EARLY RESULTS FROM A SITE-REPLICATED PECAN PROGENY TEST

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Abstract.--An open-pollinated progeny test of 40 pecan families of central Louisiana origin was replicated on 3 sites in southern Louisiana and Mississippi. A high degree of genetic variation in first-year height and root growth, field survival, and second-year height growth was found, with significant effects partitioned in the component for stand or local breeding population variance. The latter effect indicates a closer degree of relationship or genetic homogeneity within small breeding groups, reflecting a relatively high level of inbreeding in wild populations. Genetic homogeneity within small populations was also demonstrated by the comparatively good survival and growth of progenies of unselected trees from each selected stand, indicating that phenotypic stand selection may be as effective as individual tree selection in the first generation. Comparisons of the 3 test sites emphasized the magnitude of environmental effects on survival and growth of pecan, a site-specific species. No GXE interactions were found between the two bottomland sites, but major effects were noted on the better-drained upland site. These differences were reflected in estimates of heritability of second-year height growth, which ranged from 0.22 (narrow) and 0.57 (broad) to 0.41 (narrow) and 0.74 (broad) when calculated on the basis of bottomland-upland and bottomland-bottomland test site performance, respectively.

Additional keywords: *Carya illinoensis*, selection, inbreeding height growth, root growth, survival, genotype-environment interaction, heritability.

In the past 25 years, pecan (*Carya illinoensis* (Wangenh.) Koch) has increased in utility and value from an unwanted commodity to an extremely marketable material for use in the manufacture of furniture, cabinets, and paneling. With increasing demand, the supply of quality trees is decreasing at an alarming rate. To preserve and improve the excellent pecan resource of central Louisiana, a 40-family open-pollinated progeny test was established with seed from selected parents. It was designed to evaluate the extent and pattern of genetic variability in wild populations, and to obtain basic information on the general biological requirements for effective breeding and culture of pecan.

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METHODS

Parent trees were selected in the summer of 1972 from Raccourci Island in West Feliciana Parish, Louisiana., The "island" was formed in 1848, when the Mississippi River changed its course. The area consists of typical Mississippi River bottomland soil types (azonal, heavy clay deposits). It is laced with ridges, sloughs, and lakes and is subject to frequent overflow by the Mississippi River.

Raccourci Island is approximately 25,000 acres and, from this area, four stands were chosen. Within each of the four stands, ten of the best pecan trees were selected as seed parents on the basis of their phenotypes. Selection criteria included vigorous growth, straightness of bole, absence of limbs for at least 10-15 meters of bole length, and a full crown one-third of the total height of the tree. These phenotypic selections were made by visual estimate in relation to neighboring trees in the stand, and no attempt was made to apply a quantitative grading system. Stand areas were about 2 acres (0.8 hectare) or less, and stands were located from 0.5 to 5 miles (0.8 to 8 km) apart.

In the fall of 1973, seeds were collected from all 40 parent trees, and a general (control) collection was made from unselected trees in each stand. All 44 seed lots were planted in the spring of 1974 in two nursery locations, Baton Rouge, Louisiana and Lumberton, Mississippi. Height growth was measured at the end of the first growing season in the nursery, and when seedlings were lifted for outplanting the following spring, root diameter was measured 2 cm below the root collar. The two nursery treatments were quite dissimilar, and there were highly significant differences in seedling growth between the two locations (Adams and Thielges 1976).

The progeny test outplantings were designed to compensate for this nursery effect and to allow further study of its influence in subsequent growing seasons. Seedlings from the Lumberton nursery were planted in replicated tests at Lumberton and at Baton Rouge, and seedlings from the Baton Rouge nursery were planted in replicated tests at Baton Rouge and at Washington, Louisiana (southwest Louisiana). The Baton Rouge planting site therefore contains paired, 5-tree family plots of seedlings grown at each nursery. Each family (paired family at Baton Rouge) is replicated 5 times at each planting site.

At the end of the second growing season (first year in field), survival and height growth were determined at all three locations. The statistical design was a randomized block with a factorial arrangement and, for each analysis, stand variation as well as individual family variation was evaluated. In estimating heritability of height growth, the stand source was not partitioned and family (broad sense) and single tree (narrow sense) heritabilities were estimated.

RESULTS AND DISCUSSION

First Year Results

The analysis of variance for height and root diameter growth in the nurseries indicated highly significant ($P < 0.01$) differences between families. This large parent tree or family variation among progenies of trees selected from one local source indicates much genetic diversity in wild populations of pecan.

To evaluate the relative performance of the 40 families, mean values for height and root diameters were compared. An examination of family means showed that 7 of the 40 families tested were above average for both height and root diameter growth at both nursery locations.

The four general (unselected) stand collections also grew well in the nurseries. Three of the four unselected collections exceeded the overall mean for height growth at both nurseries, but only two of the unselected collections exceeded the overall mean for root diameter, and only at the Lumberton nursery.

