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Gene Effects for Fibre Properties in Upland Cotton (*Gossypium hirsutum* L.)

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Summary. Six populations - P_1, P_2, F_1, F_2, B_1 and B_2 - each of five Upland Cotton (*Gossypium hirsutum* L.) crosses were used to evaluate gene effects in the inheritance of fibre properties by Gamble's six-parameter model for the analysis of generation means. Partial dominance of long fibres over short fibres and of mature fibres over immature fibres was found in the material studied. Overdominance in gene action governed fibre fineness while additive gene action governed the fibre strength. Besides additive and dominance effects, significant epistasis was present in all crosses. These results indicate a significant potential for improving fibre properties through reciprocal recurrent selection.

Introduction

Fibre properties of cotton are among the most important factors in the cotton industry. A certain standard of fibre has to be maintained to meet the requirements of the millers. In a cotton breeding programme due emphasis is given to developing varieties or hybrids with improved fibre properties, but there are relatively few studies of the genetic systems that control such properties. Furthermore, these studies show inconsistent results for gene effects. Fibre length was found to be partially dominant by Ware and Harrell (1944). Similar gene action in the inheritance of fibre length was reported by Ware and Harrell (1963) and Self and Henderson (1954). Miller and Lee (1964) found that various fibre properties of the hybrid were similar to the mid-parent value, indicating absence of dominance. Lee, Miller and Rawlings (1967) found small but significant levels of heterosis for fibre properties and obtained significant general combining ability estimates for all the fibre properties. Verhalen and Murray (1967 and 1969) noted that overdominance gene action governed fibre fineness, whereas long fibres were partially dominant over short fibres and additive gene action governed fibre strength. Marani (1968), working with intraspecific crosses within *G. hirsutum* and *G. barbadense*, generally found more dominance and epistasis in *G. barbadense* crosses. Fibre length showed small dominance effect in both crosses and probably some epistasis for *G. barbadense*. Some dominance for fibre strength in *G. barbadense* was indicated, whereas fineness appeared to be due mostly to additive effects. Al-Rawi and Kohel (1970) found highly significant general and specific combining ability for all fibre properties within *G. hirsutum*. They noted that all fibre properties were within the range of partial dominance (except fibre fineness, which showed overdominance, possibly caused by repulsion linkage). Their results suggested that a major part of the total phenotypic variance was additive. Singh, Dahiya and Jain (1972) studied gene action in some intra-*hirsutum* crosses and found that additive, dominance and epistatic gene effects were prevalent for halo length, fibre maturity (micronaire units) and fibre fineness in all their eight crosses. Meredith, Jr., and Bridge (1972) found that significant heterosis for yield and fibre properties was due to the presence of nonadditive gene effects caused either by dominance or epistasis, or by both. Additive effects predominated for fibre strength, fibre elongation and fibre fineness. However, both additive and dominance effects were involved for lint yield and fibre length. They suggested that in the presence of significant dominance in most crosses, hybrids would be an improvement over existing commercial varieties.

The purpose of the present experiment was to obtain information on the gene action involved in the inheritance of fibre properties in some intervarietal crosses.

Materials and Methods

The materials evaluated for each of the five crosses were P_1, P_2, F_1, F_2, B_1, and B_2. The variety PRS-72 was the common parent (P_2) in each cross, chosen because of its strikingly different growth and fruiting habit from the other parents. It is an erect growing, short statured variety, bearing more than one boll on extremely short sympodials (cluster bearing), as if the bolls were born directly on the main stem. It is very early maturing and its bolls are bold. The varieties chosen as P_1, though differing in most of the characters, closely resemble each other in their growth and fruiting habit. All bear multinodal fruiting branches appearing on the monopodials or directly on the main stem. H_{14} is the locally adapted standard variety in the north Indian cotton zone. Res. H_{141} and 419/49 are single line selections from local material. Variety 5143C is an introduction from Ceylon with high yield potential while Banda-I is an introduction from West Africa. The other four populations studied were $F_1 = (P_1 \times P_2)$, $F_2 = (F_1 \text{ selfed})$, $B_1 = (P_1 \times F_1)$ and $B_2 = (P_2 \times F_1)$.

