AN ANALYSIS OF PHENOTYPIC SELECTION IN NATURAL STANDS OF NORTHERN RED OAK (*QUERCUS RUBRA* L.)

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Abstract: Comparison of growth and stem quality parameters of 19-year-old progeny from superior and comparison trees indicates that rigorous phenotypic selection of trees in natural stands may not be an efficient method of parent tree selection for *Quercus rubra* L. Total tree height, dbh, number of branches in the butt log, fork height, and number of mainstem crooks of progeny from 11 phenotypic select trees and their co-occurring comparison trees were analyzed. Pooled data from 4 test sites indicated no difference in dbh or number of mainstem crooks among select and comparison families. However, comparison families were significantly ($p \leq 0.05$) taller, had significantly less branches in the butt log, and higher fork heights than select families. Similar patterns of variation were also found within test sites. The large degree of within-stand variation in growth and stem quality traits among families indicates that selecting several phenotypically above-average candidate trees may be more effective than rigorously selecting a smaller number of phenotypically superior *Q. rubra* trees.

INTRODUCTION

Mass selection of superior phenotypes is the most widely used method of obtaining material for the initial stages of tree breeding programs (Zobel and Talbert 1984). Regional *Quercus rubra* L. improvement programs have recently been initiated in both the central and southeastern U.S. (Cox and Schlarbaum 1991, Robison and Overton 1987). These programs have used mass selection to provide material for the establishment of seed orchards and test plantings. Results of relatively young provenance/progeny tests of *Q. rubra* have shown a large degree of intra-stand and provenance growth variation (Farmer and others 1981, Houston 1987). This suggests that gains through mass selection are possible however, gains from plus-tree selections have proved inconsistent (Robison 1988). Previous tests have focused primarily on growth characteristics which, for some hardwood species, have relatively low narrow-sense heritabilities (Zobel and Talbert 1984). The use of phenotypic selections in natural stands of *Q. rubra* remains appealing in light of potential stem quality gains, certain aspects of which may have high narrow-sense heritabilities (Zobel and Talbert 1984). Little information on potential stem quality gains is available for *Q. rubra* as previous analyses of provenance/progeny tests were completed in relatively young plantings (Kriebel 1993).

This paper addresses the question of whether mass selection criteria need be extremely rigorous to provide gains in the initial stages of *Q. rubra* tree improvement programs. Specifically, we were interested in comparing the performance of open-pollinated progeny from some of the best phenotypes in the region to the performance of open-pollinated progeny from several above-average phenotypes or "comparison" trees from the same stands as the select phenotypes. Results of our analysis may aid in designing effective selection strategies for *Q. rubra*.

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METHODS

Experimental Materials

We studied 19-year growth and stem quality data from 43 open-pollinated *Quercus rubra* L. families from a provenance/progeny test of 226 *Q. rubra* families established in 1973 by the Tennessee Valley Authority (TVA) (Farmer 1980). Mother trees were located throughout the Tennessee and lower Ohio Valleys between Long. 81°58'-89°00' W, Lat. 34°15' - 38°50' N, and 152 - 1402 m elevation. Acorns were collected in the fall of 1971 from dominant and co-dominant trees with good size and form. Twenty-two of the mother trees were selections made in the 1960's by the TVA. These mother trees were the best phenotypes in their stand, based on form and size, as well as being representative of the best phenotypes in the region (K. Taft, TVA, personal communication). Fifty-nine additional mother trees were located in stands with the select trees and could be considered "comparison" trees in the mass selection process (Zobel and Talbert 1984). The remaining 145 mother trees were above-average phenotypes located in stands where intensive selection had not been conducted by TVA personnel (D. Scanlon, TVA, personal communication).

Establishment and Measurement of Provenance/Progeny Tests

Acorns were planted in 2 replicates at a TVA nursery near Norris, TN (Lat. 36° N, Long. 84° W), in the fall of 1971. Seedlings were lifted in the spring of 1973 and graded for size. The 16 largest seedlings of each family were planted at test site I (Fig. 1), and the remaining ungraded seedlings were distributed to 11 other test sites. A randomized complete block design was selected for each test site. However, the number of blocks, trees per plot, and families differed by test site. By 1991, only 4 plantations remained intact for analysis (Fig. 1, Table 1). Total number of families, family plot size, number of replicate blocks, and number of select and comparison families included in our study are shown for each test site in Table 1.

Table 1. Description of *Quercus rubra* provenance/progeny test sites.

