

REALIZED GENETIC GAINS IN VOLUME, VOLUME PER ACRE, AND STRAIGHTNESS
IN UNROGUED ORCHARDS OF THREE SOUTHERN PINE SPECIES

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Abstract.--By means of Best Linear Prediction (BLP), breeding values were obtained for single-tree volume, volume per acre, and straightness for shortleaf pine (*Pinus echinata*), eastern white pine (*P. strobus*), and three breeding populations of loblolly pine (*P. taeda*) in unrogued clonal seed orchards. For the volume traits the gains ranged from a high of 31.2 percent to a low of -3.8 percent. For straightness the gains were more stable across breeding populations, ranging from a high of 29.7 percent to a low of 0.1 percent. Substantial gains can still be obtained for volume in those breeding populations with weak or negative gains for volume when selection is restricted to a few of the best families. This kind of strategy is being implemented in those breeding populations by means of forward selections that are currently in progress. Possible reasons for the variability of relative gains for volume and straightness are discussed.

Keywords: Best linear prediction, breeding population, unrogued clonal seed orchard, realized genetic gain.

INTRODUCTION

In the Tree Improvement Program of the Southern Region (Region 8), progeny testing, which was begun in 1978, includes measurements at ages 5 and 10. Volumes can not be estimated until age 10, since dbh is not measured until then. Likewise, straightness is also evaluated at that age. Since a large number of progeny tests have been evaluated at age 10 in several species and breeding populations within those species, it is now possible to estimate genetic gains for volume and straightness for these species and populations.

Although some thinning has been done in the clonal seed orchards in which these breeding populations are maintained, there has been essentially no roguing in these orchards. Hence, any genetic gains to be obtained thus far in the breeding program are dependent on the success of the selection intensities obtained in the original octet selection process and can be evaluated by comparison with commercial or General Forest Area (GFA) check lots.

This paper will report the heritabilities and genetic gains for volume, volume per acre, and straightness in five breeding populations representing three southern pine species.

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MATERIALS AND METHODS,

Species and Breeding Populations

The three species reported in this paper are shortleaf pine (Pinus echinata Mill.), eastern white pine (P. strobus L.), and loblolly pine (P. taeda L.). The Region 8 Tree Improvement Program divides southern pine species into separate breeding populations when information is available to delineate such populations. Hence, shortleaf pine and loblolly pine are so subdivided based on the Southwide Pine Seed Source Study (Wells and Wakely 1966). White pine comprises only one breeding population, since insufficient information is available on geographic variation in this species in the southern Appalachians to designate separate populations.

In this paper shortleaf pine Breeding Population 1 (BP1), located on the Ouachita and Ozark-St. Francis National Forests in Arkansas and Oklahoma, is the only population in shortleaf pine with sufficient test data yet available to allow a comprehensive analysis. White pine Breeding Population 1 is so designated because information at some future time may allow us to subdivide the species range in the southern Appalachians. Loblolly pine is subdivided into seven breeding populations, three of which are reported on in this paper. These are BP2, BP3, and BP5.

Breeding Population 2 is located in Louisiana and Texas on the Kisatchie National Forest and the National Forests in Texas. Breeding Population 3 comprises the National Forests in southern Mississippi. Breeding Population 5 comprises the Districts on the Sumter National Forest in the Piedmont of South Carolina and the Uwharrie National Forest in the Piedmont of North Carolina.

Progeny Test Design

The field designs of the progeny tests in all three species conformed to the standard randomized complete-block design used in the Region 8 Tree Improvement Program. In this design the tests are arranged in 10-tree row plots so that all plots within a block followed the same contour. Most tests contained five replicates, but some had either four or six replicates.

