SECOND TECHNICAL SESSION

Chairman: R. Westfall

GENETIC STUDY OF WOOD SPECIFIC GRAVITY IN SLASH PINE

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ABSTRACT

Wood samples and measurements from 9-year-old open-pollinated progenies of 18 slash pine families were analyzed to determine specific gravity. Average performance was 0.45 in specific gravity, 5.1" in d.b.h., 39.4' in height. Heritability estimates were 0,68+ .2, 0.31+ .1 and 0.47+ .2 for specific gravity, d.b.h. and height. Genetic correlations between specific gravity and d.b.h. specific gravity and height, and d.b.h. and height were -0.12+ .27, 0.20+ .27 and 0.91+ .06, respectively. Family means and ranks from random samples of one, two and three trees per plot were compared with determination for all trees in all plots. Rank correlation tests showed one tree per plot was acceptable but three trees per plot gave family rank determination comparable to complete plot measurements.

INTRODUCTION

Extensive research on specific gravity of southern pines indicates that this wood characteristic has an important relationship to pulp yield and paper properties (Barefoot et al., 1966; van Buijtenen et al., 1968; Einspahr et al., 1969; Wangaard et al., 1966). There is also considerable evidence in the literature of substantial variation in wood specific gravity and moderate to high heritability (van Buijtenen, 1962; Goddard and Strickland, 1962; Perry and Wang, 1958; Squillace et al., 1962, Stonecypher and Zobel, 1966; Stonecypher et al., 1964; Zobel et al., 1972). Thus, specific gravity should be considered in choice of clones for inclusion in improved seed orchards and in second generation selection.

Numerous progeny tests of southern pines have been established and specific gravity is among the traits requiring measurement in these tests. However, rather expensive field and laboratory procedures are required for specific gravity determination, making such analysis of all of the many individual trees established in progeny tests prohibitively expensive.

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A reliable sampling system would provide a method of acquiring needed data within reasonable costs. This paper deals with a study to determine optimal sample size for efficient estimation of family means and genetic parameters of specific gravity, Components of variance, heritability, and genetic correlation with other growth characteristics were studied.

MATERIALS AND METHODS

An open-pollinated slash pine progeny test was established on the Austin Cary Forest near Gainesville, Florida, in 1964. A total of 18 families, involving 16 open-pollinated select and two check lots, were represented in ten randomized blocks of 8-tree-row plots. During the springs of 1964 and 1965, 300 pounds per acre of diammonium phosphate were applied to one-half of each block. Blocks were split so that four trees of each lot in each block were fertilized.

In March, 1972, after the trees had completed nine growing seasons, wood samples were collected from all trees in each plot. One full diameter 11 mm increment core was removed from each tree near breast height and divided at the pith into two pieces to obtain two observations from each tree. Specific gravity was determined by using the Maximum Moisture Method (Smith, 1956). Heights and diameters were measured. Analysis of variance was conducted with the average specific gravity value of each tree by use of a Least Squares Maximum Likelihood General Purpose computer program written by Harvey (1968). This program solved for most of the genetic parameters: heritability, correlations among specific gravity, height and diameter, some components of variances as well as analysis of variance. Components of variance were estimated by equating mean squares to expectation (Table 1). In this analysis, fertilizer treatment and block effects were assumed to be fixed. Computation of within-tree variation was done separately on the basis of individual core values.

The effect of subsampling was determined by comparing the different sample sizes of one, two, and three trees per plot with original 8-tree plot data. A random sampling scheme of an APL program was used to pick pertinent numbers of trees per plot. Data of the different samples were subjected to analyses of variance. Tree means and rankings were compared by means of a Rank Correlation Test (Snedecor and Cochran, 1967) for the several sample sizes.