The planting arrangement was a completely randomized block design with four replications. The plants were spaced at 60 cm between the rows and 45 cm within the rows. P_1, P_2 and F_1 were accommodated in single row plots, while the number of rows for segregating generations of F_2, B_1 and B_2 varied depending on the seed availability. Each row contained 10 plants. All plantings were made by hand to ensure accuracy in spacing. Three seeds were sown per hill and were thinned to one after one month of planting. Approved cultural practices and pest control measures were adopted. Fibre samples were taken on a total plot basis and were analysed at the North Zone Central Technological Laboratory, Abohar (Punjab), to obtain information on the following fibre properties:

(1) mean fibre length: length in mm, using Balls Sledge Sorter at 65 per cent relative humidity; (2) fineness: in millitex units, with the help of a micronaire calibrated to give mean fibre weight or coarseness in terms of micrograms per inch; (3) maturity coefficient: in percentage, by micronaire cylinder with air compression adjusted for reading after applying spacer; (4) strength: expressed in terms of force (Pressley Strength Index) necessary to break the fibre bundle with two jaws of the testing instrument, a Pressley Strength Tester.

With the data from all generations for each cross, six genetic parameters were estimated using Gamble's (1962) notation as follows:

$$P_1 = m + a - \frac{1}{2} d + aa - ad + \frac{1}{4} dd$$

$$P_2 = m - a - \frac{1}{2} d + aa + ad + \frac{1}{4} dd$$

$$F_1 = m + \frac{1}{2} d + \frac{1}{4} dd$$

$$F_2 = m$$

$$B_1 = m + \frac{1}{2} a + \frac{1}{4} aa$$

$$B_2 = m - \frac{1}{2} a + \frac{1}{4} aa$$

where m = the experimental mean, and a, d, aa, ad, and dd represent the additive, dominance, additive x additive, additive x dominance and dominance x dominance gene effects, respectively.

With the means of $\overline{P}_1$, $\overline{P}_2$, $\overline{F}_1$, $\overline{F}_2$, $\overline{B}_1$, and $\overline{B}_2$ the following six genetic parameters were estimated by:

$$\hat{m} = \overline{F}_2$$

$$\hat{a} = \overline{B}_1 - \overline{B}_2$$

$$\hat{d} = -\frac{1}{2}\overline{P}_1 - \frac{1}{2}\overline{P}_2 + \overline{F}_1 - 4\overline{F}_2 + 2\overline{B}_1 + 2\overline{B}_2$$

$$a\hat{a} = -4\overline{F}_2 + 2\overline{B}_1 + 2\overline{B}_2$$

$$a\hat{d} = -\frac{1}{2}\overline{P}_1 + \frac{1}{2}\overline{P}_2 + \overline{B}_1 - \overline{B}_2$$

$$d\hat{d} = \overline{P}_1 + \overline{P}_2 + 2\overline{F}_2 + 4\overline{F}_2 - 4\overline{B}_1 - 4\overline{B}_2$$

Significance of the genetic effects was evaluated by the corresponding standard error obtained from the analysis of variance of the generation means.

Results and Discussion

Heterosis

Heterosis results (Table 1) indicate partial to overdominance gene action governing the fibre properties. In four out of five crosses, the F_1 mean for fibre length increased over the mid-parent value, though it was not significant in any cross. The highest value for heterosis was

Table 1. Average performance of parents, F_1, percentage heterosis and overdominance of fibre properties in upland cotton

Cross	Character	Generation mean P_1	P_2	F_1	Heterosis over mid-parent	Overdominance over better parent
H14 × PRS-72	Fibre length	26.38	24.11	26.72	5.82	1.29
	Coarseness	153.25	117.50	164.25	21.33**	7.18
	Maturity	0.74	0.67	0.73	3.54*	-
	Strength	9.33	8.56	8.92	-0.33	-
Res.H141 × PRS-72	Fibre length	29.45	24.11	27.40	2.36	-
	Coarseness	138.50	117.50	150.00	17.19**	8.30
	Maturity	0.71	0.67	0.69	0.00	-
	Strength	9.73	8.56	8.20	-10.38**	-
419/49 × PRS-72	Fibre length	28.70	24.11	26.40	0.00	-
	Fineness	139.50	117.50	136.00	5.84	-
	Maturity	0.72	0.67	0.70	1.45	-
	Strength	9.55	8.56	8.20	-9.49**	-
5143C × PRS-72	Fibre length	27.92	24.11	26.45	1.69	-
	Coarseness	156.75	117.50	135.00	-2.27	-
	Maturity	0.75	0.67	0.71	0.00	-
	Strength	8.83	8.56	8.40	-3.34*	-
Banda-I × PRS-72	Fibre length	28.08	24.11	26.92	3.18	-
	Coarseness	141.50	117.50	144.25	11.39	1.94
	Maturity	0.71	0.67	0.73	5.79**	2.82
	Strength	10.03	8.56	8.75	-5.81**	-

