GENETIC VARIATION IN A LONGLEAF PINE POPULATION: A LONG-TERM FIELD STUDY OF A 13-PARENT DIALLEL

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Genetic and environmental effects on growth and survival were quantified in a population of longleaf pine (*Pinus palustris* Mill.) using a 13-parent diallel cross growing over 40 years on two sites in southern Mississippi. This long-term field experiment is unique for longleaf pine, a tree species of renewed interest for ecosystem restoration and plantation forest management in the southern United States.

Materials and Methods

The genetic foundation of this experiment consists of progenies produced by making all possible crosses among 13 parent trees in a diallel mating scheme. The parent trees were randomly chosen from a natural, open-grown longleaf pine stand located on the Harrison Experimental Forest (HEF) near Saucier, Mississippi. Of the 169 possible crosses, 143 were planted in 1960 in two replicated field trials, each located on the HEF about 2 miles apart. Of the 78 half-diallel, full-sib crosses, 76 were established in field tests. Each site was established in a randomized complete block design experiment composed of eight-tree family row plots arranged in four replications. Growth and survival data were collected for all trees at various stages of stand development, including ages 3, 7, 17, 30, and 40 years.

Quantitative genetic analyses were conducted and reported on for ages 1 through 7 years, by Snyder and Namkoong (1978). Further analyses of genetic parameters, including age 17 year results, were reported by Rousseau (1980). Later ages including age 40 years were analyzed and reported by Stine et al. (2001). Measurements for ages 3, 7, 17, 30, and 40 years are analyzed for this report. Only families that had greater than two replications per test site were included in this analysis. Of the 76 full-sib crosses, 66 families met this criterion. In this analysis, ASReml software was used to generate genetic variance components of a mixed model (Gilmour et al. 2002).

Results and Discussion

The strong genetic basis of the experiment, coupled with superb silvicultural management of the sites, allowed us to successfully partition the genetic and environmental components of variation in various growth and survival traits. We found substantial genetic variability in growth and survival among these longleaf pine families. Family means for individual-tree volume ranged from 12.7 to 24.9 cubic feet (0.36 to 0.70 cubic meters) at age 40 years.

For later ages (≥17 years) growth traits, non-additive genetic (specific combining ability, SCA) variance was high, relative to additive genetic (general combining ability, GCA) variance (Table 1). Similarly, the ratio was high for tree survival trait at age 40 years (Table 1). The variance component estimates along with their standard errors are reported in Table 2. The relatively large proportion of non-additive genetic variance after age 7 years is noteworthy and is consistent with previous reports (Rousseau 1980; Stine et al. 2001). However we are reporting larger non-additive to additive genetic variance ratios for some traits. Our current analysis includes a larger sample of families than used in the analyses of Stine et al. (2001), because of our less stringent restriction on numbers of trees required per family, an additional earlier age (age 3 years), and we have used different computational and analytical methods. It remains to be seen whether this stronger non-additive effect holds up in further analyses, but clearly we are seeing a trend of higher SCA variance versus GCA variance starting after stand closure and continuing to mature stand ages.

Broad implications of these results for longleaf pine breeding and species conservation can be stated as follows. First, breeding programs for longleaf pine should not ignore specific combining ability (SCA) in developing production and breeding populations. Second, substantial genetic variation in growth and survival were found among non-selected parent trees in a natural stand within a small area (80 acres), indicating that much genetic variation for important traits exists in natural populations of longleaf pine.

Table 1. Ratios of non-additive to additive genetic variances for the longleaf pine diallel experiment for growth and survival across different ages. Data suggest that by age 17, non-additive genetic variance is generally large compared to additive genetic variance.

Trait	**Age 3**	**Age 7**	**Age 17**	**Age 30**	**Age 40**
Height	0.0	0.22	2.1	- -	0.80
DBH	- -	0.38	1.32	1.27	3.21
Volume	- -	- -	1.35	- -	2.23
Survival	- -	0.08	0.45	0.27	2.76

Table 2. Genetic variance components (w/ std. errors), and ratios of non-additive (SCA) to additive (GCA) genetic variance at ages 17 and 40 in the longleaf diallel experiment.

Trait	**SCA**	**GCA**	**Ratio, SCA/GCA**
		Age 17	
Height	78.25 (30.8)	36.5 (22.4)	2.1
DBH	5.39 (2.02)	4.08 (2.07)	1.32
Volume	18.07 (7.81)	13.40 (7.02)	1.35
Survival	0.035 (0.037)	0.076 (0.040)	0.45
		Age 40	
Height	95 (70.0)	118.5 (61.2)	0.80
DBH	16.13 (5.76)	5.03 (3.24)	3.21
Volume	215.25	96.5 (59.3)	2.23
Survival	0.140 (0.053)	0.051 (0.031)	2.76

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