RESULTS AND DISCUSSION

Genetic variability of specific gravity.--The least squares analyses of variance indicated highly significant variation among families (Table 2). Fertilizer did not affect specific gravity variation in this study. Most of the components of variance from interaction terms were omitted since they were negligible (0.00001 or less). Actually, the variance component estimate for families was the only remarkable source of variation except the within plot (trees/plot) and within tree (cores/tree) variations. Heritability based upon the individual tree values of 18 open-pollinated families was 0.68+ .21. This estimate was calculated from the intraclass correlation of half-sib families and represents an estimate of heritability in the narrow sense on an individual tree basis. The heritability estimate was higher than that of previous reports on slash pine (0.43 from Goddard and Cole, 1966; 0.21 from Squillace et al., 1962), Genetic correlation between specific gravity and height was insignificantly negative (-0.118) and the genetic correlation between specific gravity and height was insignificantly positive (0,197) (Table 3). Some families (244-55, 110-56, and etc.) showed high performance in specific gravity as well as in diameter and height (Table 4). This implies that selections for growth and specific gravity characteristics can be achieved with genetic improvement in both.

<u>Sample size analysis.--Since</u> fertilizer treatment effects were insignificant, the total trees per plot was considered eight and smaller subsamples were drawn with no consideration of fertilization. The efficiency of sampling was checked by random sampling of one, two, and three trees per plot. Analyses of variance of subsample data indicated highly significant differences (1% level) between families for all sample sizes (Table 5). Especially the estimate of variance component of family in sample size three has almost the same magnitude as that from the original data. Family means from three different sample sizes were ranked and compared with original 8-tree plot results (Table 6). The first rank and the last two ranks remained unchanged in all three sample sizes. Ranks for sample size three were mostly shifted no more than two ranks from those based on 8-tree plots, and many families showed no change in rank. Family rank correlations between all three sets of sample sizes and 8-tree plot data were significant at the one-percent level (Table 7). However, the comparison of data from one tree per plot with the full 8-tree plot data suggests a loss of 40% of potential information on correlations among family mean. Two trees per plot gave increased accuracy and three trees per plot gave increased accuracy and three trees per plot gave essentially the same information as the full 8-tree plots ($r^2 = .92$).

Decisions on sample size should be related to purpose of the study and the cost situation, On the basis of this study, sampling of three trees per plot can be recommended as satisfactorily accurate for ranking family means when ten replications are available. This is further corroborated by examination of coefficients of variation calculated from these data (Fig. 1). Increase of sample size from one to three gave a decrease in coefficient of variation but increase above three did not substantially improve precision. These coefficients suggest that increase of sample size may be necessary when fewer replications (blocks) are available for sampling.

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Table 1.--General form of the analysis of variance used to estimate variance components.

Source of variation	d.f.	Expected mean square
Blocks (B)	b-1	$\sigma^2_{e'} + k\sigma_i^2 + ktf\sigma^2_b$
Treatments (T)	t-1	$\sigma^2_{e'} + k\sigma_i^2 + kb\frac{t}{t-1}\sigma^2_{tf} + kbf\frac{T^2}{t-1}$
B x T	(b-1) (t-1)	$\sigma^2_{e'} + k\sigma_i^2 + kf\sigma^2_{bt} + kf\sigma^2_t$
Families (F)	f-1	$\sigma^2_{e'} + k\sigma_i^2 + kbt\sigma^2_f$
T x F	(t-1) (f-1)	$\sigma^2_{e'} + k\sigma_i^2 + kb\frac{t}{t-1}\sigma^2_{tf}$
Remainder		$\sigma^2_{e'} + k\sigma_i^2$
Error* (BxF, BxTxF)	t(b-1) (f-1)	
**		
Trees/Plot	(k-1)f·b·t	$\frac{\sigma^2_c}{c} + \sigma^2_e = \sigma^2_{e'}$
Cores/Tree	b·t·f·k(c-1)	σ^2_c

σ^2_c = variance due to differences among cores

σ^2_e = variance due to differences among trees within plots

σ_i^2 = variance due to compound interactions

σ^2_{tf} = variance due to the interaction of treatment and families

σ^2_f = variance due to differences among families

σ^2_t = variance due to whole-unit random error

σ^2_b = variance due to differences among blocks

c = harmonic mean of number of cores per tree

k = harmonic mean of number of trees per plot

f = number of families

b = number of blocks

t = number of treatments

*Since preliminary analysis of variance based on plot means showed no significant differences between these interaction terms, they were included as part of error.

