

GENETIC GAIN FOR FIVE TRAITS  
IN BLACK WALNUT 1/

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Abstract .--From data gathered on two 3-year-old black walnut plantations, selection by height, diameter, or straight height generally resulted in genetic gain for all three of these traits, while date of leaf flush was set back slightly. Little or no increase was observed in the number of leaders competing for dominance when selection was based on growth parameters.

Family selection gave greater expected genetic gains in the next generation than either provenance or mass selection. Maximum gain will likely result from using a combination of selection methods.

Additional keywords: Selection methods, Juglans nigra, tree growth, heritability, tree form.

INTRODUCTION

In tree improvement programs our overall objective is to get maximum genetic gain. The "maximum" gain attainable depends on the amount of genetic variability for specific traits, the inter-trait correlations, and the method of selection. In the study reported here, we evaluated genetic gain in two seedling seed orchards for five separate traits and compared the gain using provenance, family, and mass selection methods.

MATERIALS AND METHODS

Two black walnut seedling seed orchards were established in southern Illinois in 1970 by the North Central Forest Experiment Station with Southern Illinois University and the Illinois Division of Forestry (Bey and Kung 1973). Seed was collected from 74 parent trees located in an area extending about 150 miles to the north and 150 miles to the south of the orchard site. Provenances were arbitrarily designated by grouping families on the basis of latitude.

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Germinating seeds from each parent tree were planted directly in the orchards. The Union County orchard is on a well-drained bottomland site and contains 74 families. The Jackson County orchard is on a moderately productive upland site and contains 39 families. A randomized complete block design was used. Five seed per family (a plot) were planted in each of five blocks at each site. Spacing was 4 feet apart in the row and 10 feet between rows.

The following traits were measured: total height, straight height, diameter at 6 inches above the ground, date of leaf flush, and number of leaders competing for a dominant position. Straight height was defined as the height to the point where the main leader deviated more than one foot from an imaginary line through the vertical central stem axis. Because trees that break dormancy early are more susceptible to spring frost damage than are late-flushing trees, we were interested in the date of leaf flush. Leaf flush was considered to have occurred when the first leaf on the tree was one inch long. Number of leaders competing for dominance was counted as one if there was a single dominant leader. In cases where the leader was damaged by frost, insects, wind, etc., several leaders might be competing for dominance. If one branch had gained strong apical control and it appeared that no forking would occur, the number of leaders was counted as one. If several were competing equally, we simply recorded that number.

Analysis of variance (ANOVA) was used to determine block, provenance, and family effects according to the following model:

<u>Source of Variation</u>	<u>df</u>	<u>EMS</u>
Block	$n_b - 1$	$\sigma_e^2 + n_f \sigma_b^2$
Provenance	$n_p - 1$	$\sigma_e^2 + n_b \sigma_f^2 + K\sigma_p^2$
Family/Prov.	$n_f - n_p$	$\sigma_e^2 + n_b \sigma_f^2$
Error	diff.	$\sigma_e^2$
Total	$n_t - 1$	

where N = total no. of plots

$n_b$  = no. of blocks

$n_p$  = no. of provenances

$n_f$  = no. of families

$n_{f/p}$  = no. of families within provenance

$$K = \frac{1}{n_p - 1} \left( \frac{N - \sum n_{f/p}^2}{N} \right) \quad (\text{Kempthorne, p. 104, 1952})$$

Genetic gain for the next generation was computed for each trait using the formula:

$$\text{Genetic Gain} = h^2 \times \text{Selection Differential}$$

Selection differential is the difference between the average and selected provenances, families, and individual trees. Because individuals make up families, and families make up provenances, the selection differential is necessarily lower for provenances than for families, and families lower than individuals.

Narrow sense heritability is defined as follows:

$$h^2 = \frac{\text{Additive genetic variance}}{\text{Genetic variance} + \text{Environmental variance}}$$

The family heritabilities in this project were determined for the seed parent. These heritability values can be used to calculate genetic gain for the next generation if we accept the assumption that heritabilities for a trait do not vary significantly from one generation to the next.

The following equations were used to calculate heritabilities:

$$(1) \quad h_f^2 = \frac{\sigma_f^2 + \sigma_p^2}{\sigma_f^2 + \sigma_p^2 + \sigma_b^2 + \sigma_e^2 / n_b}$$

$$(2) \quad h_p^2 = \frac{\sigma_p^2}{\sigma_f^2 + \sigma_p^2 + \sigma_b^2 + \sigma_e^2 / n_b}$$

$$(3) \quad h_i^2 = \frac{4h_f^2}{n + 3 - (n-1)h_f^2} \quad (\text{adapted from Wright, 1962})$$

where,

$h_f^2$  = heritability among families over all provenances  
(used to compute gain in family selection)

$h_p^2$  = heritability among provenances  
(used to compute gain in provenance selection)

$h_i^2$  = heritability among individuals  
(used to compute gain in mass selection)

To be a valid narrow sense heritability, Equation 1 assumes that the variance components for family and provenance represent additive genetic variance. If this is not the case, Equation 1 is a broad-sense heritability and Equation 3 will have an inflated value. However, since we included the block variance (a) in the denominators, our heritability estimates are probably conservative--but perhaps realistic.