Test Site	Number of Families			Blocks	Plot Size (# of trees)
	Total	Select	Comparison		
I LBL, KY	226	10	30	8	2
II Parke Co., IN	134	8	17	3	2
III Ames, TN	80	3	2	6	4
IV Coshocton,OH	176	10	30	7	4

All test sites were evaluated during the dormant season of 1991-1992. Growth and stem quality measurements used in this analysis included total tree height (THT); diameter at 1.3 m height (DBH); number of branches (BR#), live or dead, in the butt log (0.32-5.3 m height); height to lowest fork (FKHT, fork defined as the occurrence of 2 crown branches resulting in a mainstem deviation $\geq 10°$); and number of crooks below FKHT (CR#, crook defined as mainstem deviation $\geq 10°$). Heights were measured with a clinometer (Suunto) positioned 15.2 m from each tree. A diameter tape was used for DBH determination, and a height pole was used to designate the butt log. A protractor was used to establish angle deviation for fork and crook identification.

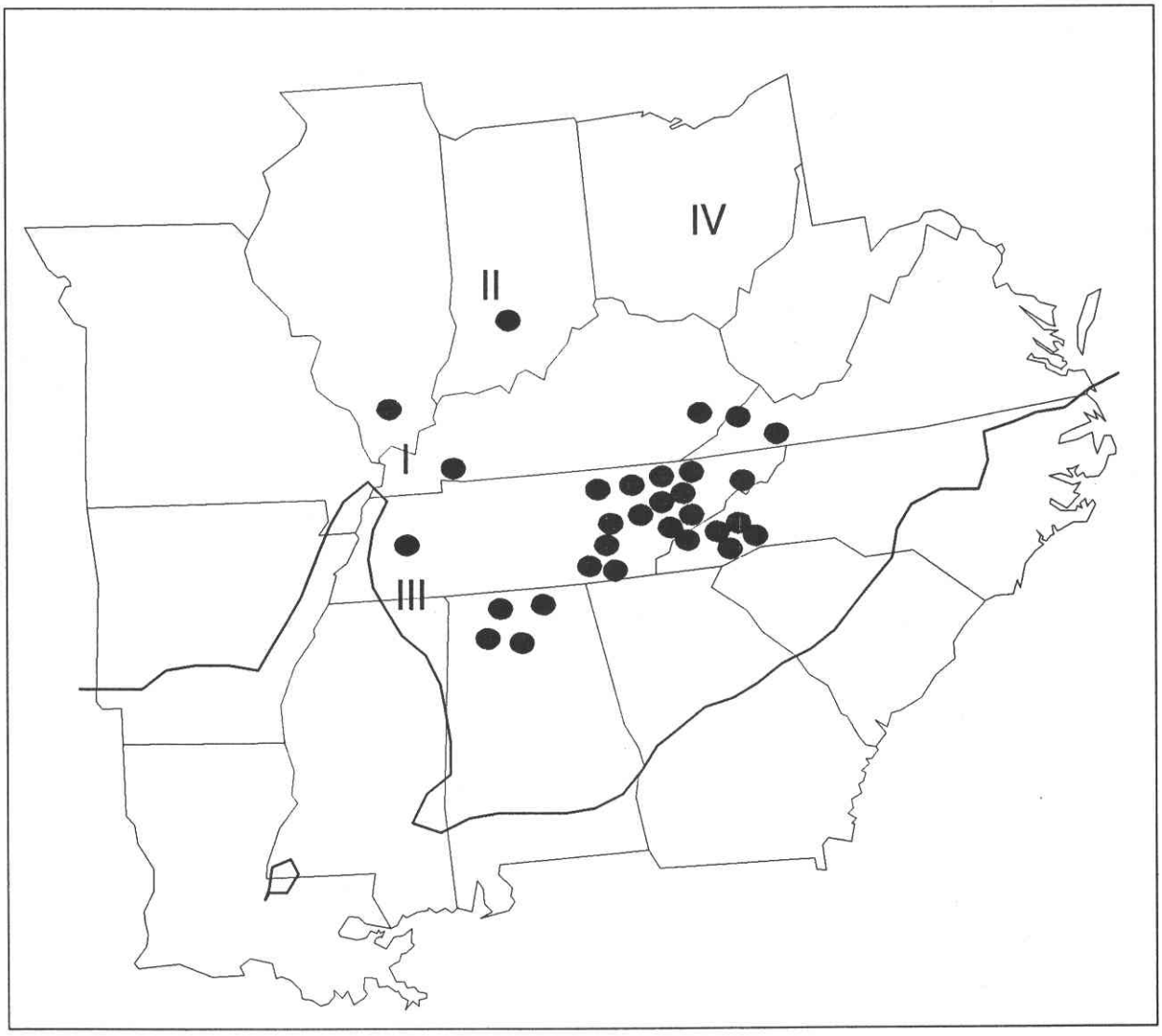

Figure 1. Stand location of mother trees (solid circles) and test site location (Roman numerals) of *Quercus rubra* L. genetic tests. Heavy lines indicate the natural range of *Q. rubra* L.

