COMPARISONS OF PROGENY OF A LOBLOLLY PINE SEED PRODUCTION AREA WITH PROGENY OF PLUS TREE SELECTIONS

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Abstract.--Four progeny tests compared performances of progeny of Georgia Forestry Commission (GFC) seed orchard clones; a seedlot from a seed production area (SPA) in Warren County, Georgia, established by the Continental Can Company; and several commercial check lots. The clonal progenies consistently outranked the SPA lot and the commercial check lots for crown/height ratio at age 5 and for height, d,b.h., stem volume and stem straightness at age 15. There were few consistent differences for number of galls/tree at age 5 or plot volume, percentage of rust-free trees, and survival at age 15. When all traits were considered, clonal progenies performed best as a group. Differences between the SPA lot and the commercial checks were not significant.

Additional keywords: Commercial check lot, phenotype, nonparametric, *Pinus taeda*, *Cronartium quercuum.*

One of the early efforts to improve the genetic quality of forest nursery stock was to set aside and manage certain stands as seed production areas. Removal of all but the selected seed crop trees was based only on phenotypic characteristics. There has been little empirical evidence that progeny of seed production areas possessed any potential for genetic gain. Four progeny test plantations of loblolly pine *(Pinus taeda L.),* established in 1965, contain progeny of a seed production area along with progenies of plus tree selections represented in two clonal seed orchards and several commercial check lots. Though designed to test progenies of seed orchard clones, these plantations offer a means of evaluating the genetic potential of the seed production area. Nine important traits were compared among three main progeny groups, and these results are the subject of this paper.

MATERIALS AND METHODS

The four plantations in which the data for this study were collected were designed to test polycross progenies of clones in two Georgia Forestry Commission (GFC) seed orchards (the Arrowhead Seed Orchard in Pulaski County and the Horseshoe Bend Seed Orchard in Wheeler County) and to compare them with several controls.

In this paper we compare three groups using progeny test data: Group 1, progeny of plus tree selections used to establish clonal seed orchards, hereafter referred to as clonal progenies; Group 2, a seedlot collected from a seed production area (SPA) in Warren County, Georgia, established by the Continental Can Company; and Group 3, commercial check lots supplied by the GFC as nursery run controls in the progeny test plantations.

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The four plantations, numbered 69, 75, 76 and 77, contain 22, 8, 22 and 17 clonal progenies, respectively. Because some progenies are common to two or more plantations, the total number of different clonal progenies is 53. Three commercial check lots were used, but no more than two in any plantation, and only one in Plantation 76.

All plantings were in randomized complete blocks, with the numbers of replications varying from 5 to 8. Plantations 69 and 76 contained 25-tree square plots; Plantations 75 and 77 had 5-tree row plots. Plantations 69, 76 and 77 are in Bleckley County in the Upper Coastal Plain, and Plantation 75 is in Jasper County in the Lower Piedmont.

Since numbers of clonal progenies in the three groups of interest varied considerably, a one-way analysis of variance with unequal subclass numbers was used to analyze most traits. In two plantations the nature of the data for two traits permitted a 2-way analysis of variance with unequal but proportional subclass numbers (Snedecor, 1956, Sokal and Rohlf 1969). However, this method produced a gain in efficiency in only one trait in one plantation.

The traits analyzed in this study are: (1) height, (2) d.b.h., (3) tree volume, (4) plot volume, (5) number of fusiform rust galls/tree (*Cronartium quercuum* (Berk.) Miyabe ex Shirai f. sp. *fusiforme*), (6) percentage of trees free of rust, (7) straightness, (8) crown/height ratio, and (9) percentage survival. Galls/tree and crown/height ratio were measured at age 5, all other traits at age 15. The growth traits were measured in metric units. The number of galls/tree was transformed to $\sqrt{X + .5}$, and the percentages of rust-free trees and survival were transformed to the arcsin $\sqrt{\text{percent}}$. Straightness was indexed by ocular estimation from 1 = straight through 6 = very crooked and transformed to $\sqrt{X + .5}$ for the analyses.

Analyses of variance and Duncan's Multiple Range Tests were performed on data for all 9 traits, except that the data for the percentage of rust-free trees in Plantations 75 and 77 had to be omitted; in these tests all or nearly all trees were infected, so that meaningful comparisons could not he made.