First-year height growth was significantly correlated with seed weight (Adams and Thielges 1976). This significant positive correlation has also been shown for another large seeded species, *Quercus rubra* (Gall and Taft 1973). Although these seed relationships may be true genetic effects, they exert a confounding effect on analyses based on additive genetic variation (such as heritability estimates) and cause difficulties in objectively evaluating first-year growth. The influence of seed size was not significant at the end of the second growing season and, therefore, these second year data provided more reliable analyses of family variation.

Second Year Results

Stand variation and field performance.--The purpose of selecting parent trees within several small, separated stands and the comparative evaluation of stand variability, was to provide some information on the genetic relationships within and between stands of this monoecious, wind-pollinated species.

In the analyses of second-year height growth at all three planting sites, there was highly significant ($P < 0.01$) variation among stands indicating that, in addition to individual tree variation, there is also detectable variation between stands or small breeding groups within local populations of pecan. If there is much inbreeding, there may be a tendency for stands within populations to develop some degree of homozygosity and, therefore, a closer genotypic-phenotypic relationship among trees within the individual stands.

This would be possible in natural pecan stands because the majority of the pollen disseminated by a tree is probably intercepted by its immediate neighbors. With little inclusion of new genetic material from neighboring but non-contiguous stands, local breeding populations could develop patterns for expression of certain traits which would be measurably different from those of other populations. Thus, individual neighboring trees remain highly variable but are more closely related to each other than to more distant pecan trees.

The four stands from Raccourci Island exhibited highly significant differences in height growth, but no logical pattern could be determined for this variation. Generally, the order of stand means for second year height growth remained the same as for first year growth. The stand considered to have been the poorest in terms of parental phenotypes, is the one that has the best progeny mean in the Lumberton planting. It is quite possible that this stand represents an inbred population that was high-graded in the recent past, and that the better phenotypes were eliminated. Our results indicate that, under these conditions, predictions based on parental phenotypes are misleading, and they also emphasize the importance of progeny testing.

Family variation and field performance.--Family variation in survival and second-year height growth was found to be highly significant at all planting sites, supporting the theory of a large degree of genetic diversity in wild populations of pecan. The family means for second year height growth at the Lumberton and Baton Rouge and Washington and Baton Rouge sites were compared, and five families exceeded the overall mean at all three locations. Only one unselected collection was growing better than the overall means at all planting sites at age 2.

A comparison of select-tree progeny performance to that of seedlings in the unselected stand collections yielded variable results. For example, individual tree selection was apparently effective in one of the stands, where selected families outgrew the unselected stand collections at two of the three locations. At the other extreme, selected families of another stand grew poorly when compared to the means for the unselected seedlings at all three planting sites.

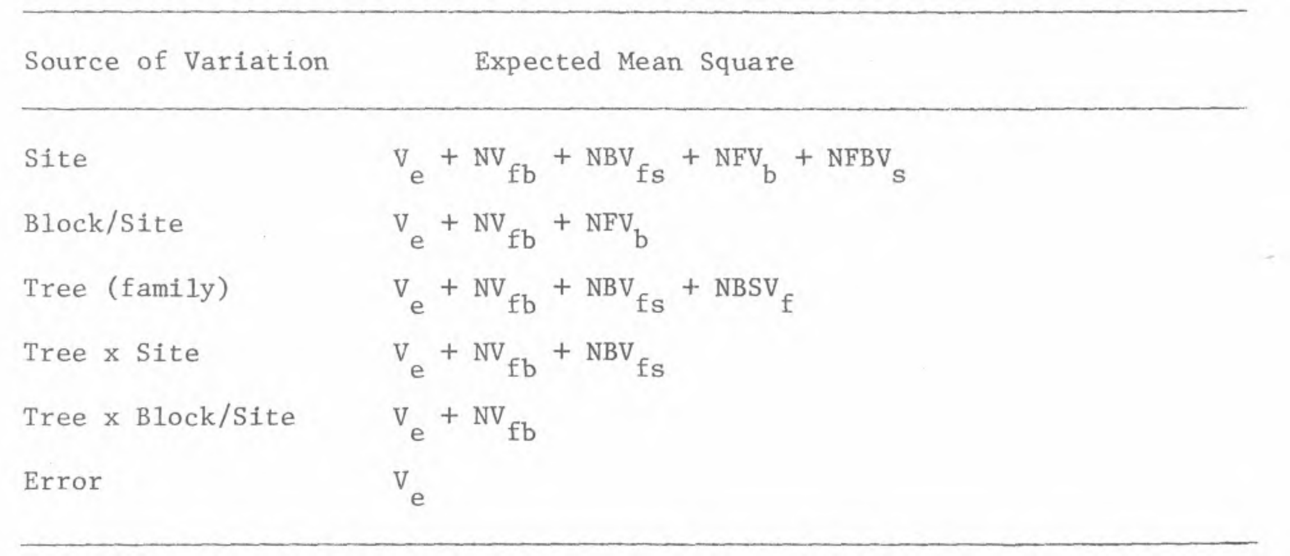
Genotype-environment interactions.--The Baton Rouge and Lumberton planting sites (established with seedlings grown at the Lumberton nursery) are very different in terms of soil type, drainage, elevation, fertility, and competing vegetation. The Lumberton site could be rated as a typical coastal plain pine site. On the other hand, the Baton Rouge and Washington sites (established with seedlings grown at the Baton Rouge nursery) are more similar in terms of soil texture and fertility, drainage, elevation and weed growth. Both are essentially typical bottomland sites.

