

Genetic Association Between Yield and Fiber Strength in Upland Cotton<sup>1</sup>R. L. Scholl and P. A. Miller<sup>2</sup>

## ABSTRACT

Genetic variances and correlations were measured on the segregating progeny of a cross between two upland cotton (*Gossypium hirsutum* L.) cultivars. One cultivar ('TH-149-8-5') had high lint yield and high fiber strength, whereas the other parental cultivar ('Lankart 57') had low lint yield and low fiber strength. Previous studies of genetic correlations between lint yield and fiber strength in upland cotton have shown that there is a negative association between these two traits. However, in the previous studies, high yield and high fiber strength were introduced from opposite parents in the cross. The present study was undertaken to determine if alteration of this relationship between parental means would change the observed genetic association in the progeny population. Eighty-nine progeny families, generated by selfing individual  $F_2$  plants, were evaluated in two replicates in each of three environments for lint yield, several yield components, and fiber quality indices. Population means were generally intermediate to the parental means, and significant genetic variance was found for each trait. Genotypic correlations generally agreed in both sign and magnitude with past estimates. The genotypic correlations between lint yield and the fiber quality traits were generally negative. Both 2.5% span length and fiber strength ( $T_1$ ) were negatively correlated with yield (both  $-0.36$ ). Significance of the correlations and the expected gain from selection were discussed.

*Additional index words:* *Gossypium hirsutum* L.

QUANTITATIVE genetic studies of upland cotton (*Gossypium hirsutum* L.) have documented a strong, consistent, negative genetic association between line yield and fiber strength (Miller et al., 1958; Al-Jibouri, et al., 1958; Miller and Rawlings, 1967b). Since both of these characters should be maximized for the production of superior commercial cultivars, this problem and its basis remain of fundamental interest to cotton breeders. While genetic correlations may be caused by several factors (Anderson, 1939), the genetic correlations observed in segregating cotton populations are probably caused by linkage or pleiotropism (Al-Jibouri et al., 1958). Miller and Rawlings (1967a) estimated the effect of intermating on the genetic correlations in a cotton population and found that the association between yield and fiber strength, as well as most other correlations, were reduced in absolute value. Meredith and Bridge (1971) obtained similar results, and Fotiadis and Miller (1973) found that  $\gamma$ -irradiation did not measurably affect negative genetic correlations in a cotton population.

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Past studies of genetic correlations have involved populations generated from biparental crosses in which the higher lint yield and higher fiber strength were not contributed by the same parent. From such a cross it might be anticipated that any genetic correlation in the  $F_2$  would be negative (Anderson, 1939). The parents for the present study were chosen so that high lint yield and fiber strength were both contributed by the same parent. The objectives of the present study were to estimate genetic variances for and correlations among lint yield and fiber quality in the progeny of a cross, for which high lint yield and fiber strength were introduced from the same parent. Results from such a cross should provide information regarding the underlying causes of these genetic correlations.

## MATERIALS AND METHODS

Two strains of *G. hirsutum*, 'Lankart 57' and TH-149-8-5, were crossed to generate the hybrid progeny used. Lankart 57 was developed at the Lankart Seed Farms, Waco, Texas, for use on the Blacklands and Rolling Plains of Texas. It is adapted to stripper harvesting, and is storm-resistant. It has low fiber strength, and yields poorly in North Carolina, although it produces acceptable yields in the area where it is adapted. TH-149-8-5 was derived from the inter-specific hybrid, (*G. arboreum* L.  $\times$  *G. thurberi* Tod.)  $\times$  *G. hirsutum* (Beasley, 1940) crossed with several upland strains. TH-149-8-5 is one of the two component lines of the cultivar 'TH149', and combines high fiber strength with relatively high lint yield. TH-149-8-5 is highly inbred and thus relatively homogeneous.