In addition to these analyses, the group means were ranked for each trait and two nonparametric methods were used to interpret results. The first method involved an interaction chi-square test for goodness of fit. The ranks of all traits were summed for each group in each plantation. The second method, which utilized the same ranked data, was Friedman's test, which is a chi-square approach to a randomized complete-block design (Steel and Torrie 1960). In this case the four plantations were considered to be replicates of the three groups. In this application each method became a form of nonparametric multivariate analysis, since all traits were combined into one variable, rank.

RESULTS AND DISCUSSION

Since nine traits were analyzed in Plantations 69. and 76 and 8 traits **in** the remaining two progeny tests, 34 analyses were performed in all. Only seven of these 34 tests produced significant variance analyses (table 1), and only six tests resulted in significant Duncan's multiple range tests (table 2). However, inspection of the group means in each plantation revealed that the clonal progenies appeared to rank first much more frequently than would seem to result from chance alone (table 3). Hence, two nonparametric analytical methods were applied to the ranked data.

The first method is a test for goodness of it. Ranks (1,2 or 3) of each group in each plantation were summed for all eight or nine traits, and these sums are listed as the "observed" data in the top row for each group in table 4. The expected values are listed in the second row for each group in table 4. Each expected value = rank x number of traits; e.g., for clonal progenies, Group 1, in Plantation 69, the expected value is 1 x 9 = 9.

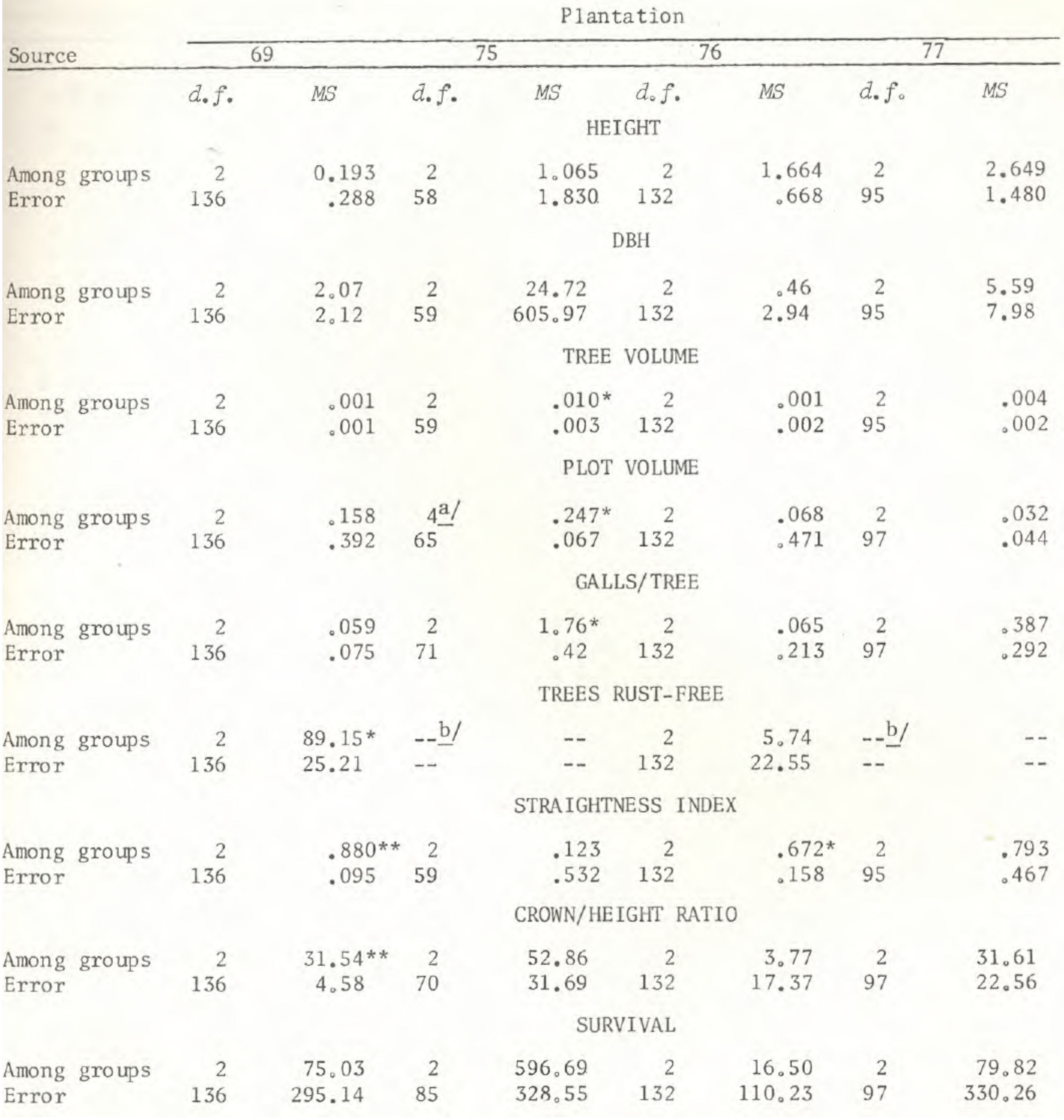
We expect Group 1, the clonal progenies, to rank first for each trait because their octets were selected in natural stands or plantations on the basis of greater size and better form than the surrounding trees and on the basis of absence of fusiform rust galls. In theory, each ortet was selected as the best of a sufficient number of trees in its stand, so that the selection differential is at least one standard deviation above the mean.

