

Partitioned Genetic Variances for Several Characters in a Cotton Population of Interspecific Origin¹

H. H. Ramey and P. A. Miller²

ABSTRACT

Estimates of additive and dominance genetic variances were obtained for 11 agronomic and fiber traits in a cotton population of interspecific origin (*Gossypium thurberi* Tod., *Gossypium arboreum* L., *Gossypium hirsutum* L.). Substantial amounts of additive genetic variation were found for the traits lint percentage, lint index, seed index, weight per boll, fiber length (U.H.M.), fiber strength (T_1), fiber elongation (E_1), fiber fineness (A), and fiber shape (D). Additive genetic variations were also found for seed cotton yield and lint yield but were small in magnitude. Positive estimates of dominance genetic variance were obtained for seven of the traits. Magnitudes of these estimates were generally small and only three (those for lint percentage, weight per boll, and fiber length) exceeded their standard errors. Negative estimates of dominance genetic variance were obtained for seed cotton yield, lint yield, seed index, and fiber shape. Estimates of average degree of dominance, where obtained, were less than unity indicating only partial dominance for genes controlling these traits.

SUBSTANTIAL amounts of genetic variation have been reported in certain breeding populations of Upland cotton (*Gossypium hirsutum* L.) (1, 8, 10). In most cases this total genetic variation has not been partitioned into the genetic variance components. Where this breakdown has been provided, additive components account for a major portion of the variation (9, 13). Genes from two diploid cotton species, *G. thurberi* Tod. and *G. arboreum* L., were brought into tetraploid Upland cotton in the course of transferring high lint strength from a tri-species hybrid. The objective of the present study was to investigate the nature of the genetic variation in this population and consider its implications on breeding procedures.

Beasley (2) induced fertility in a hybrid of *G. thurberi* ($n=13$) and *G. arboreum* ($n=13$) by doubling the chromosome number. This allotetraploid ($n=26$) was crossed with American Upland cotton ($n=26$). Lewis (7) described the F_2 and F_3 population of the cross and noted that there was an opportunity to develop increased fiber strength from this material. At the North Carolina Agricultural Experiment Station the original cross has been backcrossed to locally adapted Upland varieties in an endeavor to improve fiber strength. High strength strains isolated from this program have lacked agronomic acceptability.

Choice of breeding procedures to follow in combining higher fiber strength into agronomically acceptable lines depends in part on the covariances between fiber strength and the other traits and on the relative

magnitude of additive and dominance genetic variances. Al-Jibouri et al. (1) reported on the genotypic variances and covariances in this high strength material. The present study was designed to partition the genotypic variances into their additive and dominance components and examine their relative magnitude in terms of average degree of dominance (5, 6).

MATERIALS AND METHODS

Two parental lines, 'Empire 10' and 'TH 131-5', were used to generate the experimental material for this study. Both had been isolated through a pedigree (individual plant) system of inbreeding for at least six generations prior to initiation of the study. Empire 10 is a derivative of one of the component lines of the variety 'Empire' and is characterized by large bolls and general agronomic acceptability. No selection was practiced in the derivative of this line beyond an attempt to obtain a homozygous line which was phenotypically similar to the parent variety. TH 131-5 was derived from the sixth backcross to Upland of the tri-species material and is characterized by high fiber strength, low yield, and general agronomic undesirability. During the backcrossing and selfing generations strong selection was practiced for the high strength trait. The two parental lines differ substantially in all traits studied except fiber length. A more detailed description of the parental lines and of a population of F_3 lines derived from their cross has been given by Al-Jibouri et al. (1).

From an F_2 population of this cross, 97 plants were randomly chosen as male parents. Each male parent was backcrossed to each parental line to produce a pair of backcross progeny. In the production of seed for a backcross progeny, from 10 to 30 plants of a parental line were used as females.

These backcross progenies were grown at two locations, Clayton and Rocky Mount, North Carolina. Plots were single row, 15 feet in length consisting of 10 hills 18 inches apart. Three plants per hill were left at thinning.

In order to decrease the effects of soil heterogeneity the progenies were grown in small groups. Precision of comparison among means was reduced by grouping, but this was not important as the objective was estimation of genetic variance rather than progeny mean comparison. The 97 pairs of progenies were randomly allocated to groups within the limitations of quantity of seed available. For 21 pairs, seed were sufficient to plant 4 replications, 2 at each location. These were allocated to 1 group of 10 pairs and 1 group of 11 pairs. For the remaining 76 pairs, seed were sufficient to plant 5 replications, 3 at 1 location and 2 at the other. These were allocated to 6 groups of 11 pairs each and 1 group of 10 pairs.

Each group was grown at each location in a randomly assigned single block in the field with replication within blocks. Progenies of a group were completely randomized within each replication of the block assigned. Groupings remained constant over locations.