Eighty-nine  $F_2$  plants of TH-149-8-5  $\times$  Lankart 57 were self-pollinated to produce  $F_3$  families and bulk self-pollination of each  $F_3$  family was made to produce corresponding  $F_4$  families. The parents and segregating progenies were evaluated at the Upper Coastal Plains Research Station at Rocky Mount, N.C. in 1968 ( $F_3$  plants) and 1969 ( $F_4$  plants) and the Central Crops Research Station at Clayton, N.C. in 1969 ( $F_4$  plants). These three location-year combinations were treated as three environments. To combine the analysis for the three environments,  $F_3$  and  $F_4$  families were treated as having the same genetic expectation. The expected dominance and dominance interaction variances, based on a common  $F_2$  base population, are less among  $F_4$  than among  $F_3$  family means. If dominance effects were small in the population, use of both types of progeny in the same experiment should be valid. Previous estimates of dominance variance in upland cotton populations have been low (Ramey and Miller, 1966).

Since the family types were confounded with environments, the genotype  $\times$  environment variance component could be biased

Table 1. Relevant portion of the analysis of covariance between traits  $i$  and  $j$  (for analysis of variance if  $i = j$ ) for more than one environment.

Source	df	Mean square or product	Mean square or product expectation†
Entries in blocks	b (g-1)	M1 <sub>ij</sub>	$\sigma_{ij} + r\sigma_{gnij} + r\sigma_{gij}$
Entries by environments in blocks	b (g-1) (n-1)	M2 <sub>ij</sub>	$\sigma_{ij} + r\sigma_{gnij}$
Pooled error	bn (g-1) (r-1)	M3 <sub>ij</sub>	$\sigma_{ij}$

†  $\sigma_{ij}$  = pooled error covariance or variance,  $\sigma_{gnij}$  = interaction covariance or variance of entries by environments,  $\sigma_{gij}$  = genotypic covariance or variance, b = no. of blocks, g = no. of entries, n = no. of environments, r = no. of replications.

Table 2. Means of parents and the progeny population.

Character	Progeny population	TH-149-8	Lankart 57	L.S.D. (0.05)	
				Parental difference	Progeny mean vs. mid-parent
Lint percentage	34.1	34.5	34.3	0.4	0.4
Lint yield, kg/ha	712	794	568	42	65
S. C. yield, kg/ha	2,092	2,303	1,669	121	178
Boll size, g	7.67	6.95	8.21	0.16	0.17
Seed index, g	14.5	14.3	14.4	0.3	0.2
Seed/boll, no.	34.8	31.8	37.6	0.8	0.8
Lint index, g	7.56	7.53	7.54	0.18	0.16
50% span length, mm	13.4	13.7	12.7	0.3	0.3
2.5% span length, mm	27.2	27.7	26.4	0.3	0.3
Fiber strength, mN/tex	183.9	209.3	155.8	3.3	3.1
Fiber elongation, E <sub>1</sub>	7.86	6.41	9.46	0.32	0.25
Fiber fineness, Mic.	4.29	4.51	4.22	0.08	0.09

Table 3. Estimates of variance components and their standard errors (in parentheses) in the progeny population.

Character	Genotype × Environment interaction $\hat{\sigma}_{gni}$	Genotypic $\hat{\sigma}_{gi}$	Phenotypic $\hat{\sigma}_{pi}$
Lint percentage	0.225** (0.062)	1.252** (0.216)	1.424 (0.215)
Lint yield, kg/ha	-140 (810)	2,760** (740)	4,700 (710)
S. C. yield, kg/ha	-300 (6,500)	10,600** (4,200)	25,900 (3,900)
Boll size, g	0.0041 (0.0095)	0.0886** (0.0170)	0.1116 (0.0168)
Seed index, g/100 seed	0.059* (0.023)	0.249** (0.047)	0.310 (0.047)
Seed/boll, no.	0.204 (0.226)	1.373** (0.298)	1.936 (0.292)
Lint index, g/100 seed	0.024* (0.010)	0.134** (0.024)	0.160 (0.024)
50% span length, mm	0.03 (0.01)	0.08** (0.02)	0.12 (0.02)
2.5% span length, mm	0.03 (0.02)	0.50** (0.08)	0.55 (0.08)
Fiber strength, mN/tex	-0.87 (3.00)	43.5** (7.7)	50.5 (7.6)
Fiber elongation, E <sub>1</sub>	0.003 (0.019)	0.189** (0.036)	0.235 (0.035)
Fiber fineness, Mic.	0.0113** (0.0039)	0.0617** (0.0108)	0.0710 (0.0107)

\* \*\* Appropriate f-test of the null hypothesis that the component of variance is zero is significant at the 0.05 and 0.01 probability levels, respectively (phenotypic variance was not tested).

upward to the extent that differential inbreeding effects changed the relative ranking of families among environments. This effect was not regarded as important because estimates of non-additive genetic variance in cotton populations have been small.

