PHENOTYPIC SELECTION EFFECTIVE IN A NORTHERN RED OAK SEEDLING SEED ORCHARD

T. La Farge and R. A. Lewis 1/

Abstract.--In 1984 a progeny test of 220 northern red oak open-pollinated families, established in 1973 by the Tennessee Valley Authority, was converted to a seedling seed orchard. Located on the Watauga District of the Cherokee National Forest, this orchard was measured for seven traits in August, 1985 at age 13 years. Significant differences ($p \leq 0.001$) were found among families for height, DBH, straightness, forking, D H, survival, and defoliation. Single tree heritabilities ranged from 0.113 for D H to 0.375 for percent survival. Family heritabilities ranged from 0.240 for D H to 0.711 for survival. On the basis of these results, 21 families have been rogued, and all families have been thinned to the best one or two trees in each of eight four-tree-row plots. Selection differentials and genetic gains showed that positive gains obtained from single tree selection were greater than those obtained for family selection. It is concluded that phenotypic selection in plantations will work well in northern red oak.

Additional keywords: Quercus rubra L., seedling seed orchard, heritability, selection differential, genetic gain, roguing.

Northern red oak (*Guercus rubra* L.) is among the most important of the northern hardwoods, and it attains the largest size of the eastern upland oaks (Core 1971). Its range extends from New Brunswick, southern Ontario, and Minnesota south to Alabama and Georgia. This species is most frequently found in coves and on lower and middle slopes having northern and eastern aspects. It grows best on fine textured soils and topographies favoring a high water table.

Planting red oak and establishing a stand is not difficult if done on a suitable site. Some plantings in the southern Appalachians have averaged better than 90 percent survival (Russell 1971). Early provenance tests have indicated that differences among geographic sources are less than differences among trees within sources, so that single tree selection would seem to have the greatest potential for genetic gain (Cech 1971).

The present study was undertaken after a decision was made to convert a progeny test to a seedling seed orchard. The trees were measured, seven traits were analyzed, and the test was rogued and thinned as the first stage of selection. The procedures used and genetic gains attained are reported herein.

1/ Eastern Zone Geneticist and Supervisory Geneticist, respectively, U.S.D.A. Forest Service, Region 8, Atlanta, Georgia. The authors wish to express their appreciation to Ken Proffit, Seed Orchard Manager of the Northern Red Oak Seed Orchard, Tom Crews, Watauga District Silviculturist, and B. D. Barr, Watauga District Ranger. Without considerable help in measuring, thinning, and caring for this orchard by these people, this study would not have been possible.

HISTORY

The Tennessee Valley Authority (TVA) began a breeding program for the oaks in the early 1960s and initially used mass selection of superior phenotypes. However, by the late 1960s data obtained from hardwood progeny tests in the South had demonstrated that phenotypic mass selection is not effective for growth traits. Hence, they decided to establish a large breeding population of open-pollinated families. This population was to provide data on geographic variation and plant material to be used to produce seed orchards. To accomplish this, the tree improvement staff at TVA selected a representative sample of dominant and codominant trees having good form from several geographic sources (Farmer 1980).

In the spring of 1973 the TVA planted a progeny test of 220 open-pollinated northern red oak families on the Watauga Ranger District of the Cherokee National Forest in Tennessee. The field design was eight replications of four trees of each progeny in row plots at a 10 X 10-foot spacing. This test was one of 11 plantations. The other 10 plantations are located in Kentucky, Tennessee (3), Alabama, Georgia, North Carolina, Illinois, Indiana, and Ohio. The seed sources used represented all of these states except Georgia and Ohio.

The progeny test area is located in the Dry Hill section of the Watauga Ranger District and is a quarter of a mile from Watauga Lake. The ecological management unit is on broad ridgetops and upper slopes of low lying intermountain ridges having elevations of less than 2,500 feet. The soil texture is a medium silty clay loam to clay loam that grades to clay at depths of three to five feet. Depth to the underlying limestone bedrock ranges between six and 12 feet. The average soil moisture regime is dry. Slopes vary from two to 35 percent, but most are between six and 20 percent. The test area occupies 16.2 acres.