**Variance of cores/tree was calculated separately on the basis of individual core values.

Table 2.--Least squares analyses of variance of specific gravity, d.b.h., and height and estimates of variance components in specific gravity ⊛

Source	d.f.		M.S.	
		sp Gr	d.b.h.	Ht.
Blocks	9	0.00568*	7.08**	147.01**
Treatments	1	0.00683	2.87*	81.16
B x T	9	0.00174*	0.53	27.03
Families	17	0.01180**	2.74**	141.57
T x F	17	0.001	0.75*	21.56
Remainder	1228	0.00074	0.39	13.92
trees/plot	922	0.00064		
cores/tree	1282	0.00026		

*significant at .05 level

**significant at .01 level

⊛ Estimates of variance components in specific gravity

$\sigma_f^2 = 0.00016$

$\sigma_e^2 = 0.00051$

$\sigma_c^2 = 0.00026$

$\sigma_i^2 = 0.00003$

Table 3.--Heritability estimates (h^2) of specific gravity, d.b.h., and height and genetic (G), phenotypic (P) and environmental (E) correlations among them.

		Correlation		
	h^2	G	P	E
Sp Gr	0.68 ± 0.2			
Sp Gr - d.b.h.		-0.118 ± 0.27	0.015	0.147
Sp Gr - height		0.197 ± 0.25	0.189	0.188
d.b.h.	0.31 ± 0.1			
d.b.h. - height		0.909 ± 0.058	0.661	0.522
height	0.47 ± 0.2			

Table 4.--Means of specific gravity, d.b.h., and height of each family and treatment.

Family	Specific gravity	d.b.h.	Height
244-55	0.478	5.30	41.8
284-55	0.470	4.84	38.2
21-57	0.465	5.07	40.3
67-57	0.462	4.91	39.7
67-56	0.460	5.03	39.9
18-57	0.458	4.90	37.9
111-58	0.456	4.84	37.7
110-56	0.456	5.29	40.6
121-56	0.454	5.24	39.9
240-55	0.453	5.32	41.2
60-57	0.449	5.30	40.2
U.C.	0.449	4.73	37.5
A.C.F.	0.445	4.95	38.3
269-56	0.444	5.00	37.8
254-55	0.443	5.23	40.2
289-55	0.438	5.00	37.7
89-57	0.433	4.99	38.8
60-56	0.427	5.33	41.3
Treatment Means			
Fertilized	0.450	5.12	39.6
Unfertilized	0.455	5.02	39.1
Mean	0.452	5.08	39.4
Standard deviation	0.03	0.70	4.1

Table 5.--Analyses of variance of specific gravity with varying sample sizes

Source	n = 1		n = 2		n = 3	
	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.
Total	179		359		539	
Block	9	.00085	9	.00184*	9	.0019*
Family	17	.0024**	17	.00182**	17	.0056**
Error	153	.00088	153	.00080	153	.0008
Within plot			180	.00077	360	.0008
σ_f^2		0.00015		0.00005		0.00016

* significant at .05 level

** significant at .01 level

Table 6.--Specific gravities of family means and their ranks, calculated from various random sampling sizes.

Family	1 tree/plot		2 trees/plot		3 trees/plot		8 trees/plot	
	Sp Gr	Rank	Sp Gr	Rank	Sp Gr	Rank	Sp Gr	Rank
244-55	.479	1	.474	1	.481	1	.478	1
284-55	.472	4	.463	3	.476	2	.470	2
21-57	.475	3	.457	6	.460	4	.465	3
67-57	.451	8	.456	8	.463	3	.462	4
67-56	.457	6	.467	2	.458	6	.460	5
18-57	.471	5	.454	10	.454	7	.458	6
111-58	.447	14	.456	7	.458	5	.456	7
110-56	.447	13	.459	5	.452	9	.456	8
121-56	.476	2	.463	4	.449	11	.454	9
240-55	.452	7	.454	9	.451	8	.453	10
60-57	.448	12	.453	11	.444	13	.449	11
U.C.	.449	10	.446	15	.446	12	.449	12
A.C.F.	.447	15	.446	15	.451	10	.445	13
269-56	.451	9	.450	12	.439	16	.444	14
254-55	.439	16	.447	13	.443	15	.443	15
289-55	.448	11	.447	14	.444	14	.438	16
89-57	.433	17	.441	17	.432	17	.433	17
60-56	.422	18	.434	18	.427	18	.427	18
Mean	.454		.453		.452		.452	