Data Analysis

Analyses were conducted on families from stands containing one select tree and at least one comparison tree. In the TVA test, several select trees were represented by a limited number of seedlings, and a small number of stands contained more than one select tree. Families of these trees were deleted from the analyses as were associated comparison tree families. The 145 families from stands lacking select trees also were deleted from the analyses. Measurements from families of the remaining 11 select trees and their 32 associated comparison trees formed the data set for our study.

Fork heights were converted to percent of total tree height (FKPER) and normalized using an arc sine transformation (Steel and Torrie 1980). All other variables were subjected to Wilk-Shapiro/rankit plots to check for normality. Data were subjected to a series of analyses and were analyzed untransformed. Pooled select and pooled comparison families were compared over all test sites as well as within test sites. Within-stand comparisons (i.e. analyses of select families and their associated comparison families) were also completed within test sites and for data pooled over all test sites. Two sample t-tests were used to detect differences at $p \leq 0.05$.

RESULTS AND DISCUSSION

Growth Variables

No significant differences ($p > 0.05$) in mean THT were found among pooled select and pooled comparison families within any of the test sites. Mean DBH of select versus comparison families was significantly different only at test site I (Fig. 2). Mean DBH for select families (12.05 cm) was 6.8% higher than comparison families (11.22 cm). None of the other test sites analyzed showed any differences among select and comparison families for DBH. While test site I was the location where the 16 largest seedlings of each family were planted, the importance of this in regards to a DBH difference among groups is not clear.

No significant differences ($p > 0.05$) were observed in analyses of data pooled over all test sites for mean DBH among select and comparison families, but mean THT's of select families were significantly less than those of comparison families (Fig. 3). However, the difference was relatively small, approximately 4 percent.

Stem Quality Variables

There were 12 possible variable/test site analyses evaluating pooled select versus pooled comparison family data within each test site. Of these 12 analyses, we found only 4 instances of significant differences ($p \leq 0.05$) for the stem quality variables (BR#, CR#, and FKPER) and only 2 instances where select families outperformed comparison families. Mean CR# was significantly less for select families (0.02) at test site I than for comparison families (0.12) but at test site II the opposite was true (Fig. 4). Differences for mean FKPER were also found at test sites I and II (Fig. 5). Only at test site II did select families perform better than comparison families, averaging 64.2 and 53.4 percent FKPER, respectively. No differences in select versus comparison families for mean BR# were found within test sites.

Data pooled over all test sites indicated no significant differences for mean CR# among select and comparison families. However, significant differences among groups in both BR# and FKPER were found ($p \leq 0.05$) (Fig. 6). Comparison families had the smaller mean BR# (7.14), compared to select families (7.99), representing a 10 percent difference. Comparison families also outperformed select families in FKPER having a mean of 70.7 compared to 66.0 for select families, representing a 7 percent difference.

Within-Stand Comparisons

Analysis of data pooled over all test sites found only 16 of the 51 within-stand comparisons of growth and stem quality variables significant ($p \leq 0.05$). Results of these analyses were expressed in terms of percent differences in means between select and comparison families (Table 2). Of the 16 significant differences, only 6 were positively associated with select families, while comparison families outperformed select families in 10 analyses.

The results of within-stand comparisons among select and comparison families within test sites were similar to the within-stand analyses that were pooled over test sites. Six significant differences ($p \leq 0.05$) were found out of 50 analyses performed on growth and stem quality variables for select versus comparison families in test site I. Only 2 of these significant results were positively associated with select families. Similar patterns occurred in within-stand analyses at each of the other test sites.