At near maturity, where there were missing hills, a skip distance was estimated as the number of feet between the overlap of two adjacent plants. Yields of plots having missing hills were adjusted upward by the reciprocal of the percent perfect stand (12).

A randomly picked sample of 15 bolls was harvested from each plot prior to general harvest. These samples were used to obtain plot values for weight per boll, lint percentage, seed index (weight in grams of 100 seeds) and lint index (weight in grams of lint from 100 seeds). Yield of seed cotton for each plot was measured in grams per plot and yield of lint in grams for each plot was calculated by multiplying the weight of seed cotton by the respective plot lint percentage. A lint sample from each plot was analyzed by the U. S. Department of Agriculture Fiber Laboratory at Knoxville, Tennessee. Fiber property measurements were as follows:

Fiber length, U.H.M. (Upper Half Mean) — Length in inches of the half of the fibers, by weight, that contains the longer fibers.

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²Formerly graduate assistant (now Geneticist, National Cotton Council of America, Memphis, Tenn.) and Professor of Crop Science.

Fiber strength, T_1 units — Strength of a bundle of fibers measured on the Stelometer with 2 jaws holding the fiber bundle separated by an $\frac{1}{8}$ -inch space. Strength is expressed in terms of grams per grex.

Fiber elongation, E_1 units — Percentage elongation at break of the center $\frac{1}{8}$ -inch of the fiber bundle measured for T_1 strength on the Stelometer.

Fiber fineness, A — "A" is a measure of the external surface area of the fibers of a given volume of fibrous material expressed in terms of square millimeters per cubic millimeter of fibrous material. It is measured on the Arealometer.

Fiber shape, D — "D" is the difference between the value of the specific area determined at high pressure and at standard pressure on the Arealometer. It is presumably a measure of the flatness of the fiber ribbon.

Plot values were used in an analysis of variance for each character as described by Gardner et al. (6), except that lines were treated as fixed effects in the model. The form of this analysis of variance is shown in Table 1. Estimates of additive genetic (σ_A^2) and dominance (σ_D^2) variance can be expressed as follows:

$$\hat{\sigma}_A^2 = 4(M_1 - M_5)/2re \quad \hat{\sigma}_D^2 = (M_3 - M_5)/re$$

where it is assumed that genotype-environment interaction variances are proportional to the variances from the genetic effects involved whether the latter are of the additive or dominance type (6).

Variances of the genetic variances are estimated as:

$$V(\hat{\sigma}_A^2) = (\frac{2}{re})^2 \cdot 2 \left[\frac{M_1^2}{p_1 + 2} + \frac{M_5^2}{p_5 + 2} \right] \text{ and}$$

$$V(\hat{\sigma}_D^2) = (\frac{1}{re})^2 \cdot 2 \left[\frac{M_3^2}{p_3 + 2} + \frac{M_5^2}{p_5 + 2} \right]$$

where p = the degrees of freedom for the respective mean squares and the other symbols are defined in Table 1. Mode and Robinson (11) present a discussion of the derivation of these formulae and the use of $p + 2$ as a divisor.

If only additive and dominance effects give rise to genetic differences in the segregating populations, the average degree of dominance (\bar{a}) can be estimated (6) as

$$\bar{a} = \sqrt{(M_3 - M_5)/(M_1 - M_5)}$$

where the degree of dominance is reflected by the magnitude of \bar{a} as follows:

$\bar{a} = 0$	No dominance
$0 < \bar{a} < 1$	Partial dominance
$\bar{a} = 1$	Complete dominance
$\bar{a} > 1$	Over-dominance

An F test of M_3 vs M_5 will test the null hypothesis, $\bar{a} = 0$.

RESULTS AND DISCUSSION

Estimates of additive genetic variance (σ_A^2) and dominance genetic variance (σ_D^2), together with their standard errors and the average degree of dominance (\bar{a}), are shown in Table 2. Estimates of additive genetic variance are positive and all but two, those for yield of seed cotton and yield of lint, greatly exceed their standard errors.

Seven estimates of dominance genetic variance are positive and four are negative. These negative estimates for seed cotton yield, lint yield, seed index and shape factor D do not exceed their standard errors so they may be considered for practical purposes to be zero. Only three of the positive dominance genetic variance estimates, those for lint percentage, weigh per boll, and U.H.M., exceed their standard errors.

Estimates of average degree of dominance (\bar{a}) were not obtained where there were negative estimates of dominance genetic variance. The 7 obtained are in the range of partial dominance and only 1, for U.H.M., exceeded 0.5. Only two of these, the ones for lint percentage and fiber fineness were greater than zero as

Table 1. Form of pertinent portion of the analysis of variance used for each character.

