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Genetic Analysis of Fibre Properties in the Exotic and Indigenous Germplasm of *hirsutum* Species

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ABSTRACT

A full diallel cross involving four exotics and four local lines were used to study the inheritance of staple length and fibre fineness in *G. hirsutum* L. The analysis of variance showed that 56 F_1 and F_2 hybrids and their parents differed significantly for the two traits. Non significant deviation of regression coefficient (b) from zero revealed that additive dominance model was not adequate for analysing data on staple length in both the generations. The estimates of components of variation in fibre fineness showed predominantly additive genetic effects with some degree of dominance in F_1 and F_2 generations. Narrowsense heritability in F_1 and F_2 was 88 and 100%, respectively. The additive gene action and high estimates of heritability should make either pedigree breeding or recurrent selection successful for improving fibre fineness in *hirsutum* species.

Key Words: Diallel cross; *Hirsutum;* Fibre fineness; Additive genes; Heritability

INTRODUCTION

Amongst the four species of cotton which produce spinnable fibre, *G. hirsutum* L. contributes 90% of the total cotton production in the world (Poehlman & Sleper, 1995). Thus all attention of the cotton breeders remained focused on the development of varieties giving increased lint production on unit area basis. Cotton fibre is not only the raw material of the local textile industry but also is an important agricultural exporting commodity of Pakistan. Although a good deal of work had already been done to improve the fibre characteristics of cotton since the breeding work started in the country, these properties of cotton must continually improve to keep Pakistan cottons competitive in domestic and world market, and meet the needs of new spinning and weaving methods.

Previous studies on the inheritance of fibre traits in cotton have found different pattern of inheritance of key fibre traits such as fibre length and fibre strength. Mirza and Khan (1984) found the over-dominance for staple length and fibre fineness, whilst the studies of Nadarajan and Rangaswamy (1990) revealed additive genetic effects for fibre fineness. By contrast, the studies of May and Green (1994) revealed that dominance genetic variance was greater than additive genetic variance for all the fibre traits.

In present investigations, the F_1 and F_2 data on staple length and fibre fineness obtained by crossing eight parents belonging to *hirsutum* species were analysed to study the genetic basis of the two characteristics following simple additive-dominance model (Hayman, 1954a, b; Jinks, 1954).

MATERIALS AND METHODS

The experimental materials used in the present study were developed by crossing eight parents belonging to *Gossypium hirsutum* L according to diallel system of mating. The eight parents namely BJA, Reba-B50, A89/FM, Changmiah, CIM250, S12, NIAB78 and AUH50 were distinguishable for the two characters studied. The genotypes were genetically and geographically unrelated.

The parents were grown in earthen pots in a glasshouse, and were crossed when they started to flower. A large number of pollinations were made to produce sufficient quantity of F_1 seed. Half of the seeds of 56 hybrids and their parents were field planted in single row plot to develop F_2 seed, and the other half were kept to develop F_1 generation next year.

The F_1 and F_2 populations were grown together in a field following RCBD with three replications. The seeds of 56 F_1 hybrids and their parents were spaced at a distance of 30 cm within a row and 75 cm among the rows, and thus there were 12 plants in a row. Similarly 56 F_2 entries and their parents were planted in a plot measuring 3.3 x 6 m^2, having 96 plants, of each family in each replication. One plant on either end of each row of both the populations was left as non experimental. At maturity of plants, whole produce of the seed cotton was picked from each plant, and ginned. Length of fibres (staple length) was measured using Digital Fibrograph Model 530 at 2.5% span length and uniformity ratio at 50%. Fibre fineness was measured with the help of 'Shaffield Micronaire Apparatus'. A sample of lint was blended thoroughly using a mechanical blender.

Then 3.24 g of the blended lint was placed in micronaire chamber and was compressed by a plunger, and air current

was allowed to pass through, at the pressure of 40-60 pounds per square inch. The amount of airflow was indicated by the position of the float in the vertical tube connected to the compression chamber and fineness of fibre was read directly on the scale in microgram per inch.

Statistical analysis. Before analysing the data following diallel technique, these were subjected to Fishers' analysis of variance in order to determine whether the genotypic differences for the two characters were significant. Only significant genotypic differences allow the use of simple additive-dominance model for genetic analysis.