The SPA lot, Group 2, also represents some theoretical increment of genetic gain, since the dominant trees remaining in the area for seed production should be superior phenotypes compared to those which were rogue& However, because of the number of trees which must be left for seed production, selection intensity is limited, so that the selection differential is necessarily something less than one standard deviation above the mean. Hence, we expect a second rank for the SPA lot, and its expected value in Plantation 69 is 2 x 9 = 18.

The commercial check lots, which represent nursery run stock, have in theory a selection differential of zero. Since they are ranked third, the expected value in Plantation 69 is 3 x 9 = 27.

Only one chi-square, that of the clonal progenies in Plantation 69, indicated a significant difference between the observed and expected rank sums (table 4). However, chi-square for the goodness of fit test of all observations, taken as a whole, is 15.12 at 8 degrees of freedom and is not significant at the .05 level. The chi-squares for each group are also not significant (at 3 degrees of freedom for each group). The high observed rank sum for Group 1 in Plantation 69 probably results from the very poor performances of the clonal progenies in both rust resistance traits and in survival (table 3). The clonal progenies do not rank third for any other trait in any other plantation. Finally, the heterogeneity chi-square for each group is not significant. This means that the relative ratios of observed rank sums among the three groups are homogenous from one plantation to another,

Table 1.--*Degrees of freedom (d.f.), mean squares (MS), and significances of differences among groups for nine traits in four* loblolly *pine progeny test plantations in Georgia*



Source	Plantation 69 d.f.	69 MS	Plantation 75 d.f.	75 MS	Plantation 76 d.f.	76 MS	Plantation 77 d.f.	77 MS
				HEIGHT				
Among groups	2	0.193	2	1.065	2	1.664	2	2.649
Error	136	.288	58	1.830	132	.668	95	1.480
				DBH				
Among groups	2	2.07	2	24.72	2	.46	2	5.59
Error	136	2.12	59	605.97	132	2.94	95	7.98
				TREE VOLUME				
Among groups	2	.001	2	.010*	2	.001	2	.004
Error	136	.001	59	.003	132	.002	95	.002
				PLOT VOLUME				
Among groups	2	.158	4[a]/	.247*	2	.068	2	.032
Error	136	.392	65	.067	132	.471	97	.044
				GALLS/TREE				
Among groups	2	.059	2	1.76*	2	.065	2	.387
Error	136	.075	71	.42	132	.213	97	.292
				TREES RUST-FREE				
Among groups	2	89.15*	--[b]/	--	2	5.74	--[b]/	--
Error	136	25.21	--	--	132	22.55	--	--
				STRAIGHTNESS INDEX				
Among groups	2	.880**	2	.123	2	.672*	2	.793
Error	136	.095	59	.532	132	.158	95	.467
				CROWN/HEIGHT RATIO				
Among groups	2	31.54**	2	52.86	2	3.77	2	31.61
Error	136	4.58	70	31.69	132	17.37	97	22.56
				SURVIVAL				
Among groups	2	75.03	2	596.69	2	16.50	2	79.82
Error	136	295.14	85	328.55	132	110.23	97	330.26

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[a]/ The mean squares and degrees of freedom were synthesized by means of the Satterthwaite-Cochran approximation in a 2-way ANOVA with unequal hut proportional subclass numbers (Snedecor 1956).

