

Inheritance of Fiber Properties Among Crosses of Acala and High Plains Cultivars of Upland Cotton¹

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ABSTRACT

Although High Plains and Acala cultivars of cotton are taxonomically classified as *Gossypium hirsutum* L., their pedigrees suggest that they have remained largely discrete populations during cultivar development. To evaluate the genetic control associated with certain fiber properties when High Plains and Acala cultivars are hybridized, a factorial mating design was used to cross randomly-selected High Plains and Acala lines. The hybrid populations that resulted from those crosses were used to obtain estimates of genetic variances for fiber length, strength, elongation, and fineness.

Additive genetic variance predominated for fiber length, strength, and elongation. Most of the phenotypic variance for fiber fineness was due to the environmental component; however, a statistically significant, nonadditive component was observed. The results suggested that in general, within segregating populations derived by hybridizing High Plains and Acala cultivars, lines can be selected that have desirable combinations of fiber length, strength, and elongation, but that genetic gain for fiber fineness will probably be difficult.

Additional index words: *Gossypium hirsutum* L., Heterosis, Cotton breeding, Gene action.

CERTAIN fiber properties are indicative of characteristics considered important when raw cotton (*Gossypium hirsutum* L.) is processed into finished products. These fiber properties affect the quality of the finished products, the efficiency of the production process, or both. The degree to which fibers conform to these quality requirements forms the basis of the marketing system in upland cotton. This system places a premium value on the fiber properties of long length, maturity, and over-all appearance. Although the marketing system does not assign values to fiber strength and elongation, both have been shown to affect either production efficiency or quality of the end products (Rusca and Reeves, 1968).

To meet the demands of this marketing system, cotton geneticists and breeders have a large array of fiber types with which to work. These range from the extremely long, fine fibers of the Pima cultivars (*G. barbadense* L.) to the short, coarse fibers associated with many of the primitive stocks of *G. hirsutum* L. In reality however, a commercial or public plant breeder of upland cotton (*G. hirsutum*) has a more limited number of fiber types available because of the low fertility associated with interspecific crosses or

because of the photoperiodic flowering mechanism associated with many of the primitive race stocks.

In the United States, three general groups of upland cultivars form the basis of the material available to a breeder. These are: i) the medium fiber length, medium to small-boll, medium maturing, open-boll cultivars grown in the eastern Cotton Belt, the Mississippi Delta, and the Gulf Coast of Texas; ii) the short fiber length, medium to large-boll, early maturing, storm resistant or stormproof cultivars grown in the Plains area of Texas, Oklahoma, and New Mexico; and iii) the long fiber length, large-boll, late maturing, open-boll Acala-type cultivars grown in the irrigated areas of the Southwest (Lewis and Richmond, 1968). Although these are not discrete groupings, they are descriptive of geographical areas where particular types of cultivars are grown. To a limited extent, these groups are based on fiber properties; however yield of lint, earliness of crop maturity, and other agronomic characters that contribute to the adaptation to a given production area vary among and within these groups.

The purpose of this research was to evaluate the nature of gene action associated with fiber length, strength, elongation, and fineness when High Plains cultivars are crossed with Acala cultivars. This information should be of particular value in the High Plains production area where attempts are being made to improve the fiber quality among the cultivars adapted to the region.

LITERATURE REVIEW

Numerous studies on the inheritance of fiber properties have been conducted in cotton. In a cross between two cultivars, Ware, Jenkins, and Harrell (1943) found that long fiber was partially dominant to short fiber. Self and Henderson (1954) and Ware and Harrell (1944) reported that fiber strength was inherited in a partially dominant fashion and was controlled by numerous genes. Miller and Marani (1963) reported an appreciable amount of additive genetic variance for fiber length and strength. Verhalen and Murray (1967, 1969) in a 10-parent diallel noted that long fibers were partially dominant over short fibers, additive gene action appeared to govern fiber strength, and over-dominant gene action controlled fiber fineness. Al-Rawi and Kohel (1970) studied the gene action associated with the fiber properties of 9 selected cultivars of upland cotton. They showed that fiber length, strength, and elongation were within the range of partial dominance and that fiber fineness was controlled by overdominant gene action, possibly caused by repulsion linkage. Baker and Verhalen (1973) reported that complete dominance was operative for fiber length and strength and that partial dominance controlled fiber fineness. The results of these studies have not been entirely consistent from experiment to experiment, perhaps because they have included different material, were conducted in different environments, or both.

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MATERIAL AND METHODS

The experimental lines used in this study were randomly chosen from within an F_2 composite population of High Plains cultivars and from within an F_2 composite of Acala cultivars. The composite High Plains population was developed by making all possible crosses among six High Plains cultivars ('Paymaster 111,' 'Western Stormproof,' 'Gregg 35,' 'Blightmaster A-5,' 'Lankart sel. 57,' and 'Paymaster 101B'). These six cultivars were randomly chosen from among a group of 24 cultivars that were grown in the High Plains production area during the 1969-70 growing seasons. The F_1 hybrids from those crosses were self-pollinated, harvested in bulk, and the resulting F_2 seed were planted in the greenhouse. From this F_2 population, six plants were randomly chosen to represent the germplasm associated with High Plains cultivars.