Two replicates of each F<sub>3</sub> or F<sub>4</sub> family or parent, each consisting of a single row-plot (7.63 × 1.02m) with approximately 75 plants, were grown in each of the three environments. The progeny families were arbitrarily divided into six groups, which corresponded to blocks of the experimental plots. The replications were planted within blocks. This design was used to minimize the effect of soil heterogeneity.

The parental lines were included in all six blocks at each location. Therefore, the parental information was analyzed as a randomized complete block design with 12 replicates (6 blocks × 2 replicates per block). Seed cotton yield was expressed as kilograms per hectare, based on total plot production. Lint percentage was the weight of ginned lint as a percentage of the seed cotton in a 25-boll sample, and lint yield (kg/ha) was the product of seed cotton yield × lint percentage. Boll size was the average weight, in grams, per boll. Seed index and lint index were the average weights, in grams, of 100 seeds and of the lint from 100 seeds.

Fiber characteristics were measured at the USDA Fiber Laboratory at Knoxville, Tenn. Fifty percent span length and 2.5% span length were the distance (mm), spanned by 50% and 2.5% of the fibers as measured on the Digital Fibrograph. Fiber strength (T<sub>1</sub>) and fiber elongation (E<sub>1</sub>) were measured on the 3.2 mm gauge strometer. T<sub>1</sub> is a measure of fiber strength (mN/tex), and E<sub>1</sub> is expressed in terms of maximum percentage elongation. Fiber fineness was determined on the Micronaire and expressed in standard micronaire units.

The analysis of the experiment was combined over environments for the segregating progeny and the parents. Analyses of variance on the parents were conducted separately. Analyses of covariance analogous to the variance analyses were conducted for the segregating progeny population. The relevant portion of the progeny analysis is given in Table 1. From the analysis the genotypic components of variance ( $i=j$ ) and covariance ( $i \neq j$ ) were estimated as

$$\hat{\sigma}_{gi} = (M_{1i} - M_{2i})/rn,$$

the phenotypic variance ( $i=j$ ) and covariance ( $i \neq j$ ) of entry means as

$$\hat{\sigma}_{pi} = M_{1i}/rn, \text{ and}$$

the genotype by environment interaction component of variance as

$$\hat{\sigma}_{gni} = (M_{2i} - M_{3i})/r.$$

The phenotypic variance, as defined above, is specific for two replications conducted within each of three environments.

Variance and covariance components were used to estimate genotypic correlations as

$$\text{Genotypic } r_{ij} = \frac{\hat{\sigma}_{gi}}{(\hat{\sigma}_{gi} \cdot \hat{\sigma}_{gj})^{1/2}}.$$

The method of Mode and Robinson (1959) was used to estimate the standard errors of variance components and correlation coefficients. Genetic advance from selection was predicted as given by Fotiadis and Miller (1973).

## RESULTS AND DISCUSSION

**Parental and Progeny Means.** TH-149-8-5 produced more lint and had longer and stronger fiber than Lankart 57 (Table 2). This was expected when the parents were chosen. Significant differences between the parents were detected for all characteristics except lint percentage, seed index, and lint index. With the exception of micronaire the overall means for the progeny families were not significantly different from the mid-parent values. For micronaire the population mean was closer to the low parent. Such a lack of heterotic effects is consistent with an additive model of gene action.

**Estimates of Variance Components.** Genotype by environment interaction variances were significantly greater than zero for four characteristics (Table 3). The four significant interaction components were,

however, smaller than the corresponding genotypic variance component, indicating that relative performance of the entries was similar in all environments.

The genotypic variances of the progeny populations were of a magnitude similar to estimates from other populations (Miller et al., 1958) and high. Therefore, this population should provide sufficient genetic variability for selection of any of the traits. For comparison, the phenotypic components of variance were included. They were slightly higher than the corresponding genotypic components. Therefore, heritability estimates based on progeny means over three environments would be relatively high.