Breeding Population Size and Number of Tests

The numbers of clonal seed orchard parents, the numbers of commercial or General Forest Area (GFA) check lots, and the number of progeny tests in each breeding population are listed in Table 1. Since the number of 6 X 6 diallel crossing groups varied from test to test, those numbers are not listed. Although the attempt was made to include all crosses within a crossing group in the same set of tests for any one year, some crosses were tested in years different from the majority of crosses in that crossing group. In the present analysis, the effects of differing sites and years were minimized by analysis of all data as deviations from each test mean. However, this analysis did not include the effect of genotype x year of establishment interactions.

Table 1. The numbers of parents, progeny tests, and commercial (GFA) check lots comprising each breeding population in three southern pine species.

Species and Breeding Populations	Parents	Progeny tests	GFA check lots
	Number	Number	Number
Shortleaf Pine Breeding Population 1	78	12	1
White Pine Breeding Population 1	60	14	4
Loblolly Pine Breeding Population 2	61	8	1
Loblolly Pine Breeding Population 3	42	9	1
Loblolly Pine Breeding Population 5	51	13	1

Procedures Used

The results of these analyses were based on data from measurements made at ten years of age. The traits measured were total height to the nearest foot, dbh to the nearest inch, survival, and straightness based on an index estimated ocularly to produce scores from 1 (=very crooked) to 4 (=straight). Traits analyzed were cubic volume inside bark of entire stem from volume equations for each species and breeding population. The volume equations are listed in Table 2. Volume per acre was calculated by summing the individual tree volume per acre at 8 X 8-foot spacing and factoring in survival.

All three traits were analyzed by means of Best Linear Prediction (BLP). BLP has been utilized as a method of data analysis because of considerable imbalance in the data available in all five breeding populations. Except for the white pine progeny tests, the mating scheme for all breeding populations is a 6 X 6 diallel crossing group. The white pine tests are wind-pollinated tests. Each year full-sib and half-sib tests were planted at as many as five locations, but not all families could be planted at each location, and most diallel crossing groups were less than complete. Hence, the prospect of obtaining balanced ANOVAs and unbiased estimates of breeding values were formidable until the recent availability of BLP as a method of data analysis (White et al. 1986; White and Hodge 1989).

Previously La Farge and Gates (1991) discussed the application of BLP in obtaining breeding values for height and survival in shortleaf pine (*Pinus echinata* Mill.) in Arkansas. Since those methods of data analysis were also utilized for the present investigation, they will not be discussed in depth in this paper. However, a brief review of the procedures required for these analyses is appropriate. BLP involves the prediction of breeding values, and

the defining equation is $\hat{g} = C^{-1}V^{-1}y$, where C is a non-symmetric matrix which defines the genetic relationships between the observed full-sib family means at each site and the true yet unknown breeding values, g ; V is a symmetric matrix which represents the variances and covariances between the observed phenotypic values; y is a vector of data representing observed deviations of the family means at each test location from the test location mean; \hat{g} – the breeding values to be predicted.

Generation of the second moments needed to construct the C and V matrices requires a combined ANOVA on the data. This was accomplished by means of the VARCOMP Procedure of the Statistical Analysis System for Personal Computers and the MIVQUEO Method (SAS 1987). The variance components generated by this procedure were then combined in appropriate equations to produce the second moments needed to construct the C and V matrices. These second moments were loaded into the C and V matrices by means of language provided in the SAS IML Guide for Personal Computers (1985).

Genetic gains for each trait in each breeding population in each species were calculated as:

$$\% \text{ Gain} = (\text{Parental mean} - \text{GFA mean}) \times 100 / \text{GFA mean},$$

where Parental mean – the mean of all parental breeding values in a breeding population, and GFA mean – the breeding value for the GFA check lot or the mean of the breeding values of more than one check lot.

Table 2. Volume equations used to calculate single-tree volumes for each species and breeding population.