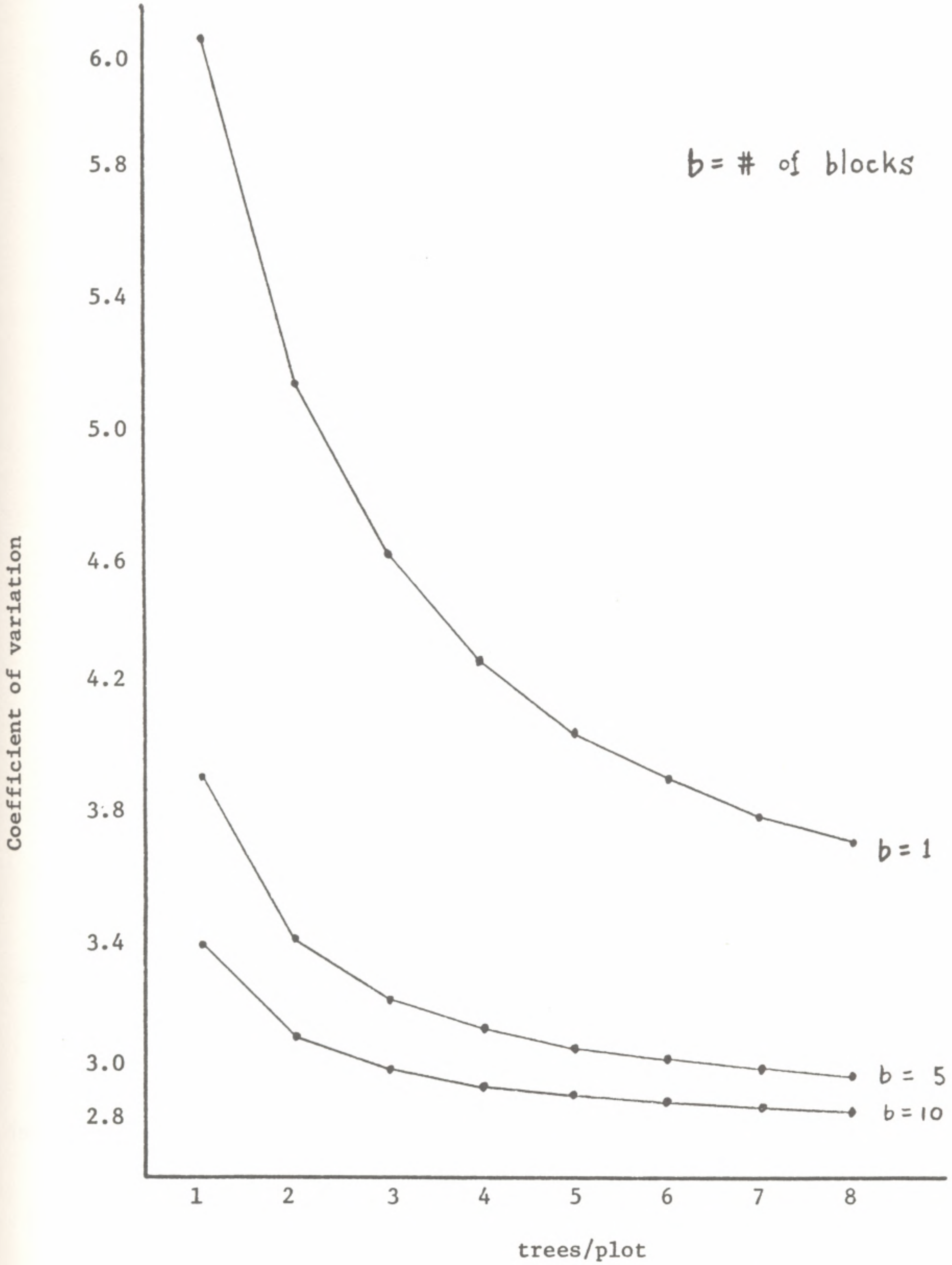

Figure 1. The coefficients of variation of family means showing the combined effect of tree and replication (b) numbers on specific gravity.

Table 7.--Rank correlations between three sets of sample sizes and complete 8-tree plot.

	r	r^2
1 vs. 8	0.77**	0.60
2 vs. 8	0.89**	0.80
3 vs. 8	0.96**	0.92

** significant at .01 level.