed mean and the changes which are anticipated to realize the expected gain.

The actual rating frequencies (adjusted to a per 1000 tree basis) are presented in Table 4. This frequency distribution produced the observed mean of 3.02 for the quality rating. If the expected gain is realized, then the progeny will have a mean of 3.30. A straight percentage increase of 29 percent from each rating to the next is required to achieve the new mean. This would result in the expected frequencies presented in Table 4.

Table 4. Actual and expected rating frequencies per 1000 trees.



Rating	Actual	Expected
1	93	66
2	191	162
3	374	321
4	288	313
5	54	138
Average Rating	3.02	3.30

Assuming that a 29 percent average increase from one rating class to the next is realistic, then there would be a 29 percent reduction in 1 rated trees which are all culls. There would also be approximately a 15 percent reduction in 2 rated trees - those which require major corrective procedures. It is impossible to correct all trees rated 2 to make them salable. In fact, it would be more accurate to assume that only 50 percent of 2 rated trees can be made into a salable product. A 29 percent reduction in 1 rated trees and a 15 percent reduction in 2 rated trees, assuming half of these are not salable, represents an average increase of 42 merchantable trees per 1000 or approximately per acre.

A clearer understanding and more meaningful measure of the above gains can be obtained by assigning a dollar value to them. Assuming a value of $2.00 per foot, or $12.00 per tree as a wholesale price for a 6-foot Virginia pine Christmas tree, an additional 42 trees marketed per acre represents an increase in income of $504.00. An increase in height of 13.5 cm on 853 trees per acre would represent a gain of $756.00. Of possible greater importance, but not easily measured, is the percentage of the trees that will be of better quality and will have required less maintenance. Also, more trees will be merchantable at an earlier age, increasing the rate of return on a grower's investment.

CONCLUSIONS

Although there were significant differences among seed sources of Virginia pine ranging from South Carolina to Mississippi and north to Tennessee, the differences were not large and accounted for less than 2.5 percent of the total variation observed in any of the characteristics which were evaluated. Seed source differences within this test area are not considered to be important. Based on the calculated estimates of heritabilities and potential gains, the genetic improvement of Virginia pine for Christmas trees is possible and practical. The greatest improvement can be achieved if the selection of superior trees primarily focuses on the characteristics of overall quality rating and stem straightness, followed by height growth with the least emphasis being placed on branches per whorl and needle color. Progeny from select trees should average 13.5 cm taller and result in approximately 4 percent fewer cull trees per acre, representing an increase in commercial value of over $1,200.00 per acre.

The Virginia pine is a species which is characterized by a large amount of tree-to-tree variation, which is particularly pronounced in juvenile trees. One objective of future research efforts should be to minimize the environmental source of variation within a test location. This variation causes reduced estimates of heritabilities and may mask much of any realized genetic gains without accurate measurements. The estimates of heritabilities for growth related factors may also be greatly influenced by site conditions, primarily soil conditions.

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