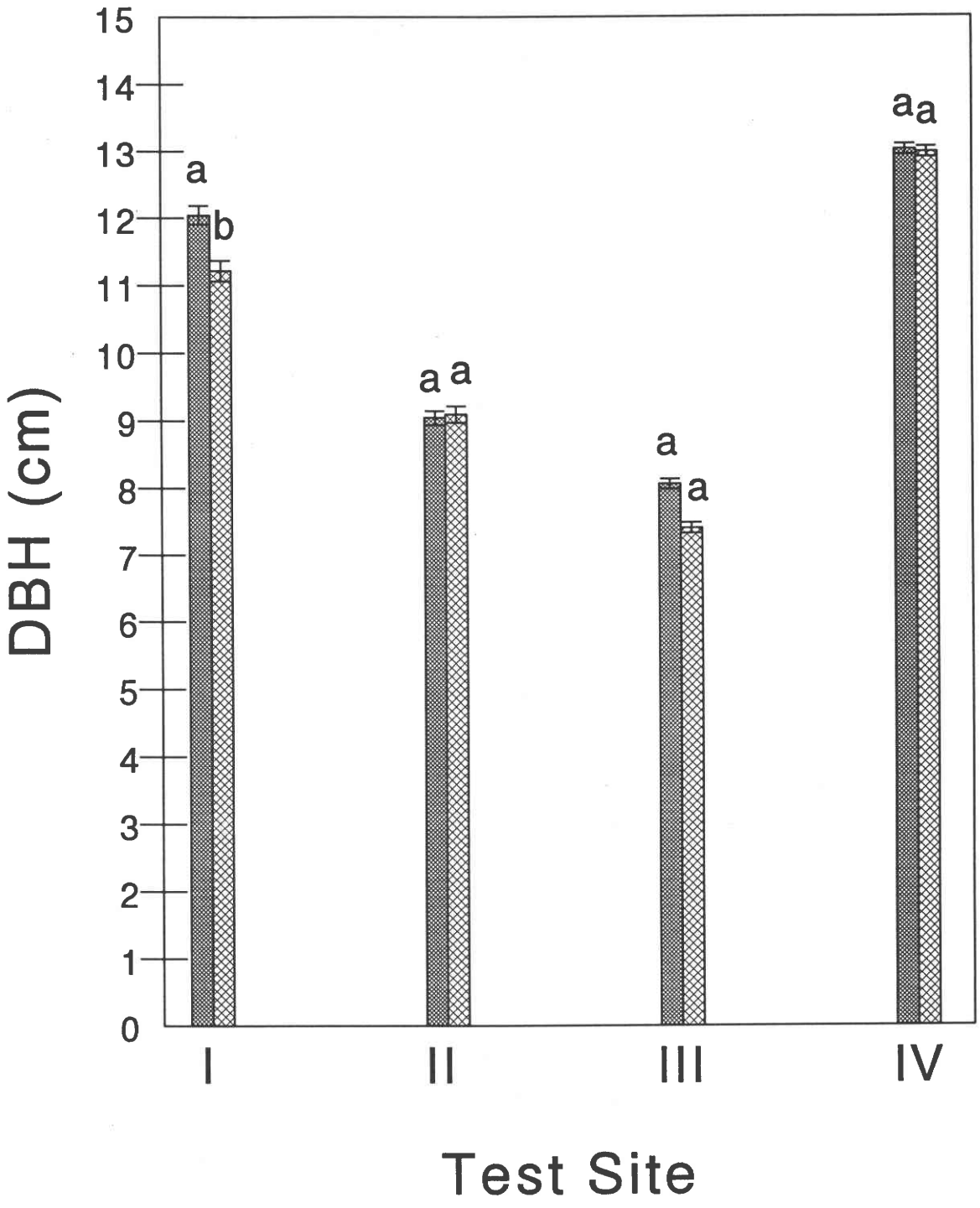

Figure 2. Contrasts of mean DBH among select (shaded) and comparison (hatched) families for each test site. Bars represent means with standard errors for each group. Significant differences ($p \leq 0.05$) are indicated by different letters.