The TVA performed annual maintenance of the test by disking or mowing until 1979, when they dropped funding for the project. In 1983 the Watauga District resumed annual mowing to prevent weed-tree species from taking over the site. Deer browsing, rodents, and mowing accidents have taken their toll, and growth has been slowed by a heavy sod of fescue grass. Overall survival was 44.4 percent as of September, 1985, when the measurements for the current data analyses were taken.

In 1982 the TVA asked Region 8 to assume full responsibility for the test. Region 8 accepted and decided to thin and rogue the test to convert it to a seedling seed orchard. Although height and diameter measurements were made in 1982 at age 10, a more complete set of measurements was made at age 13.

METHODS

Six traits were measured in August and September of 1985. They were: (1) height to the nearest foot; (2) diameter at breast height (DBH) to the nearest inch; (3) straightness, by an index of 1 = crooked to 6 = straight; (4) forking, by an index in which 1 = 3 or more forks, 2 = 2 forks, 3 = 1 fork, and 4 = 0 forks; (5) insect defoliation, by an index of 0 = no defoliation, 1 = partial defoliation, and 2 = complete defoliation; and (6) apical dominance, by an index in which 1 = no dominance and 2 = complete dominance. Apical dominance was later dropped from consideration after it proved impossible to estimate subjectively. The indexes used in this study are similar to many used in biology, despite questions about their frequency distributions (Sokal and Rohlf 1969).

Two additional traits were included in the analyses: percent survival and D^2H, the latter trait being computed from the DBH and height measurements as an approximation of single-tree volumes. Percent survival was also analyzed as arcsine X (square root of proportion), but this transformation accomplished no reduction in mean square error of the analysis of variance and was, therefore, dropped.

All data were analyzed by a one-way analysis of variance on a UNIVAC 1100/84 computer with the BioMedical Data Processing (BMDP) package, program P7D (Dixon 1983). Selection differentials, phenotypic and genotypic standard deviations, selection intensities, and genetic gains were all calculated by methods given by Becker (1984). All analyses had to be performed in two overlapping data sets, since BMDP program P7D could not handle the size of the complete data set. Therefore, blocks 1 - 6 were analyzed as Data Set #1, and Blocks 1,2,3,4,7,8 were analyzed as Data Set #2, blocks 1 - 4 being common to both sets. Results from both data sets are listed in all tables.

After analysis, we decided to use all seven traits to identify the poorest families, so that the orchard could be rogued and thinned with a combined family and single tree selection. The roguing system used was a variant of the independent culling levels selection method and was accomplished by means of a spread sheet. Threshold limits were arbitrarily chosen for each trait so that they fell toward the lower limit of the range of variation of all families. Any family which fell below these limits for at least three traits was marked for roguing. On this basis 21 of the 220 families were rogued from the orchard.

Single tree selection was accomplished by thinning all but one, or occasionally two, trees from each plot. In a very few cases no trees were left in a plot, because none appeared capable of survival. Of course, many plots were already empty, since survival was only 44.4 percent.

RESULTS

The means and numbers of observations of the seven traits analyzed are listed in Table 1. At age 13 tree height ranged from one to 26 feet and DBH from zero to six inches. All except one of the seven traits showed significant differences among families at the 0.001 probability level in both data sets (Table 2). The family heritabilities are somewhat low, but the single tree heritabilities, while not high, are in the usual range reported for most species (Table 3). The heritabilities for height and survival are especially encouraging.

Once all roguing and thinning had been accomplished and all remaining trees identified, it was possible to calculate selection differentials and intensities of selection. These are listed for families in Table 4 and for single trees in Table 5. The percentage genetic gains for family, single tree, and combined selection (Table 6) were obtained from the appropriate heritabilities and selection differentials.