It was therefore not surprising to find an absence of genotype environment interactions when the Baton Rouge and Washington sites were compared. The overall means for second year height growth were very similar--15.9 cm at Washington and 17.4 cm at Baton Rouge. There were much greater differences between the Lumberton (29.7 cm) and Baton Rouge (20.4 cm) planting sites; analysis of variance for second-year height growth revealed highly significant ($P< 0.01$) genotype-environment interactions between families at the two sites. A specific example of the effect of the different environments on particular genotypes is provided by families of one stand which ranked 1, 2, 3, 4, and 5 in terms of second year height growth at Baton Rouge and 4, 2, 9, 7, and 10, respectively, at the Lumberton planting.

The environment not only affected the relative ranking of families, but altered overall mean height growth at Baton Rouge and Lumberton. Two of the better families growing at Lumberton had mean heights of 31.00 and 30.94 cm at Lumberton and 15.75 and 17.18 cm at Baton Rouge, respectively. This is a difference in growth of 49 and 44 percent between the two sites. These two families ranked 2 and 3 at Lumberton and 10 and 9 at Baton Rouge.

The large range of response in height growth of families on the two sites indicates that selection of pecan genotypes to match a specific environment may be possible. On the other hand, there is also some evidence that a few individual families will perform well over a wide range of environments, which presents possibilities for developing populations generally adaptable to a broad spectrum of planting sites. Both approaches may be valid in light of current land use trends in the fertile river bottoms of the central and southern states.

<u>Heritability estimates of second year height growth</u>.--Components of variance and heritabilities for second-year height growth of pecan were estimated using the following mean-square components:



Source of Variation	Expected Mean Square
Site	$V_e + NV_{fb} + NBV_{fs} + NFV_b + NFBV_s$
Block/Site	$V_e + NV_{fb} + NFV_b$
Tree (family)	$V_e + NV_{fb} + NBV_{fs} + NBSV_f$
Tree x Site	$V_e + NV_{fb} + NBV_{fs}$
Tree x Block/Site	$V_e + NV_{fb}$
Error	V_e

Where: F, B, S, and N represent the numbers of trees, replications per site, sites, and trees per plot, respectively; V_e, V_{fb}, V_{fs}, V_f, V_b, and V_s are variances due to tree-within plot, tree x replication-within-site, tree x site, tree, replication within site, and site, respectively.

The following estimates for family (broad sense) and single tree (narrow sense) heritabilities closely follow Wright's (1976) variance analysis for replicated half-sib progent tests:

$$\text{Family (broad-sense) heritabilities} = \frac{V_f}{V_e/NBS + V_{fb}/BS + V_{fs}/S + V_f}$$

and

$$\text{Single tree (narrow-sense) heritabilities} = \frac{4\ V_f}{V_e + V_{fb} + V_{fs} + V_f}$$

Heritability estimates for second year height growth of pecan (Table 1) are in the range of those reported by Bey (1970) and Bey et al. (1971) for height growth of black walnut. There were considerable differences in the heritability estimates calculated for the Lumberton and Baton Rouge plantings and those for the Washington and Baton Rouge plantings. The values for the latter were higher, and this is partly due to the absence of significant genotype-environment interaction. In the estimating equations (Table 1), the more uniform environment between the Baton Rouge and Washington planting sites is reflected in the variance for tree (V_f) and tree x site (V_{fs}). These statistical effects emphasize the major constraints on the broad application of heritability estimates that are imposed by environmental variation.

Table 1.--Estimated variance components and heritabilities for second year height growth of 40 open-pollinated pecan families at three planting sites.

Planting sites	V_f	V_{fb}	V_{fs}	V_e	Broad h^2	Narrow h^2
Lumberton and Baton Rouge	306.08	444.04	110.71	4792.54	0.57	0.22
Washington and Baton Rouge	380.01	406.74	0.0	2921.24	0.74	0.41

Based upon observations of a greater degree of genetic similarity in progeny performance among selections within than between stands, and the relatively good growth of unselected progenies from these selected stands, there seems to be a fairly high level of inbreeding in natural populations of pecan. Combined with the relatively high heritabilities for height growth estimated in this study, these population characteristics can be advantageous to the breeder. Selection of superior stands may be as advantageous and efficient for first generation selection as plus-tree selection. Also, with prior knowledge of stand or population characteristics, there may be some possibilities for utilizing the remaining phenotypes in high-graded pecan stands, a factor that will become increasingly important as the harvesting of old-growth timber proceeds. Present practices favor the cutting of all mercantable stems on the site. For artificial regeneration, progeny testing is mandatory, and breeding programs should be designed to explore, delimit and utilize the full range of genetic variation in this site-specific species.

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