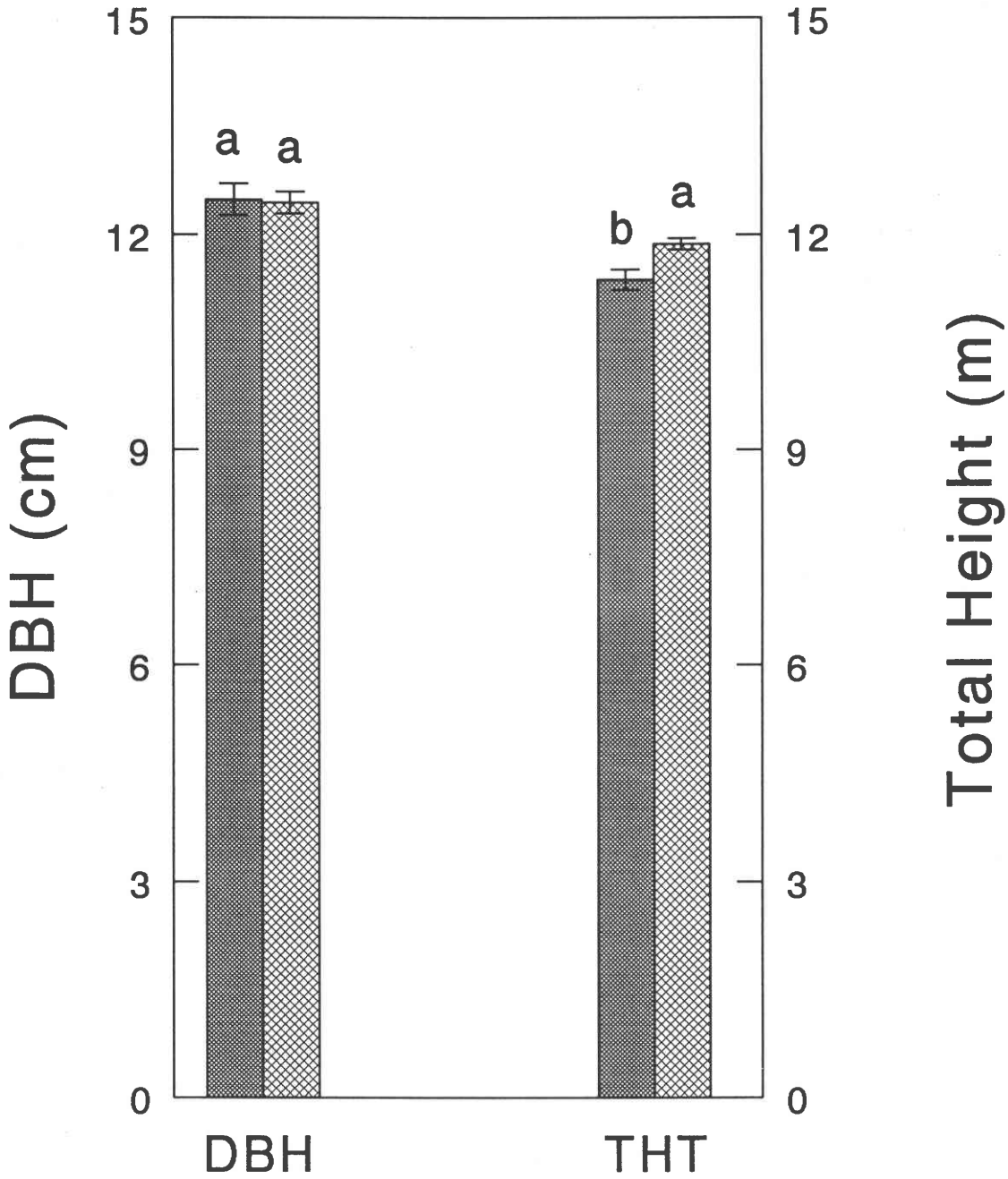

Figure 3. Comparison of mean DBH and mean THT among 11 select (shaded) and 32 comparison (hatched) families. Bars represent means with standard errors for each group pooled over all test sites. Significant differences ($p \leq 0.05$) are indicated by different letters.