[b]/ No comparisons due to very high infection,

* Difference is statistically significant at the .05 level.

** Difference is statistically significant at the .01 level.

Table 2.--Duncan's multiple range tests comparing means of three groups for nine traits in four loblolly pine progeny test plantations in Georgia

	Plantation			
Group	69	75	76	77
		HEIGHT, m		
Clonal progenies	14.3 a[a]	13.6 a	15.0 a	14.8 a
Seed production area lot	14.2 a	13.0 a	14.7 a	14.8 ab
Commercial check lots	14.1 a	13.3 a	14.4 a	14.0 b
		DBH, cm		
Clonal progenies	21.3 a	23.7 a	20.2 a	19.3 a
Seed production area lot	20.5 a	21.3 a	19.8 a	19.8 a
Commercial check lots	21.2 a	23.5 a	20.0 a	18.3 a
		TREE VOLUME, m^3		
Clonal progenies	0.21 a	0.21 a	0.18 a	0.16 a
Seed production area lot	.19 a	.15 b	.16 a	.16 a
Commercial check lots	.20 a	.20 ab	.16 a	.13 a
		PLOT VOLUME, m^3		
Clonal progenies	2.54 a	0.34 a	2.24 a	0.46 a
Seed production area lot	2.39 a	.17 a	2.28 a	.41 a
Commercial check lots	2.66 a	.20 a	2.09 a	.39 a
		GALLS/TREE, $\sqrt{X + .5}$		
Clonal progenies	2.1 a	2.1 b	2.4 a	2.8 a
Seed production area lot	2.0 a	1.5 a	2.5 a	3.1 a
Commercial check lots	2.1 a	2.4 b	2.4 a	3.0 a
		TREES RUST-FREE, ARCSIN $\sqrt{\text{percent}}$		
Clonal progenies	8.8 a	--	9.1 a	--
Seed production area lot	14.3 a	--	7.9 a	--
Commercial check lots	9.8 a	--	5.7 a	--
		STRAIGHTNESS INDEX		
Clonal progenies	2.8 a	3.4 a	3.4 a	3.2 a
Seed production area lot	3.0 ab	3.7 a	3.8 b	3.5 a
Commercial check lots	3.2 b	3.4 a	3.6 ab	3.5 a
		CROWN/HEIGHT RATIO		
Clonal progenies	52.6 a	44.1 a	52.7 a	56.6 a
Seed production area lot	55.1 b	44.7 a	53.8 a	59.7 a
Commercial check lots	54.2 b	47.7 a	53.1 a	58.2 a
		SURVIVAL, ARCSIN $\sqrt{\text{percent}}$		
Clonal progenies	58.5 a	34.7 a	46.9 a	51.5 a
Seed production area lot	62.0 a	27.6 a	49.0 a	46.2 a
Commercial check lots	61.3 a	25.9 a	45.8 a	52.8 a