Data on staple length and fibre fineness were arranged in diallel tables and first degree statistics i.e. variance of the components of each array (V_r), and co-variance of all the offspring included in each parental array with the non-recurrent parent (W_r), and variance of the parental means (V_{0L0}), were calculated. The second degree statistics, means of array variances (V_{1L1}), variances of the means of arrays (V_{0L1}), and the means of array co-variances (W_{0L0}) were also calculated, and these were used for the estimation of four genetic components of variation, D (additive effects of genes), H_1 and H_2 (dominance effects of genes), and F. The F value provides an estimate of the relative frequency of dominant to recessive alleles in the parental lines and the variation in dominance over the loci. Hence F will be positive, whenever the dominant alleles are more frequent than the recessive alleles, irrespective of whether or not the dominant alleles have increasing or decreasing effects. In following the additive-dominance model, reciprocal F_1 families have identical expectations and are generally averaged before computing these statistics, hence halving the environmental component, E (Mather & Jinks, 1982). For calculating the genetic parameters in F_2 population the formulae used in F_1 were modified as proposed by Verhalen and Murray (1969), and Verhalen *et al.* (1971). Variance and covariance of the eight parents for staple length and fibre fineness are given in Table I. Variance of parents and second degree statistics are presented along with the components of variation in Table II.

The suitability of simple additive-dominance model to account for the data analysis was determined using one of the two scaling tests, joint regression analysis of variance (V_r) and co-variance (W_r). According to Hayman (1954a) the regression co-efficient (b) must deviate significantly from zero but not from unity, if all the assumptions underlying the genetic model were met. Estimate of narrowsense heritability was calculated after Mather and Jinks (1982) and given in Table II.

RESULTS AND DISCUSSION

The mean squares obtained from the analysis of variance of the two generations were significant ($P \leq 0.01$), revealing significant differences among the hybrids and their parents for staple length and fibre fineness. The results of the analysis of variance are not presented here. The regression coefficient (b) for staple length in F_1 and F_2 were equal to zero statistically, and therefore, the data were not suitable for genetic interpretation as suggested by Hayman (1954a). Regression line for fibre fineness in F_1 (b=0.880±0.162) and F_2 (b=0.976±0.035) deviated significantly from zero and were of unit slope (Fig.1), and thus additive dominance model was found adequate for genetic analysis.

The genetic components of variation in fibre fineness in both the generations are given in Table II. In both the generations, D, H_1 and H_2 items were positive and significant showing the presence of the genes with additive and dominance properties. Since the magnitude of D is greater than that of H_1 and H_2, therefore, effects of the genes acting cumulatively were pronounced in F_1 and F_2 populations. As H_1 is greater than H_2, unequal distribution of the genes in the parents was revealed, and is also evidenced by the low estimate of $H_2/4H_1 = 0.59$ and 0.23 in F_1 and F_2, respectively. The negative value of F shows the occurrence of recessive genes in F_1, and its positive value in F_2 population indicates that dominant genes were more frequent than recessives. This conclusion was also supported by the ratio of $[\sqrt{4DH_1} + F/\sqrt{(4DH_1)} - F]$, which is low in F_1 and high in F_2. The position of intercept of regression lines on Wr axis in Fig.1a, b, and low ratio of $\sqrt{H_1/D}$ indicates that dominance was of varying degree in both the populations. The sign of h^2 is positive in both the generations, and thus showing that the direction of dominance was towards the parents having finer lint. The

Table I. Variances (V_r) and co-variances (W_r) of eight parents for staple length and fibre fineness in F_1 and F_2 generations

Parents	Generations	—Staple length—		—Fibre fineness—	
		Vr	Wr	Vr	Wr
NIAB78	F_1	0.441	0.655	0.059	0.089
	F_2	0.576	0.605	0.061	0.119
S12	F_1	0.779	0.749	0.095	0.131
	F_2	0.381	0.750	0.079	0.137
AUH50	F_1	0.267	0.518	0.137	0.172
	F_2	1.094	1.085	0.086	0.143
CIM250	F_1	0.722	0.699	0.138	0.169
	F_2	0.476	0.783	0.052	0.109
Changmiah	F_1	0.341	0.483	0.092	0.126
	F_2	0.371	0.743	0.056	0.111
BJA	F_1	0.761	0.542	0.066	0.106
	F_2	0.520	0.879	0.063	0.122
A89/FM	F_1	0.292	0.512	0.086	0.143
	F_2	0.399	0.726	0.050	0.109
Reba-B50	F_1	0.479	0.720	0.077	0.140
	F_2	0.400	0.770	0.045	0.105