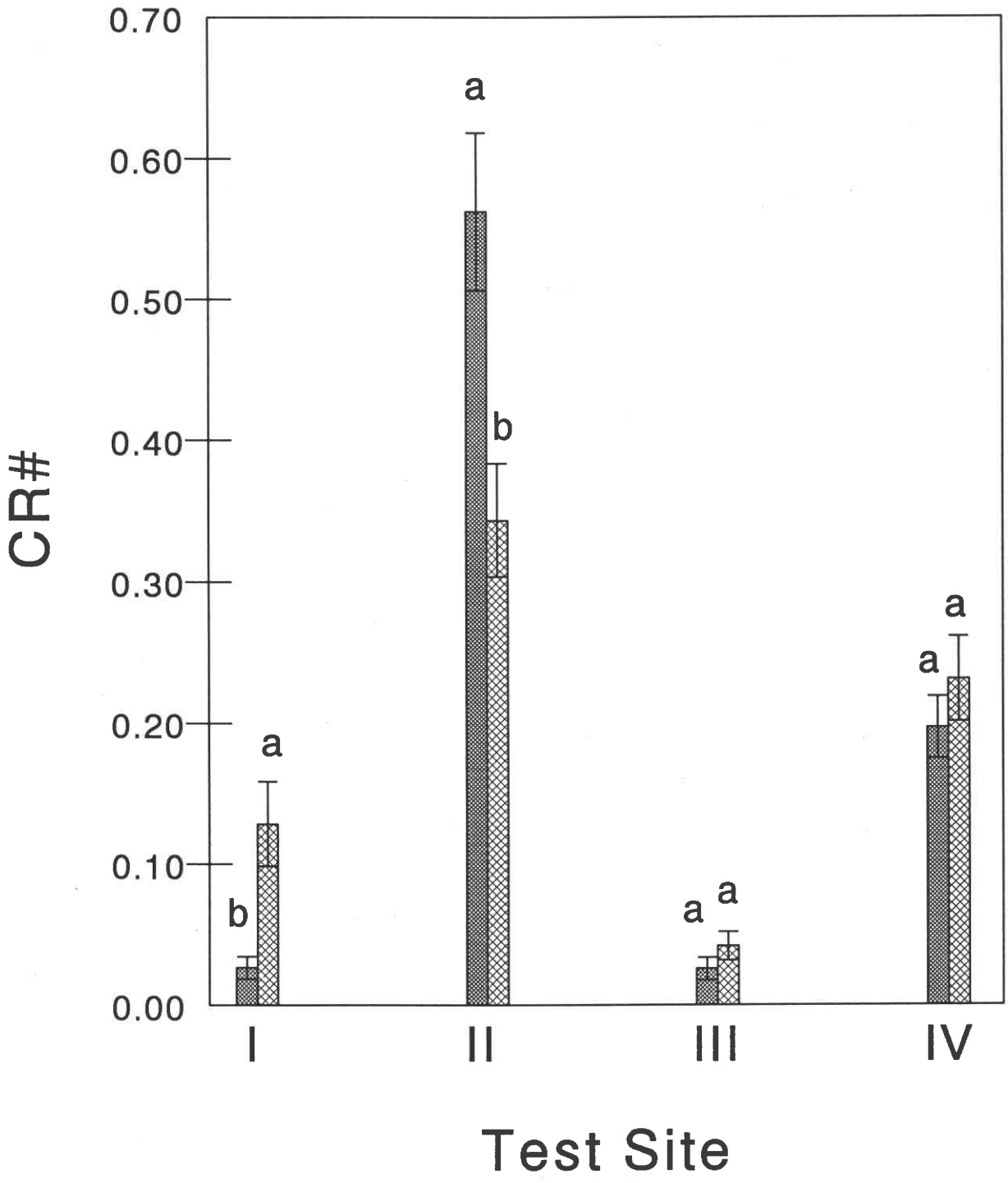

Figure 4. Contrasts of CR# (producing ≥ 10° deviation of mainstem) among select (shaded) and comparison (hatched) families for each test site. Bars represent means with standard errors for each group. Significant differences ($p \leq 0.05$) are indicated by different letters.