## RESULTS AND DISCUSSION

Date of leaf flush had a relatively high heritability while growth and quality traits were generally moderate to low (Table 1). Heritability estimates were about the same in the two plantations. The provenance heritability estimates for growth and quality traits showed the largest discrepancies between plantations.

Sixty percent of the phenotypic variance for flushing date was accounted for by provenance and family components (Table 2). Except for number of dominant branches, all traits showed a relatively high genetic component due to families. The provenance was understandably low because of the limited geographic area covered by trees in this study.

Although there is the opportunity to breed for frost resistance, selection for a late date of leaf flush is generally accompanied by genetic losses for diameter, total height, and straight height. This pattern held true for all selection intensities at both plantations using family, mass, and provenance selection methods. When looking at individual seed parent progeny performance, we see that it is rare to have both rapid growth and late flushing traits in the same family. Little or no genetic gains were made for the number of leaders competing for dominance when selecting for late date of leaf flush.

Selection for diameter, total height, or straight height generally resulted in gain for all three of these characters. When the best 10 percent of the families were selected for diameter, diameter gained 0.6 a or 0.1 inches at the Union County plantation. Mass selecting the top 10 percent of the trees for diameter resulted in genetic gains of 0.04 inches for diameter, 0.3 feet for total height, and 0.1 feet for straight height.

Selection for diameter, total height, or straight height carried along losses for date of leaf flush. Losses went as high as 0.8a or 2.6 days at the Union County plantation when selecting the best families for diameter. At both orchards, families flushed about 3 days earlier than average when selecting the top 10 percent of the families for total height growth. Similarly when selecting for straight height, family selection resulted in an earlier date of leaf flush--a loss of 1.7 days when selecting the top 20 or 30 percent.

Family selection to genetically improve tree form by decreasing the number of leaders competing for dominance does not appear to be a worthwhile objective. Analysis of variance showed no significant differences among families for the number of competing leaders, although significant family differences were detected for the remaining characters. Furthermore, family, provenance, and individual heritability values were low for competing leaders.

Regardless of the intensity or method of selection, selection differentials for the number of dominant leaders were always under one. Genetic gains of up to 0.08 feet in straight height were achieved at both plantations

Table 1.--Heritability values for five characters of black walnut from two plantations

Source	: Flushing : date	: Diameter : at 6"	: Total : height	: Straight : height	:No. of dominant : leaders
Jackson County (Union County)					
Among families over all provenances	.83 (.80)	.27 (.37)	.37 (.44)	.37 (.35)	.36 (.11)
Among provenances	.49 (.51)	.00 (.26)	.07 (.26)	.02 (.23)	.26 (.11)
Among individuals	.41 (.36)	.05 (.07)	.07 (.10)	.07 (.07)	.04 (.01)

Table 2.--Variance components due to provenances, families, blocks, and error (expressed as percent of total variance)

Source	: Flushing : date	: Diameter : at 6"	: Total : height	: Straight : height	:No. of dominant : leaders
Jackson County (Union County)					
Provenance	12 (13)	9 (9)	3 (10)	1 (18)	7 (3)
Fam./Prov.	48 (37)	15 (6)	20 (12)	18 (6)	0 (0)
Blocks	4 (3)	30 (11)	28 (15)	18 (10)	1 (5)
Error	36 (47)	55 (73)	50 (63)	63 (76)	92 (92)

When compared to genetic gain obtained from selecting for other characters, selection by total height showed equal or superior gains for total height, straight height, and diameter. Because of the high correlation for total height and straight height, straight height gave similar genetic gains.

by mass selecting those trees having the least number of dominant leaders. Yet, at both plantations, mass selection produced no significant gains for date of leaf flush, diameter, or total height.

Family selection consistently gave the greatest genetic gain for all five characters when compared to mass and provenance selection (Fig. 1). Mass selection heritabilities were necessarily lower due to their method of calculation. As selection intensity increased, differences between genetic gains for family and for mass or provenance selection increased.

The maximum genetic gain for date of leaf flush was less than two days for provenance selection. Similarly, provenance selection showed small genetic gains for growth traits. However, we already know that a lot of genetic variation in black walnut exists over its wide range (Bey 1970, Bey 1973, Bey et al. 1971). The relatively small genetic gains for provenance selection in this study can be explained by the sampling of only a limited portion of the range of the species. The greatest gain can undoubtedly be made by using a combination of provenance, family and mass selection.