The Acala F_2 composite population was generated by crossing in all possible combinations four Acala cultivars that were randomly selected from a group of 12. The four cultivars were 'Acala 1517D,' 'Hopicala,' 'Del Cerro,' and 'Acala SJ-1.' The group of 12 cultivars represented those available to producers during the 1969-70 growing season. The F_1 hybrids were grown, self-pollinated, harvested in bulk, and four plants were randomly chosen from the resulting F_2 population to represent Acala germplasm.

Although High Plains and Acala cultivars are taxonomically classified as *G. hirsutum*, their pedigrees suggest that the two groups have remained largely discrete during cultivar development (Ramey, 1966). Therefore they were treated in this study as distinct populations of germplasm of upland cotton. The cultivars used in the development of the High Plains and Acala composite populations were randomly chosen and should represent a random sample of the germplasm associated with their cultivar-types. Thus the reference populations of this study were the F_2 composite populations and the inferences derived from the data should be generally expected when High Plains germplasm is crossed with Acala germplasm.

The six plants chosen to represent High Plains germplasm and the four plants representing Acala germplasm were self-pollinated, and a progeny row of each was planted. Within each F_3 row, one plant was arbitrarily selected and self-pollinated. Self-pollinated seed from each plant was grown in F_4 progeny rows; one plant was again chosen and self-pollinated from each of these rows. One additional cycle of plant to progeny row selection was conducted. Self-pollinated seed from the F_4 plants chosen in the last cycle were used to form the six High Plains lines and four Acala lines as parents in this study. After these self-pollination cycles were conducted to remove most of the genetic variability from within a line, we believed that the parental lines were essentially homogeneous, but probably not completely homozygous. Most of the variability which remained was among lines within cultivar-types and between cultivar-types.

The crossing or mating design of the study was the "North Carolina design II" (Comstock and Robinson, 1952). Basically, this design consists of crossing maternal parents with each of a group of paternal parents. The results of these crosses are a factorial-type design with m (maternal parents) crossed with p (paternal parents) resulting in an mp (number of F_1 crosses).

Following this design, the six High Plains lines were used as maternal and the four Acala lines as paternal parents; therefore the experimental maternal consisted of 6 maternal and 4 paternal lines and 24 F_1 hybrids. Moll and Robinson (1967) and Stuber (1970) have suggested that a large number of F_1 hybrid progenies are desirable for highly reliable variance component estimation when the "North Carolina design II" is used. F_1 progeny numbers in cotton are limited by the number of F_1 seed that can be produced and by the expense involved in analyzing fiber samples.

The 34 entries were planted in a randomized complete block design in the genetics nursery at the Texas A&M University Agricultural Research and Extension Center, Lubbock on May 15, 1973. Three replications of each entry were planted in single row plots 10-m long with 1 m between plots. One 10.2-cm irrigation was applied in July; routine cultural practices were followed throughout the season. After frost, seedcotton from five random individual plants within each entry in each replication was hand harvested separately. The samples were ginned and the fiber was sent to the U. S. Cotton Quality, Knoxville, Tenn., for fiber analyses.

The fiber properties investigated were: i) fiber length - the length (inches), of the longest 2.5% of the fibers by weight as

measured on the digital fibrograph; ii) fiber strength - expressed in terms of the force (g/tex) required to break a fiber bundle with the clamps of the stelometer set 3.2 mm apart; iii) fiber elongation - the percentage of elongation which occurs before a fiber bundle breaks while being measured for fiber strength; and iv) fiber fineness - resistance in $\mu\text{g}/\text{inch}$ of a given quantity of fiber to air flow, measured on the micronaire instrument.

The additive and nonadditive genetic variances associated with these fiber properties were estimated from analyses of variance of maternal, paternal, and maternal \times paternal sources of variation using the F_1 hybrids data (Becker, 1967). The mean squares estimated from those sources were reduced by subtraction to the σ^2_m , σ^2_p , and σ^2_{mp} components. The σ^2_m and σ^2_p components estimate the additive confounded with the additive \times additive genetic variances for the maternal and paternal populations, respectively. The σ^2_{mp} component estimates nonadditive genetic variance. The data taken from the individual plants within each F_1 hybrid entry were used to estimate the within-entry source of variation (Hanover and Barnes, 1962 and Becker, 1967).

RESULTS AND DISCUSSION

The six lines representing germplasm of High Plains cultivars produced fibers that were short, weak, high in elongation, and fine (Table 1). Among these lines, significant variation occurred for each of the characters measured; however none appeared to have a desirable combination of fiber properties. In comparison, the four Acala lines produced long, strong fibers that were lower in elongation and medium in fineness. Significant variations were observed among the Acala lines for each of the fiber properties with the exception of elongation.

Fiber length appeared to be partially dominant in the direction of the longer fibered Acala lines; whereas fiber strength, elongation, and fineness were partially dominant in the direction of the High Plains lines (Table 2). Heterosis (measured as percent deviation from the mid-parental values) was 3, 5, 3, and 3% for greater length, less strength, higher elongation, and more fineness, respectively.