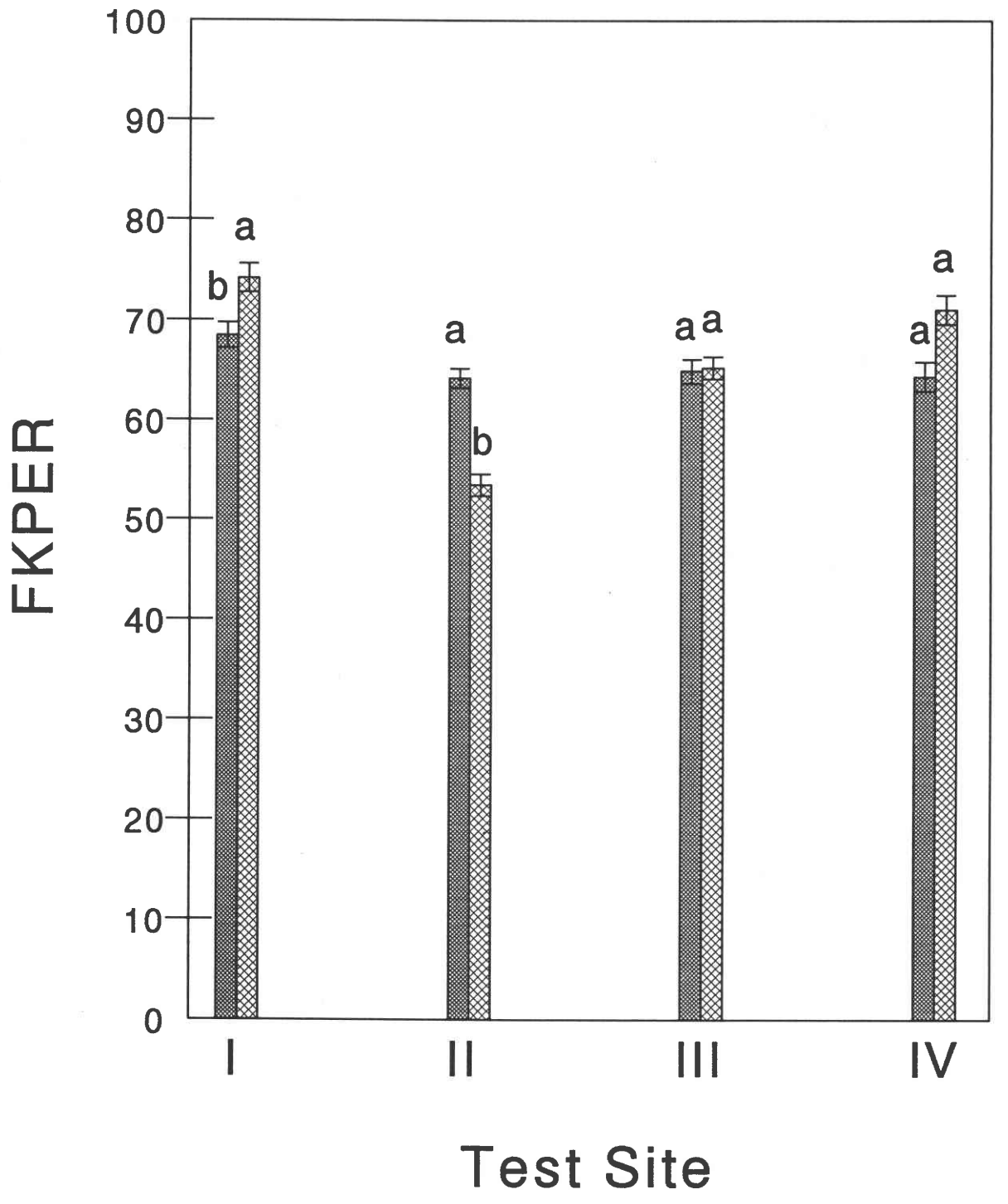

Figure 5. Contrast of FKPER (fork height, expressed as percent of total tree height) among select (shaded) and comparison (hatched) families for each test site. Bars represent means with standard errors for each group. Significant differences ($p \leq 0.05$) are indicated by different letters.