* Significant at P = 0.05; ** Significant at P = 0.01

recorded in the cross H14 × PRS-72 and was 5.82 percent, while the other three crosses showed very little increase in the F_1 over the mid-parent value. This suggests partial dominance of long fibres over short fibres. Fineness in the F_1 decreased in four out of five crosses (i.e. coarseness increased) compared with their mid-parent values, significantly so in two crosses, namely, H14 × PRS-72 and Res. H141 × PRS-72. Three crosses also showed overdominance values of 1.94 to 8.3 percent for this fibre property. This suggests that overdominance gene action may be involved in governing fibre fineness and that coarseness is dominant over fineness. Four crosses showed increased values of the maturity coefficient in F_1 over their mid-parent values, though this was significant in only two crosses. This suggests partial dominance of mature fibres over immature fibres. The fibre strength was the only character for which negative heterosis was exhibited by all the five crosses and in all but one (H14 × PRS-72) this was significant. This indicates that weak fibres are partially dominant over strong fibres.

Genetic Parameters

The estimates of six genetic parameters, $\hat{m}$, $\hat{a}$, $\hat{d}$, $\widehat{aa}$, $\widehat{ad}$, and $\widehat{dd}$ are summarised in Table 2. The sign of parameters $\hat{a}$ and $\widehat{ad}$ depends upon the parents being considered as P_1 or P_2. If P_1 is superior the estimate of $\hat{a}$ will be positive while if P_2 is superior the estimate of $\hat{a}$ will be negative. The sign of $\widehat{ad}$ will also change correspondingly in most of the cases while the signs of the other parameters remain unaffected. Since PRS-72 was designated as P_2 in all crosses, a positive effect is expected when it is the lower parent for the character under consideration. In all crosses in the present experiment P_1 had high values for all characters, the estimates of $\hat{a}$ and $\widehat{ad}$ were positive as $(P_1 - P_2)$ was used in all crosses. The sign in the case of parameter $\hat{d}$, dominance effect, is a function of the relationship of the F_1 to the mid-parent and indicates which parent might be contributing to dominance variation.

Mean Fibre Length: The estimates of additive gene effects, $\hat{a}$, were significant in three out of five crosses. However, in all crosses, the relative magnitude of parameter $\hat{d}$, in relation to parameter $\hat{m}$ was, in most cases, higher than the relative magnitude of parameter $\hat{a}$ relative to parameter $\hat{m}$. The estimates of dominance effects $\hat{d}$ were highly significant for four crosses. The estimates of epistatic gene effects dominance x dominance ($\widehat{dd}$) were mostly significant and higher than those of additive x additive ($\widehat{aa}$)

Table 2. Estimates of six genetic parameters for fibre properties in upland cotton

Cross	Character	Genetic parameters					
		$\hat{m}$	$\hat{a}$	$\hat{d}$	$\widehat{aa}$	$\widehat{ad}$	$\widehat{dd}$
H14 × PRS-72	Fibre length	27.30**	0.95**	-3.22**	-4.76	2.35	4.11**
	Fineness	153.25**	3.00	33.88**	5.00	14.87*	-23.79**
	Maturity	0.75**	0.03**	0.02*	-0.01	0.04	-0.08
	Strength	9.30**	0.50	-1.79*	-1.80**	0.30	2.19**
Res.H141 × PRS-72	Fibre length	26.10**	0.70*	1.56**	1.70	-2.21	-1.93
	Fineness	150.25**	7.50*	14.00**	8.00+	18.00**	29.00**
	Maturity	0.75**	0.02	-0.02	-0.03	0.04	-0.13**
	Strength	9.30**	0.18*	-0.98**	0.15	0.23	0.45
419/49 × PRS-72	Fibre length	27.05**	0.33+	2.99**	2.75*	1.21	-8.58**
	Fineness	142.50**	4.50	19.50**	12.00**	6.50	-65.00**
	Maturity	0.72**	0.03**	-0.01	0.01	0.02	-0.11**
	Strength	9.20**	0.23	0.21	1.25**	0.54	-4.43**
5143C × PRS-72	Fibre length	26.92**	0.20	-0.43+	-0.10	2.35*	-5.05**
	Fineness	142.50**	5.00+	3.87	6.00	14.63*	-41.75**
	Maturity	0.70**	0.02	0.07**	0.08+	0.02	-0.15**
	Strength	8.55**	0.50	0.43	0.90	0.05	-1.45**
Banda-I × PRS-72	Fibre length	26.82**	0.98**	-0.88**	0.95	1.25	-11.85+
	Fineness	142.50**	12.80**	18.15**	3.40	0.80	-29.30**
	Maturity	0.72**	0.01	-0.01	-0.03	0.02	-00.08+
	Strength	9.22**	0.15	-2.43**	1.70**	0.70	2.95**