Table 1.--Means and numbers of observations for seven traits in two data sets of a northern red oak seedling seed orchard

Trait	Data Set: # 1 Mean	Data Set: # 1 Number of trees	Data Set: # 2 Mean	Data Set: # 2 Number of trees
Height, feet	11.64	2,379	11.17	2,309
DBH, inches	1.52	2,379	1.46	2,309
Straightness, index	2.20	2,380	2.15	2,310
Forking, index	1.71	2,379	1.67	2,309
D^2H, inches-feet	63.21	2,379	57.58	2,309
Survival, percent	45.80	5,179	50.00	5,215
Insect defoliation, index	.63	2,377	.60	2,307

Table 2.--Degrees of freedom (d.f.), mean squares (MS) and significances of differences among families in a one-way analysis of variance of seven traits in two data sets of a northern red oak seedling seed orchard

Source	Data Set: # 1 d.f.	Data Set: # 1 MS	Data Set: # 2 d.f	Data Set: # 2 MS
		HEIGHT		
Among families	218	48.61 ***	217	43.75 ***
Error	2,160	29.83	2,091	27.92
		DBH		
Among families	218	1.81 ***	217	1.77 ***
Error	2,160	1.30	2,091	1.27
		STRAIGHTNESS		
Among families	218	1.19 ***	217	1.19 ***
Error	2,161	.83	2,092	.83
		FORKING		
Among families	218	.93 ***	217	.90 ***
Error	2,160	.68	2,091	.66
		D^2H		
Among families	218	11,550.34 **	217	10,547.66 ***
Error	2,160	8,776.59	2,091	7,734.16
		SURVIVAL		
Among families	219	.68 ***	219	.76 ***
Error	4,977	.23	4,995	.22
		INSECT DEFOLIATION		
Among families	218	.63 ***	217	.59 ***
Error	2,158	.41	2,089	.41

** Significant at the 0.01 probability level
*** Significant at the 0.001 probability level

CONCLUSIONS

The selection intensities in Tables 4 and 5 vary among traits because different families and trees were selected for each trait by independent culling levels. These intensities are lower than they would be for selection for only one trait, and they reflect the compromises needed to achieve selection for more than one trait. The best tree in each plot for every trait is not always selected.

The fact that none of the gains obtained from combined family and single tree selection in Table 6 are large also results from the selection by independent culling levels for seven traits simultaneously. If we had selected only the very best trees in the best families for one trait, the gain for that trait would have been considerably higher. Hence, we believe that the achievement of small positive gains for all seven traits is in itself a worthy accomplishment.

The family heritabilities appear to be small compared to those reported for some other species (Table 3). This probably results from the low effective family size (harmonic mean = nb - 10.6 trees per family). With low family sizes, the denominator of the heritability equation becomes larger, thus reducing the value obtained for family heritability.

On the other hand, the single tree heritabilities are fairly normal, and the single tree genetic gains are quite respectable (Table 6), especially when we consider the history of mowing and deer browse problems in this orchard and the fact that selection intensity did not exceed the best one of four trees per plot. We conclude from these gains that phenotypic selection seems to work quite well in a progeny test or seedling seed orchard, in contrast to the conclusion by Farmer (1980) that phenotypic selection in natural stands is not effective for growth traits. However, the small effective family sizes in this study do not permit us to conclude that family selection would not work in a progeny test or seed orchard with larger numbers of trees per family.

This study has at least one major limitation. The results reported here are from only one of 11 locations. Hence, we have no means of accounting for genotype x environment interactions and their potentially negative effects on heritability estimates and genetic gains. In fact, in an initial study of six of the other 10 progeny tests, Farmer (1980) obtained rather low correlations of family means between the Watauga test and the Ohio test (r = 0.18) and the Watauga test and the Land-Between-the-Lakes (Tennessee) test (r = 0.42).

Nevertheless, the results in this test should be reasonably applicable to any plantations of seedlings from this orchard which might be established in the future on the Watauga District or on any surrounding areas at similar elevations.

A question not directly addressed in this study is the effect of geographic variation. An examination of the 21 rogued families revealed that they broadly represented the geographic seed sources in the whole test. Hence, no geographic effect is apparent.