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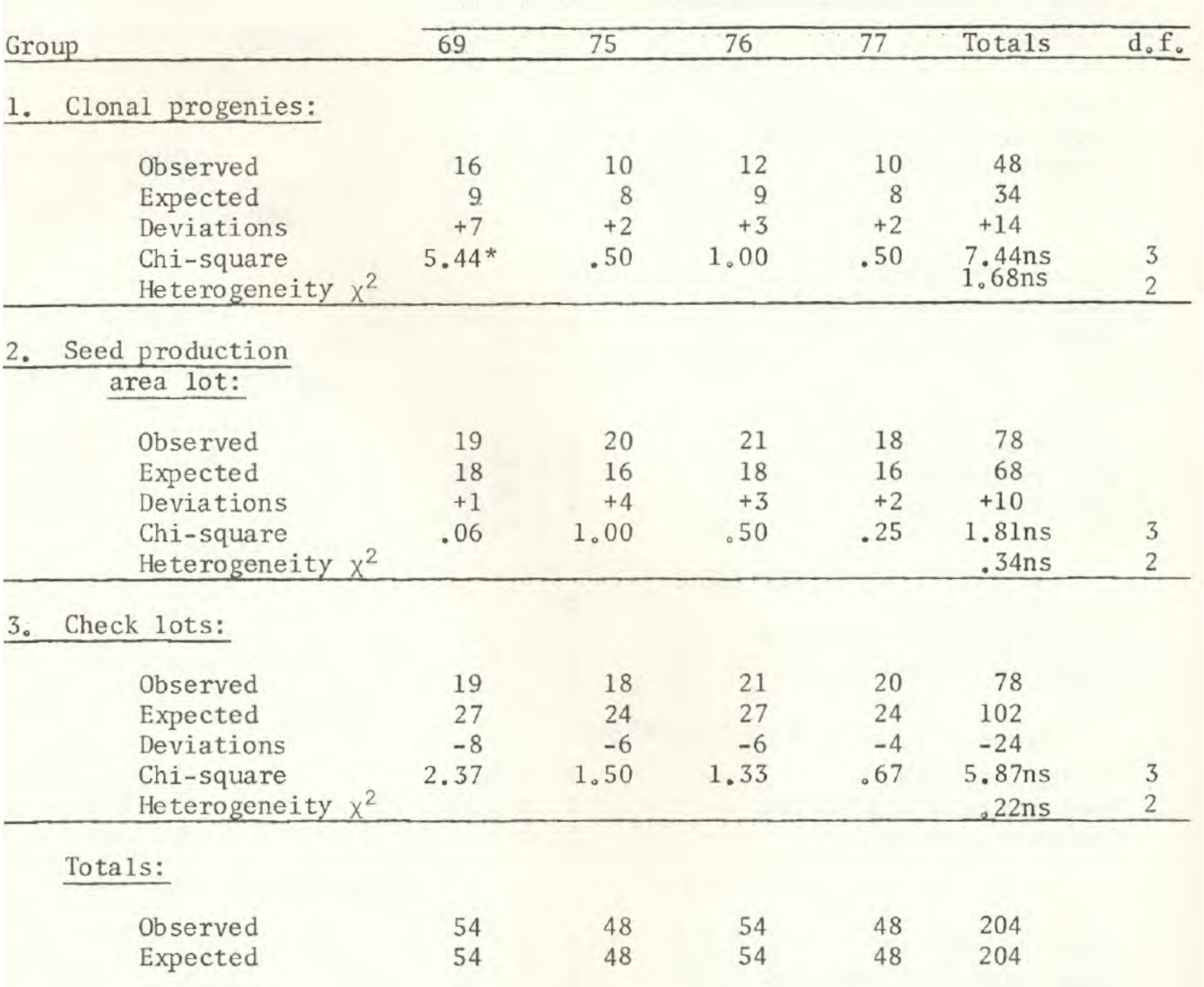
[a] Within plantations, group means followed by the same letter are not significantly different at the .05 level.

Table 3.--Rank comparisons (1 = best) of three groups for nine traits in four loblolly pine progeny test plantations in Georgia

Group	Plantation 69	75	76	77
		HEIGHT		
Clonal progenies	1	1	1	1
Seed production area lot	2	3	2	2
Commercial check lots	3	2	3	3
		DB.H		
Clonal progenies	1	1	1	2
Seed production area lot	3	3	3	1
Commercial check lots	2	2	2	3
		TREE VOLUME		
Clonal progenies	1	1	1	1
Seed production area lot	3	3	3	2
Commercial check lot	2	2	2	3
		PLOT VOLUME		
Clonal progenies	2	1	2	1
Seed production area lot	3	3	1	2
Commercial check lots	1	2	3	3
		GALLS/TREE		
Clonal progenies	3	2	2	1
Seed production area lot	1	1	3	3
Commercial check lots	2	3	1	2
		TREES FREE OF RUST		
Clonal progenies	3		1	--
Seed production area lot	1		2	--
Commercial check lots	2		3	--
		STRAIGHTNESS		
Clonal progenies	1	2	1	1
Seed production area lot	2	3	3	2
Commercial check lots	3	1	2	3
		CROWN/HEIGHT RATIO		
Clonal progenies	1	1	1	1
Seed production area lot	3	2	3	3
Commercial check lots	2	3	2	2
		SURVIVAL		
Clonal progenies	3	1	2	2
Seed production area lot	1	2	1	3
Commercial check lots	2	3	3	1