* Significant at P = 0.05; ** Significant at P = 0.01; + Estimate larger than its standard error

gene effects, while the additive x dominance ($\widehat{ad}$) gene effects were lower than $\widehat{aa}$. This indicates that though dominance, and dominance x dominance gene effects are of more importance in the inheritance of mean fibre length, the additive gene effects were also important. The other two interactions, namely, $\widehat{aa}$ and $\widehat{ad}$ gene effects, were of equal importance.

Fineness: Four out of five $\hat{d}$ parameter estimates were significant and much higher than those of the $\hat{a}$ parameter estimates. Also all the $\hat{d}$ parameters were positive. This indicates that coarse fibre was dominant over fine fibre and dominance effects contribute much more than additive gene effects to the inheritance of fibre fineness. The $\widehat{dd}$ gene effects were more important than $\widehat{aa}$ and $\widehat{ad}$ gene effects which contributed little in some and more in other crosses. Thus both $\hat{d}$ and $\widehat{dd}$ gene effects were important in the inheritance of fibre fineness.

Fibre Maturity Coefficient: In the inheritance of fibre maturity coefficient, both the $\hat{a}$ and $\hat{d}$ gene effects were found to be important. The $\widehat{dd}$ gene effects contributed the greatest part of gene interaction components. This suggests that in the inheritance of fibre maturity, though the dominance and additive gene effects were important, the dominance x dominance interaction cannot be ignored.

Strength: The estimates for the additive gene effects, $\hat{a}$, were in most cases appreciably higher than those for parameter $\hat{d}$. The estimates of $\widehat{dd}$ interaction were higher than the two other interaction components; the $\widehat{aa}$ gene effects were greater than those of $\widehat{ad}$ in three out of five crosses. Thus additive gene effects were more important than dominance effects in the inheritance of fibre strength.

Besides additive gene effects, a preponderance of dominance gene effects for all the four fibre properties was observed. However, the nature and magnitude of gene effects varied from cross to cross and thus will demand specific handling for its full exploitation. Epistasis gene effects were found for all the four characters in all the five crosses. Considering the individual epistatic gene effects, additive x additive and dominance x dominance appeared to contribute more for all characters than did the additive x dominance effects or even some of the estimates of main gene effects. The dominance x dominance gene effects were mostly negative. This indicates that a diminishing effect on fibre properties due to this type of gene action could occur. Gene interaction additive x additive, or any digenic complementary gene interaction, is fixable and thus can be exploited effectively.

The present study has revealed that the importance of epistasis in the basic genetic mechanisms cannot be ignored. The estimates of additive and dominance variances presuming that epistasis is absent will give biased upward estimates which may be misleading. The additive gene effects obtained in the present experiment were less than those obtained by other cotton workers. This may be caused by the inclusion of epistasis in our model, which would have decreased the estimates of additive gene effects. It is also possible that, since the present study involved highly selected homozygous lines, the estimates of additive gene effects would be lower. Estimates of additive gene effects would be expected to be larger if random unselected varieties were used. From the data now available for cotton it should be evident that detection of epistasis is dependent on the particular genetic material involved, the traits studied, and the particular model used. Epistasis appears to be detected more in crosses between parents of great genetic diversity than in those between parents more closely related.

On the basis of these limited studies, it was found that for these fibre characters all three types of gene action, viz., additive, dominance and epistasis, contribute significantly to their inheritance. In such a situation rapid improvement may be expected through Reciprocal Reccurent Selection, which utilizes simultaneously the three kinds of gene effect most efficiently. The improved population could then be utilized for developing either single line varieties or first generation hybrids with improved fibre properties.

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