A primary concern about planting seedlings from this orchard will be that common to regenerating upland oaks in general. Johnson (1986) has described the use of a medium density shelterwood overstory, which, together with herbicidal control of competing understory vegetation, can result in successful establishment of up to one half of the planted trees two years after the shelterwood is removed.

A serious problem with planting northern red oak is slow initial growth, which averages only one foot per year until the seedlings become established. However, there is an emerging technology using plastic tree shelters which may alleviate this problem. These are available in several forms, and they are being investigated (Tuley 1984). In addition to protecting seedlings from

Table 3.--Family and single tree heritabilities and their standard errors for seven traits in two data sets in a northern red oak seedling seed orchard

	Heritabilities in Data Set:			
	# 1		# 2	
Trait	Family	Single tree	Family	Single tree
Height	0.386 ± 0.044	0.219 ± 0.054	0.362 ± 0.029	0.203 ± 0.054
DBH	.282 ± .039	.139 ± .050	.282 ± .039	.143 ± .049
Straightness	.303 ± .040	.154 ± .049	.303 ± .040	.157 ± .043
Forking	.269 ± .038	.131 ± .047	.267 ± .038	.133 ± .049
D^2H	.240 ± .037	.113 ± .047	.267 ± .038	.133 ± .042
Survival	.662 ± .051	.306 ± .042	.711 ± .057	.375 ± .047
Insect defoliation	.349 ± .042	.189 ± .052	.305 ± .040	.159 ± .051

Table 4.--Selection differentials (SD), genotypic standard deviations (sd_f), and selection intensities (i) of families selected for seven traits in two data sets in a northern red oak seedling seed orchard

	Data Set:					
	# 1			# 2		
Trait	SD	sd_f	i	SD	sd_f	i
Height, feet	0.221	1.315	0.168	0.252	1.223	0.206
DBH, inches	.039	.217	.180	.046	.217	.212
Straightness, index	.029	.182	.159	.036	.184	.196
Forking, index	.018	.152	.118	.018	.151	.119
D^2H, inches-feet	2.582	15.984	.162	2.751	16.304	.169
Survival, percent	.011	.138	.080	.013	.151	.086
Insect defoliation, index	-.009[1]	.142	.063	-.011	.130	.085

[1] The choice of this index was such that lower values meant less insect defoliation; hence, negative values mean positive selection differentials.

LITERATURE CITED

Becker, W. A. 1984. Manual of Quantitative Genetics, Fourth ed. Academic Enterprises, Pullman, WA. 190 p.

Cech, F. C. 1971. Tree improvement research in oak species. In Oak symposium proceedings, p. 55 - 59. N. E. For. Exp. Sta., Upper Darby, PA.

Core, E. L. 1971. Silvical characteristics of the five upland oaks. In Oak symposium proceedings, p. 19 - 22. N. E. For. Exp. Sta., Upper Darby, PA.

Dixon, W. J. 1983. P7D 9.2 Description of groups (strata) with histograms and analysis of variance. In W. J. Dixon (ed.) BMDP statistical software - 1983 printing with additions, p. 105 - 115. Univ. of California Press, Berkeley.

Farmer, R. E. Progress report. An open-pollinated progeny test in northern red oak (Quercus rubra L.). Division of Land and Forest Resources, Tennessee Valley Authority, Norris, TN. 1980. (Unpublished; 75 p.)

Johnson, P. S., C. D. Dale, K. R. Davidson and J. R. Law. 1986. Planting northern red oak in the Missouri Ozarks: a prescription. North. J. Appl. For. 3: 66-68.

Russell, T. E. 1971. Seeding and planting upland oaks. In Oak symposium proceedings, p. 49 - 54. N. E. For. Exp Sta., Upper Darby, PA.

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

Tuley, G. 1984. Shelters improve the growth of young trees. Aboric. Res. Note 49, DOE Arboric. Adv. and Inform. Service, 4 p.