To maximize genetic gain for a plantation, one needs to consider gains for the character which is being selected on and gains (or losses) for other traits which accompany the selection. Determining the best combination of families for various traits in order to maximize genetic gain can be accomplished with the help of the computer (Bey, Kung, and Kucera 1974). With this selection system, genetic gains are computed for all possible combinations of selection; the best combination (percent of families selected for each trait) then represents maximum expected gain for the plantation.

Determining the "best" character to use as a basis for selection will depend upon the objectives of the selection and the problems associated with the plantation area. For example, if early spring frosts frequently present a problem, emphasis will want to be placed on selecting those families with a late flushing date. However, when major emphasis is placed on selecting genetically superior trees for growth, total height can be used as a basis for selection. Selection by total height also facilitates selection since family differences for total height can be easily measured.

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GENETIC GAIN BY TRAIT

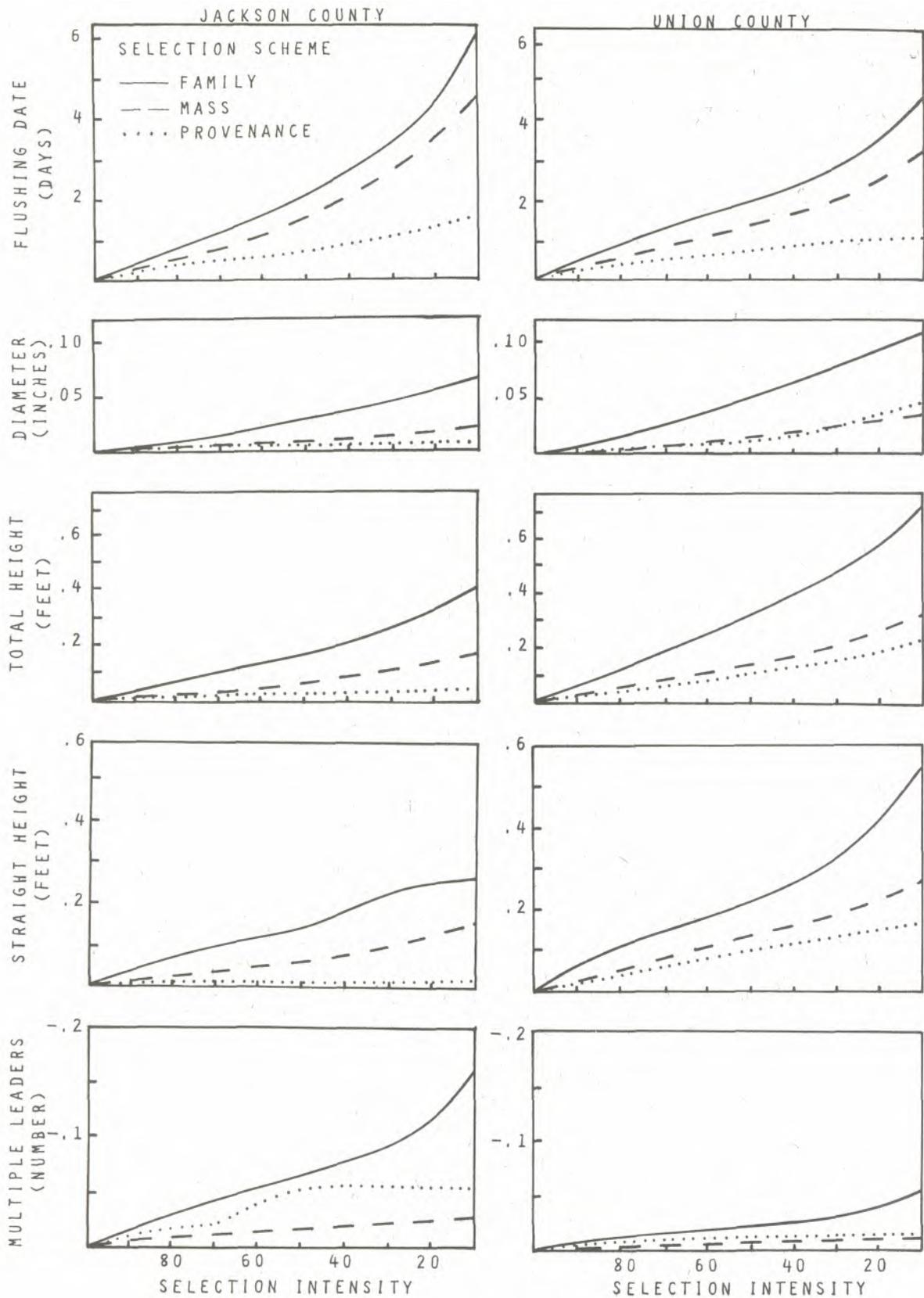


Figure 1.--Genetic gain for five traits at various selection intensities using family, mass, and provenance selection.

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