Species and Breeding Breeding Population	Volume Equation
Shortleaf Pine BP1	Total Vol.(ib) = 0.00914 + (0.0019281*dbh*dbh*height) 1/
White Pine BP1	Total Vol.(ib) – 0.74000 + (0.0027610*dbh*dbh*height) 2/
Loblolly Pine BP2	Total Vol.(ib) – 0.03789 + (0.0020911*dbh*dbh*height) 3/
Loblolly Pine BP3	Total Vol.(ib) – 0.03789 + (0.0020911*dbh*dbh*height) 4/
Loblolly Pine BP5	Total Vol.(ob) – 0.00914 + (0.0019281*dbh*dbh*height) 5/

1/ Smalley and Bower (1968). 2/ Lacher and Schlaegel (1983).
 3/ Schmitt and Bower (1970). 4/ Schmitt and Bower (1970).
 5/ Bailey and Clutter (1970).

Table 3. Individual and family heritabilities in three southern pine species for volume, volume per acre, and straightness.

	Heritability, h^2	
	Individual	Family
<u>Shortleaf Pine Breeding Population 1</u>		
Volume	0.16	0.74
Volume per acre	.04	.46
Straightness	.13	.77
<u>White Pine Breeding Population 1</u>		
Volume	0.04	0.58
Volume per acre	.02	.23
Straightness	.03	.57
<u>Loblolly Pine Breeding Population 2</u>		
Volume	0.21	0.79
Volume per acre	.04	.42
Straightness	.13	.73
<u>Loblolly Pine Breeding Population 3</u>		
Volume	0.12	0.73
Volume per acre	.07	.63
Straightness	.10	.69
<u>Loblolly Pine Breeding Population 5</u>		
Volume	0.05	0.57
Volume per acre	.01	.24
Straightness	.11	.70

Table 4. Realized genetic gains for three southern pine species for volume, volume per acre, and straightness.

Realized genetic gain, percent	
<u>Shortleaf Pine Breeding Population 1</u>	
Volume	31
Volume per acre	30
Straightness	15
<u>White Pine Breeding Population 1</u>	
Volume	8
Volume per acre	-3
Straightness	0
<u>Loblolly Pine Breeding Population 2</u>	
Volume	0
Volume per acre	-4
Straightness	27
<u>Loblolly Pine Breeding Population 3</u>	
Volume	8
Volume per acre	2
Straightness	6
<u>Loblolly Pine Breeding Population 5</u>	
Volume	23
Volume per acre	18
Straightness	15

RESULTS

Individual and family heritabilities for single-tree volume, volume per acre, and straightness for each breeding population are listed for each species (Table 3), and realized genetic gains are shown for each breeding population in each species (Table 4).

DISCUSSION AND CONCLUSIONS

The considerable variability in genetic gain values suggests that basing genetic gain on comparisons with GFA or commercial check lots may be misleading. For three of the breeding populations, we could just as easily make backward selections on the basis of comparisons with the breeding population means as with GFA check lots. For one thing, records no longer exist which show the numbers of trees or stands comprising each GFA check lot.

The gains in some breeding populations may be weak because seeds were collected from trees or stands of average or above-average growth rate or straightness. Likewise, the very strong gains shown for Shortleaf Breeding Population 1 and Loblolly Breeding Population 5 may be exaggerated by comparison with GFA checks from stands or trees that are below average for growth or straightness.

Strictly speaking, there is no F-test for significance of differences among breeding values for parents in BLP. However, the weakly negative genetic gains shown in Table 4 for volume per acre in white pine BP1 and loblolly pine BP2 and for volume in loblolly pine BP2 are probably not significantly different from zero. Hence, although these gains are somewhat erratic in that they show some variability among breeding populations, they are basically quite strong. Moreover, in all breeding populations there are many parental breeding values that are well above average. Hence, there is ample room for obtaining genetic gains when making forward selections both for volume growth and for straightness.

The variability of these gains among breeding populations is perhaps an indication that collection of seed for use as commercial check lots in progeny evaluation testing should sample stands throughout the area of a breeding population, not just in one or two convenient cutting units.

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