**Expected Progress from Selection.** Predicted changes for three unselected traits when truncation selection with a 5% intensity of selection is practiced on another trait are given in Table 4. Direct selection for lint yield was predicted to be as effective as its correlated response to selection for any of its components. Response of yield to selection for lint percentage was predicted to be as great as direct selection for yield. Predicted change in lint yield as a function of selection for both  $T_1$  and 2.5% span length was negative and substantial. This reflects the negative genetic correlations. Predicted correlated responses for 2.5% span length and  $T_1$  were lower in magnitude than predicted responses to direct selection for these traits. Past studies suggest that selection for lint yield should reduce fiber strength and length (Al-Jibouri et al., 1958; Miller et al. 1958; and Miller and Rawlings, 1967b). Despite the fact that high fiber quality and high productivity were introduced from the same parent, the predicted response of 2.5% span length and  $T_1$  to selection for lint yield were substantial and negative.

**Genotypic Correlations.** The sign and magnitude of the genotypic correlations (Table 5) agreed with

prior results. Lint yield was negatively correlated with fiber strength, fiber length, and seed index and positively associated with lint percentage, lint index, fiber elongation, and fiber fineness. A scatter diagram of the progeny means for lint yield and fiber strength was plotted, and the range of values observed was large for both characteristics. The extreme combinations of strength and yield found in the parents were not approached by any of the progeny families. Correlations that involved seed cotton yield and other traits were similar to those for lint yield. For comparison, Al-Jibouri et al. (1958), Miller et al. (1958), and Fotiadis and Miller (1973) reported negative associations between lint yield and fiber quality, particularly fiber strength (0 to  $-0.64$ ). The present estimate of the lint yield — fiber strength correlation ( $-0.36$ ) was at the center of the past range of estimates, and the phenotypic correlation ( $-0.26$ ) was similar to the genotypic correlation. Such negative correlations for this trait-pair were surprising since the present population was generated from a set of parents that, based on Anderson's (1939) predictions, should yield a positive correlation (if it is non-zero). These facts suggest that the negative association between lint yield and fiber strength might be the result of some basic genetic relationship that permeates the upland cotton germplasm currently being exploited. This seems particularly true since attempts to alter this relationship have met with difficulty. Miller and Rawlings (1967a) reduced a  $-0.69$  correlation in an  $F_2$  to  $-0.35$  with six generations of random mating. Likewise, Fotiadis and Miller (1973) found that a population that had been subjected to recurrent seed irradiation still exhibited a substantial negative genetic correlation between lint yield and fiber strength ( $-0.24$ ).

Al-Jibouri et al. (1958) have suggested that pleiotropy and/or linkage might cause such genetic correlations in upland cotton, and these appear reasonable as explanations of the current data. In this regard, it is necessary to consider whether unique circumstances associated with the particular set of environments could have invalidated the results. This possibility can probably be ruled out because three environments were studied, and they represented typical North Carolina cotton-growing conditions. The agreement of data among the three environments was good.

Extremely close linkages could be responsible for the negative yield-fiber strength correlations observed, if natural and/or artificial selection favored their accumulation in the species over a long time period. Assuming that linkages are responsible for the negative correlations, it should be expected that when the rare

Table 4. Expected response of three traits to selection for another trait.

Selected trait	Response of unselected trait		
	Lint yield	$T_1$	2.5% span length
	kg/ha	mN/tex	mm
Lint percentage	92	-5.0	-0.378
Lint yield	90	-3.8	-0.403
Seed cotton yield	70	-2.6	-0.337
Boll size	-5	-2.3	0.002
Seed index	-29	-4.7	0.094
Seed per boll	-12	4.8	0.094
Lint index	69	-1.5	-0.302
50% span length	-15	7.6	0.780
2.5% span length	-40	4.7	1.384
Fiber strength, $T_1$	-38	12.6	0.490
Fiber elongation, $E_1$	38	-2.0	-0.226
Fiber fineness, Micronaire	59	-1.9	-0.653

Table 5. Estimates of genotypic correlations and their standard errors from the progeny population (SE in parentheses).