Table 1. Fiber characteristics of the lines selected to represent High Plains and Acala germplasm.

Lines	Fiber characters			
	Length	Strength	Elongation	Fineness
	in.	g/tex	%	$\mu\text{g}/\text{in.}$
High Plains				
1	0.97 b*	15.7 bc	11.1 a	3.7 a
2	0.99 ab	15.2 c	8.7 d	3.1 b
3	1.01 a	18.1 a	9.1 cb	3.0 bc
4	0.97 b	17.5 a	9.6 c	3.4 ab
5	0.99 ab	16.6 b	9.6 c	3.4 ab
6	1.02 a	16.0 bc	10.3 b	2.6 c
x	0.99	16.5	9.7	3.2
Acala				
1	1.25 a	23.9 a	8.3 a	3.4 b
2	1.13 b	20.8 b	8.3 a	3.9 a
3	1.10 b	21.3 b	7.9 a	3.5 ab
4	1.11 b	20.5 b	8.2 a	3.9 a
x	1.15	21.5	8.2	3.7

* Means within columns not followed by the same letter were significantly different at the 0.05 probability level according to Duncan's new multiple range tests.

Table 2. Fiber properties of mean mid-parent and of mean F_1 hybrids and mean degree of heterosis.

Fiber characters	MP*	F_1	Heterosis
Length, in.	1.07	1.10	3
Strength, g/tex	19.1	18.2	5
Elongation, %	9.0	9.3	3
Fineness, $\mu\text{g}/\text{in.}$	3.5	3.4	3

* MP = mid-parent.

Table 3. Analyses of variance of maternal (High Plains), paternal (Acala), and maternal \times paternal sources of variation.

Source of variation		Mean squares			
		Length	Strength	Elongation	Fineness
		in.	g/tex	%	$\mu\text{g/in.}$
Maternal	5	.0058*	6.5393**	3.9053**	.0702
Paternal	3	.0186**	6.0740**	.8005	.0872
Pat. \times Mat.	15	.0018**	.4286	.4912**	.0718**
Pat.-Mat. Comb. \times reps	48	.0004	.2329	.1420	.0278
Among lines	71	.0068	3.5258	1.8159	.1608
Within lines	288	.0005	.2668	.1964	.0316

* ** Significant at the 0.05 and 0.01 probability levels, respectively.

Table 4. Estimated additive, nonadditive, the environmental variance components.

Fiber characters	Additive		Non-additive	Environmental
	High Plains	Acala		
Length, in.	.0003*	.0009**	.0005**	.0005
Strength, g/tex	.5092**	.3136**	.1164**	.2668
Elongation, %	.2845**	.0172	.1164**	.1964
Fineness, $\mu\text{g/in.}$.0001	.0009	.0147**	.0316

* ** Significant at the 0.05 and 0.01 probability levels, respectively.

Analyses of variance of the F_1 hybrid values for the maternal (High Plains), paternal (Acala), and maternal \times paternal sources of variation showed that significant genetic variation existed for all four fiber traits (Table 3). For length, the maternal, paternal, and interaction components were significant. Strength had significant variation for the maternal and paternal sources. Elongation had significant variation in the maternal and maternal \times paternal components. For fineness, only the interaction component was significant.

Additive, nonadditive, and environmental variance components were estimated (Table 4) from the analyses of variance of the maternal, paternal, and maternal \times paternal sources of variation (Table 3). Additive genetic variances for fiber length were contributed by both the High Plains lines and the Acala lines. Of the phenotypic variance, 41% was additive genetic variance associated with the long fiber Acala lines while only 13% was associated with the short fiber High Plains lines. The nonadditive component for length was significant, but only amounted to 23% of the phenotypic variance. Additive genetic variance for strength was more equally divided between the High Plains and Acala lines. Nonadditive gene action was not a significant factor in the inheritance of strength. The majority, if not all of the additive genetic variance associated with elongation, was due to the High Plains lines. The nonadditive component associated with fiber elongation although significant, was less than half the additive component. Most of the variance associated with fineness was due to the environmental component. The nonadditive genetic variance component was significant, but small in relation to the environmental component.

When genetic variance estimates are made from only one environment, genotype \times environmental interaction variances are confounded with the genetic estimates. These confounded variance estimates generally bias upward the genetic estimate; however the magnitude of the genetic \times environmental interac-

tion have been shown to be small for fiber properties of cotton and thus should not seriously influence the interpretation of fiber data (Lee, Miller, and Rawlings, 1967 and Baker and Verhalen, 1973).

Since the primary goal of a cotton breeder at present, is the development of a cultivar and not a hybrid, effective selection within or among populations is based on the additive or fixable portion of the genetic variance. Crosses between High Plains and Acala cultivars should in general, produce segregating populations that can be selected for fiber length, strength, and elongation, but selection for fineness will likely be difficult.

This study showed that fiber length and elongation contained additive and nonadditive genetic variance, but that the greater portion was additive. Likewise, the genetic variance associated with strength appeared to be entirely due to additive components. In comparison, the phenotypic variance associated with fineness was primarily environmental with a statistically significant, nonadditive component.

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