Table *4.--Sums of ranks, their expected values, deviations from expected and Chi-squares for each group in each of four plantations in an interaction Chi-square test for goodness of fit a/*



Group	69	75	76	77	Totals	d.f.
1. Clonal progenies:						
Observed	16	10	12	10	48	
Expected	9	8	9	8	34	
Deviations	+7	+2	+3	+2	+14	
Chi-square	5.44*	.50	1.00	.50	7.44ns	3
Heterogeneity χ^2					1.68ns	2
2. Seed production area lot:						
Observed	19	20	21	18	78	
Expected	18	16	18	16	68	
Deviations	+1	+4	+3	+2	+10	
Chi-square	.06	1.00	.50	.25	1.81ns	3
Heterogeneity χ^2					.34ns	2
3. Check lots:						
Observed	19	18	21	20	78	
Expected	27	24	27	24	102	
Deviations	-8	-6	-6	-4	-24	
Chi-square	2.37	1.50	1.33	.67	5.87ns	3
Heterogeneity χ^2					.22ns	2
Totals:						
Observed	54	48	54	48	204	
Expected	54	48	54	48	204	

Total Chi-square = 15,12ns at 4(3-1) = 8 d.f.

* Difference is statistically significant at the 0.05 level.

ns Difference is not statistically significant at the 0.05 level.

The means of all trait ranks for each group in each plantation are listed in Table 5, These averages are then themselves ranked for the three groups in each plantation; these ranks are listed in parentheses. There are ties in Plantations 69 and 76 for the second and third ranks. This nonparametric 2-way ANOVA of ranks obtained a Chi-square = 6.00, which is significant at the .05 level with 2 degrees of freedom. This method, called Friedman's procedure, is a randomized complete-block design in which we have treated the four plantations as replications. Since the rank totals for Groups 1, 2 and 3 are 4.0, 10.0 and 10.0 respectively, it seems legitimate to conclude that the clonal progenies perform better for most traits than do the SPA or commercial check lots. We may also conclude that we can find no significant difference between the SPA lot and the commercial checks.

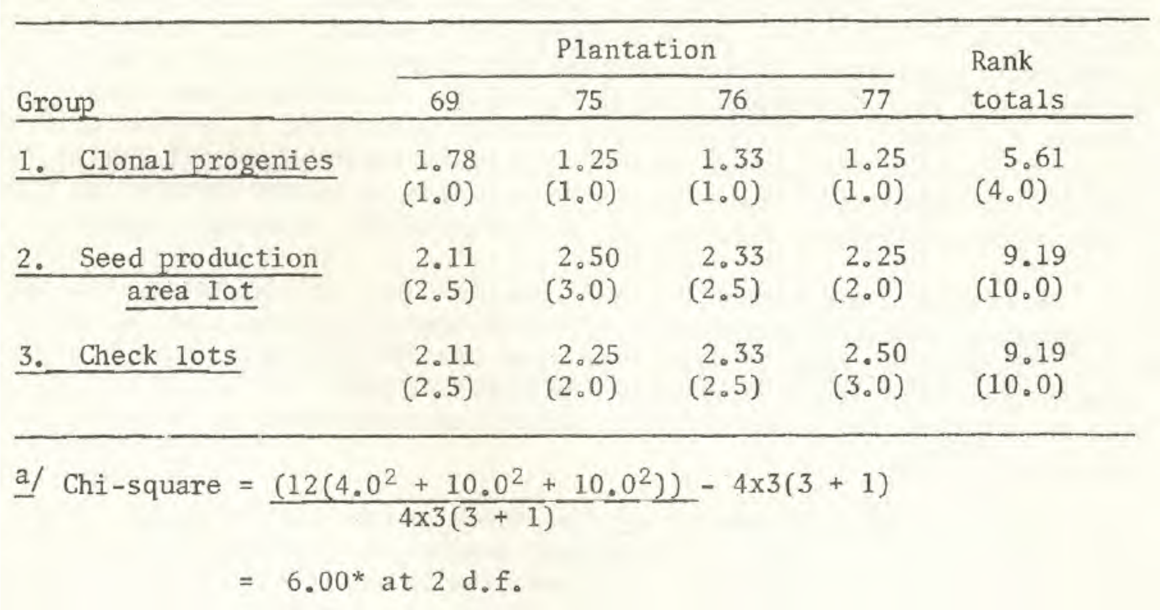
We should caution that Group 2, the SPA lot, is the least well replicated group in each plantation. If these tests had been planned to detect real differences among groups, more than one SPA lot would have been included, together with controls from stands adjacent to each SPA lot. One SPA lot can not sample the stand variation which has been shown to exist in Georgia (La Farge 1974).