Trait	Lint percentage	Lint yield	Seed cotton yield	Boll size	Seed index	Seed per boll	Lint index	50% Span length	2.5% Span length	Fiber Strength $T_1$	Fiber Elongation $E_1$	Fiber fineness
Lint percentage	--	0.84 (0.08)	0.58 (0.17)	0.09 (0.13)	-0.36 (0.17)	-0.04 (0.15)	0.75 (0.06)	-0.41 (0.13)	-0.28 (0.11)	-0.39 (0.11)	0.24 (0.12)	0.27 (0.11)
Lint yield, kg/ha	--	--	0.94 (0.05)	-0.04 (0.14)	-0.28 (0.15)	-0.22 (0.18)	0.65 (0.12)	-0.15 (0.02)	-0.36 (0.13)	-0.36 (0.14)	0.38 (0.16)	0.54 (0.12)
Seed cotton yield, kg/ha	--	--	--	-0.11 (0.19)	-0.18 (0.19)	-0.27 (0.22)	0.46 (0.18)	0.02 (0.19)	-0.36 (0.17)	-0.29 (0.18)	0.39 (0.19)	0.63 (0.16)
Boll size, g	--	--	--	--	0.48 (0.17)	0.61 (0.09)	0.42 (0.11)	-0.23 (0.14)	0.01 (0.11)	-0.18 (0.12)	-0.33 (0.12)	0.16 (0.12)
Seed index, g/100 seed	--	--	--	--	--	-0.28 (0.13)	0.34 (0.12)	-0.01 (0.08)	0.07 (0.12)	0.39 (0.12)	-0.27 (0.13)	-0.04 (0.12)
Seed per boll	--	--	--	--	--	--	-0.24 (0.13)	-0.06 (0.15)	0.08 (0.14)	-0.42 (0.12)	-0.23 (0.14)	0.08 (0.13)
Lint index, g/100 seed	--	--	--	--	--	--	--	-0.42 (0.14)	-0.22 (0.12)	-0.12 (0.13)	0.05 (0.14)	0.25 (0.12)
50% span length, mm	--	--	--	--	--	--	--	--	0.67 (0.08)	0.68 (0.10)	-0.04 (0.14)	-0.07 (0.14)
2.5% span length, mm	--	--	--	--	--	--	--	--	--	0.36 (0.11)	-0.17 (0.12)	-0.48 (0.10)
Fiber strength, $T_1$	--	--	--	--	--	--	--	--	--	--	-0.16 (0.13)	-0.15 (0.09)
Fiber elongation, $E_1$	--	--	--	--	--	--	--	--	--	--	--	-0.14 (0.06)

recombinations between yield and strength loci occur, the resultant lines when used as parents in crosses should produce sets of progeny in which the genetic correlation between yield and strength is positive. Since the present genetic correlation between yield and strength was negative in spite of the manner in which parents were selected, the genetic relationships between yield and strength probably results from pleiotropic effects. If high lint yield genes reduce fiber strength, then, regardless of the mating system applied or germplasm source chosen, any relationship between the two traits would be expected to be negative.

Given a general predominance of genes with pleiotropic effects, rare genotypes might occasionally occur to produce a high yielding, strong fibered line such as TH-149-8-5. Recombinants that had the extreme values of strength and yield of TH-149-8-5 were not found among the progeny. This suggests that TH-149-8-5 might be the result of rare genetic circumstances, possibly involving complex epistatic effects.

Several possibilities exist for the joint improvement of fiber quality and quantity, one being the examination of previously untapped exotic sources for suitable parents in breeding programs, as was accomplished when the "triple-hybrid" lines were created (Beasley, 1940; Lewis, 1957). Also, whenever selection is practiced for either lint yield or fiber strength, the other should be evaluated simultaneously. Such a practice should be successful since current information suggests that while significant negative associations between yield and quality may always be present in cotton breeding populations, they are seldom so large that joint selection techniques would be totally ineffective. Appropriate weighting of these traits in an

index (Hazel and Lush, 1942), for example, should produce a more desirable balance of quality and quantity in the selected population even though the procedure would somewhat retard the rate of progress for the trait of major interest.

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