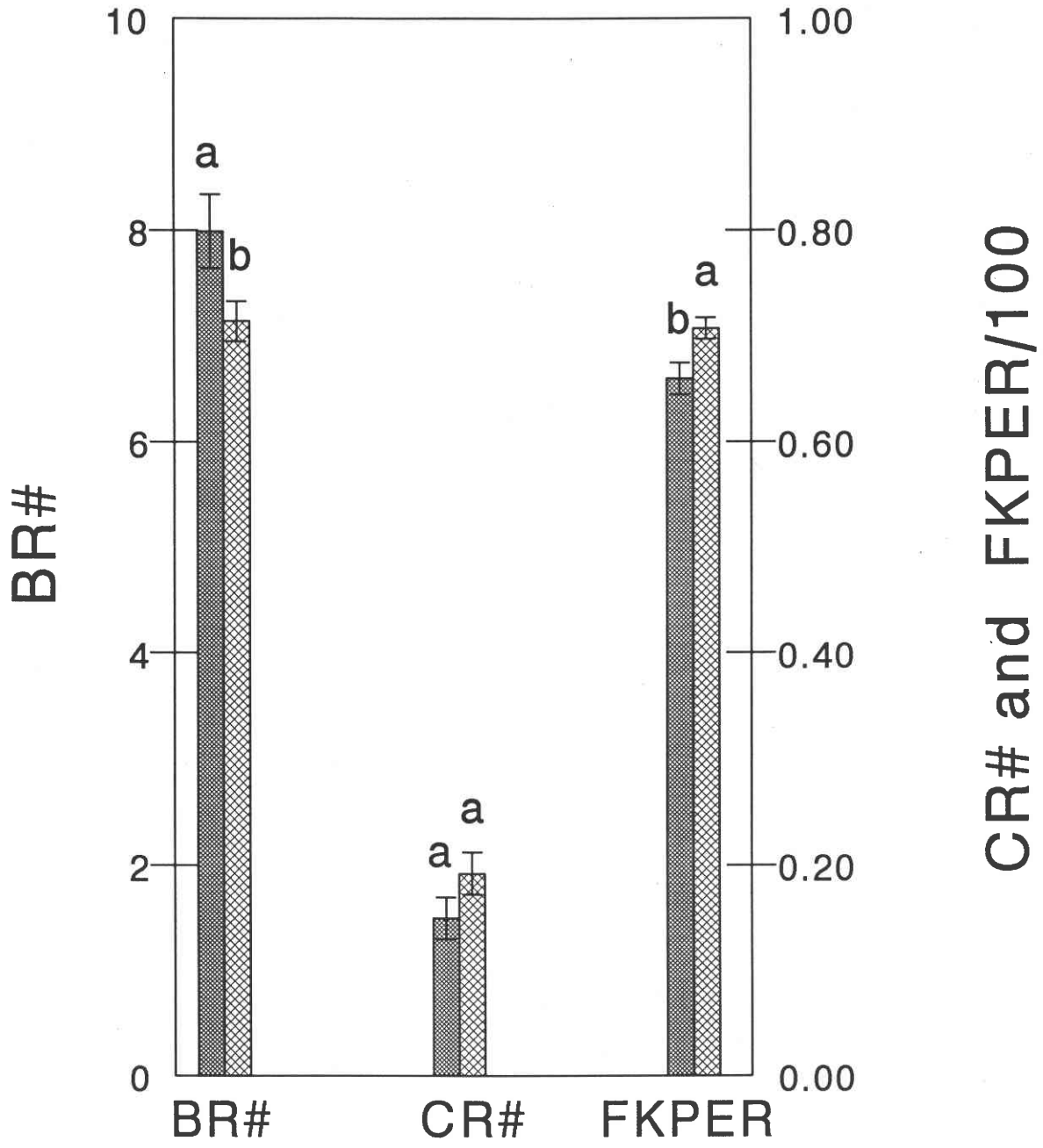

Figure 6. Comparison of BR#, CR#, and FKPER, among select (shaded) and comparison (hatched) families pooled over all test sites. Bars represent means with standard errors for each group. Significant differences ($p \leq 0.05$) are indicated by different letters.

Table 2. Percent differences in performance between select and comparison *Quercus rubra* families pooled over all test sites.

Select Family ID# (# progeny)	Number of Comparison Families (# progeny)	Percent Difference of Select Versus Comparison Families				
		DBH	THT	BR#	CR#	FKPER
2412 (22)	4 (82)	9.3	3.5	**-24.6**[1]	-47.5	10.7
2419 (30)	3 (45)	3.5	-4.5	32.0	48.3	65.6
2421 (6)	4 (60)	**19.2**	-5.2	-21.0	----	-40.0
2427 (31)	1 (17)	----	----	**-71.7**	27.1	-18.9
2429 (24)	2 (43)	-0.4	-4.2	1.4	-35.0	-14.0
2451 (42)	2 (38)	**-22.1**	**-22.1**	**48.2**	-69.8	-7.5
2452 (18)	2 (28)	-4.8	-8.8	**46.1**	-92.6	**-28.5**
2457 (32)	4 (93)	-9.9	**-11.4**	-7.1	42.9	3.3
2458 (37)	2 (58)	**-19.5**	**-16.3**	22.0	-146.7	**15.8**
2462 (31)	6 (163)	**15.2**	**8.3**	-0.4	-14.8	-22.1
2471 (24)	2 (76)	**-17.9**	**-10.4**	20.4	---	11.6
(297)	32 (703)	-2.7[2]	-7.1	4.1	-32.0	-2.2

[1] Bold values represent a significant difference at the 95% probability level using a two sample t-test.
[2] Arithmetic means.

CONCLUSIONS

Our analyses indicate that selecting one tree per stand using rigorous phenotypic selection was no more effective in providing initial improvements in growth and stem quality of *Q. rubra* than selecting a number of good phenotypes in a stand. These results are similar to those obtained for *Q. alba* (Schlarbaum 1993). Similar results and recommendations have also been obtained for other species (e.g. Pitcher 1982). The relatively large differences among select and comparison families within stands, indicating large genetic variances, suggest that several of the best phenotypes in a stand should be used to obtain seed. Progeny testing should be used to establish rankings for candidate mother trees for future collections. However, our study focused on families from relatively large and well formed trees in each stand. We can not speculate on the relative gains possible from selection across the entire range of phenotypes.

Our analyses of select versus comparison progenies indicate low genotype-phenotype correlations in the parental trees, and thus provide little encouragement for rigorous phenotypic selection in natural stands. This may not be surprising given the nature of development of many oak dominated stands. Canopy tree recruitment comes predominately from advanced regeneration subjected to disturbance (Sander 1972, Watt 1979). Oak advanced regeneration developing in non-disturbed stands does so slowly. Many biotic and anthropogenic factors may

influence phenotype during this time. Disturbance which ultimately leads to rapid development of oak cohorts may also alter phenotype.

Selection of *Q. rubra* trees for tree improvement might successfully utilize a mother tree or candidate tree approach. This involves selecting a number of good phenotypes, relying on progeny testing to indicate superior or elite mother trees. Selecting a number of good individuals from a stand eliminates detailed grading procedures, but ensures that the best phenotypes are represented in collections. This approach would increase the number of initial selections and make identification of each selected tree easier compared to a more rigorous regional grading system. Widening the options for individual tree selection may be especially advantageous in years with little mast production. While the nature of *Q. rubra* may necessitate this approach, it may be possible to accelerate gains through juvenile trait selection (Bailey and Steiner 1989, La Farge and Lewis 1987). However, the time interval necessary to determine reliable estimates of family rankings for growth parameters in this species is still under scrutiny (Houston 1987, Kriebel and others 1988).

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