The relative performances of the three groups for specific traits are also of interest. Group 1, the clonal progenies, performs most predictably for the growth traits (height, dbh and tree volume), and least predictably for traits measuring incidence of fusiform rust (galls/tree, percentage of trees free of rust). Survival is also unpredictable because in these tests it is largely a function of incidence of rust. Similarly, plot volume seems less consistent in its rankings than tree volume because it is partly a function of survival. Generally, the progeny testing of GFC clones has not shown the selection of rust-free phenotypes in natural stands to be very successful. Probably many of the ortets scored as rust-free had in fact lost branch galls through natural pruning.

The results in this study are consistent with those of the Texas Forest Service Tree Improvement Program (1962), in which the SPA seedlings had poorer height and diameter growth than the commercial control. However, they do not agree with results reported by Easley (1963), in which the SPA lot dramatically outgrew the nursery run stock on both clay and sandy sites. Since this study did not compare the SPA lot with any controls from stands adjacent to the seed production area, our results are not comparable with those of Gansel (1967), who reported slight but nonsignificant gains of a seed production area over an adjacent stand control.

CONCLUSIONS

The results of this study have very limited application. They tell us more about the selection of superior phenotypes for clonal seed orchards than they do about SPA selections. They suggest limited but acceptable gains for selection of plus trees in natural stands for inclusion in clonal seed orchards. However, they do not prove, nor do they disprove, the potential genetic gains obtainable in seed production areas. More sensitive field tests are needed to make such evaluations. Until then, seed production areas represent good forestry practice, Table *5.--Means of ranks in* all *traits of each group in each plantation, and ranks of the means in each plantation (in parentheses), Friedman's test for differences among groups a/*



Group	Plantation 69	75	76	77	Rank totals
1. Clonal progenies	1.78 (1.0)	1.25 (1.0)	1.33 (1.0)	1.25 (1.0)	5.61 (4.0)
2. Seed production area lot	2.11 (2.5)	2.50 (3.0)	2.33 (2.5)	2.25 (2.0)	9.19 (10.0)
3. Check lots	2.11 (2.5)	2.25 (2.0)	2.33 (2.5)	2.50 (3.0)	9.19 (10.0)

a/ Chi-square $= \frac{(12(4.0^2 + 10.0^2 + 10.0^2))}{4x3(3 + 1)} - 4x3(3 + 1)$

$= 6.00^*$ at 2 d.f.

* Difference is statistically significant at the 0.05 level.

LITERATURE CITED

Easley, L. T. 1963. Growth of loblolly pine seed produced in a seed production area vs. nursery run stock. *J.* Forest. 61(5): 388-389.

Gansel, C. R. 1967. Are genetic gains from seed production areas small? J. Forest. 65(9): 634-635.

La Farge, T. 1974, Genetic variation among and within three loblolly pine stands in Georgia. For. Sci, 20(3):272-2750

Snedecor, G. W. 1956, Statistical methods. 534 p. Ames: The Iowa State College Press,

Sokal, R. R,, and Rohlf, F. J. 1969. Biometry. 776 p. San Francisco: W. H. Freeman and Company.

Steel, R. G. D., and Torrie, J. H. 1960. Principles and procedures of statistics. 481 p, N.Y.: McGraw-Hill Book Company, Inc.

Tenth Progress Report of Cooperative Forest Tree Improvement Program. 1962, Texas Forest Service. Cir. 77, pp. 18,