Source of variation	d.f.	Mean square	Mean square expectation*
F_2 parents in blocks	$b \Sigma (n-1)$	M_1	$\sigma^2 + 2re^2_{me} + 2re\sigma^2_{ml}$
Environment $\times F_2$ parents in blocks	$b \Sigma (n-1)(e-1)$	M_2	$\sigma^2 + 2re^2_{me}$
F_1 parents \times inbred lines in blocks	$b \Sigma (n-1)$	M_3	$\sigma^2 + re^2_{mle} + re\sigma^2_{ml}$
Environment $\times F_1$ parents \times inbred lines in blocks	$b \Sigma (n-1)(e-1)$	M_4	$\sigma^2 + re^2_{mle}$
Remainder among plots	$be(r-1) \Sigma (2n-1)$	M_5	σ^2

* b = number of blocks (groups), r = number of replications, n = number of progeny pairs per block (not constant for every block), e = number of environments, σ^2 = error variance among plots, σ^2_{me} = variance due to genetic differences among F_2 (male) plants, σ^2_{ml} = variance due to interaction of genotypes of F_2 and inbred parents, σ^2_{mle} = variance due to interaction of F_2 genotype and environment, σ^2_{mle} = variance due to interaction of genotypes of F_2 and inbred parents and environment.

Table 2. Estimates of additive genetic variance (σ_A^2), dominance genetic variance (σ_D^2), respective standard errors, and average degree of dominance (\bar{a}) for each trait.

Trait	$\hat{\sigma}_A^2$	$\hat{\sigma}_D^2$	\bar{a}
Seed cotton yield	278 \pm 1349	-313 \pm 613	\uparrow
Lint yield	320 \pm 228	-42 \pm 86	\uparrow
Lint percentage	2,369 \pm 390	0.075 \pm .030	.252*
Lint index	0.4278 \pm .0735	0.0013 \pm .0054	.078
Seed index	0.3582 \pm .0709	-0.0011 \pm .0092	\uparrow
Weight per boll	0.1308 \pm .0325	0.0151 \pm .0089	.481
Fiber length, U.H.M.	0.000494 \pm .000125	0.000097 \pm .000041	.627
Fiber strength, T_1	0.0313 \pm .0065	0.0009 \pm .0011	.236
Fiber elongation, E_1	0.2086 \pm .0446	0.0067 \pm .0081	.253
Fiber fineness, A	.368 \pm .90	.18 \pm .21	.314*
Fiber shape, D	17.10 \pm 4,90	-0.03 \pm 1.22	\uparrow

* Deviation from hypothesis of no dominance ($\bar{a} = 0$) significant at 5% level.
 \uparrow Negative estimate due to negative estimate of dominance genetic variance.

indicated by the test of the hypothesis, $\bar{a} = 0$. As pointed out by Comstock and Robinson (5), the effect of possible linkage in an F_2 would be to cause upward bias in estimates of \bar{a} . No information is available for evaluating the importance of such bias in these estimates.

The total range of variation in this population for U.H.M. was slight, perhaps reflecting the phenotypic similarity of the two parental lines for this trait. Genetic variances for this trait might be expected to be low, and the relative magnitudes of the additive and dominance variances as expressed by average degree of dominance may reflect the fixation of a major portion of the additive variance by the prior selection process.

The ranges of variation were substantial for the other traits. The relative magnitudes of additive and dominance genetic variances found in this population are in line with those found by the authors in an inter-Upland population (unpublished) and in other cotton populations studied by Miller and Marani (9) and White and Richmond (13). These data, although limited in scope, suggest that genes transferred from the two diploid species appear to have had little effect on the genetic variances compared to those found within Upland cotton.

A choice of a breeding procedure for this population appears to be one that is effective with additive gene action. With the relatively small amounts of dominance variation present, a breeding procedure designed to produce a heterozygous final product could not be justified. Cockerham (3) points out that a combination of mass, family, and progeny-test selection would be effective in this situation.

The model used included only additive gene action with dominance. If epistasis exists, no serious consequences are encountered. Although extension of this

design to include epistasis is almost unmanageable (4), certain observations are relevant. Epistatic components contribute to both estimated variances, particularly those of the additive \times dominance types. Since the estimated dominance variance was, for the most part, negligible, it can be fairly safely assumed that the additive \times dominance components are not of sufficient magnitude to offer any appreciable contribution to the genetic variations. The breeding procedures suggested above would be effective with additive \times additive types of epistasis. Therefore, including epistasis in the genetic model would not alter the choice of the breeding procedure to be used.

It should be emphasized that the present data are very meager for characterizing the genetic variation in this population and forming the base of long range breeding plans. Genetic variance estimates have large sampling errors and may fluctuate considerably from environment to environment. Additional information on the type of genetic variation in cotton breeding populations will be required to fully evaluate the efficiency of alternative breeding procedures.

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