Table II. Estimation of components of variation in fibre fineness in F_1 and F_2 generation of *G. hirsutum* L

Components	Estimates	
	F_1	F_2
V_{0L0}	0.255	0.246
V_{1L1}	0.094	0.061
V_{0L1}	0.074	0.058
W_{0L0}	0.134	0.119
D	$0.2549^{*} \pm 0.0092$	$0.2462^{*} \pm 0.00096$
H_1	$0.0907^{*} \pm 0.0212$	$0.0506^{*} \pm 0.00883$
H_2	$0.0780^{*} \pm 0.0185$	$0.0467^{*} \pm 0.00768$
F	$-0.0274^{NS} \pm 0.0218$	$0.0302^{*} \pm 0.00453$
h^2	$0.0255^{*} \pm 0.0124$	$0.0268^{*} \pm 0.00515$
E	$0.0009^{NS} \pm 0.0031$	$0.0004^{NS} \pm 0.00032$
$\sqrt{H_1/D}$	0.5965	0.2267
	0.2151	0.2304
$H_2/4H_1$	-0.2411	1.7415
$\sqrt{4DH_1} + F/\sqrt{4DH_1} - F$	-0.2411	0.4886
	0.8784	1.0030
$\frac{1}{2} F/\sqrt{[D(H_1 - H_2)]}$	0.242	0.246
Narrowsense heritability		
Response to selection		

* denotes differences significant at 5% level of probability, whilst NS shows non-significant differences

Fig. 1. Wr/Vr graph for fibre fineness

estimate of narrowsense heritability in F_1 is 88% and in F_2 100%.

The distribution of the varieties in Fig.1a reveals that NIAB78 and BJA being closer to the origin contained the most dominant genes, and AUH50 and CIM250 being farthest from the original carried the maximum number of recessive genes for the fibre fineness. In F_2 population, Reba-B50, CIM250 and A89/FM appeared to carry the maximum number of dominant genes, whilst S12 and AUH50 contained maximum number of recessive genes for fibre fineness, Varieties BJA, NIAB78 and Changmiah were intermediate in this respect (Fig.1b), the remaining four lines/varieties formed another group intermediate between the two extremes.

The analysis of variance of the data revealed the existence of significant variation in staple length and fibre fineness. Regression analysis showed that the simple additive-dominance model was not adequate for data on staple length, and this inadequacy of the model may have been due to the presence of linkage, epistasis and non-independent distribution of genes in the diverse germplasm used here (Mather & Jinks, 1982).

Although both additive and dominance properties of the genes were revealed in controlling fibre fineness, the genes acting cumulatively showed preponderance influence on the expression of the character in both F_1 and F_2 generations (Table II), with a degree of dominance (Fig.1a,b). The degree of dominance was towards the parents producing finer lint (low mic value). It had been suggested that plant variation, which is greatly conditioned by additive genetic component, seemed to be inherited simply (Liang & Walter, 1968; Azhar & McNeilly, 1988). Thus, it is clear from these studies that plant material measured for fibre fineness in F_2 is readily available for selection, and single plant selection followed by pedigree method may be used to improve the character.

The grouping of the eight parents in Fig.1a,b with respect to the distribution of dominant and recessive genes is not surprising in view of the genetic and geographic diversity in the plant material, as suggested by Boye-Goni and Marcarian (1985).

The previous reports on heritability of fibre fineness in *G. hirsutum* are not well documented. Since an estimate of heritability is related to the magnitude of additive variance in a character (Falconer & Mackey, 1996), therefore, in view of the type of gene effects the inflated heritability estimates for fineness are justified. However, Falconer and Mackey (1996) had stated that these estimates are subject to environmental influences, and therefore, these must be reported and used with greater care and imagination in plant improvement exercise. Nevertheless, the high estimates of $h^2_{(NS)}$ for fineness in F_1 and F_2 suggest that significant achievement in improving the character may be made in the following generations of the selected material.

The response to selection (R) in F_2 and F_3 populations may be calculated as selection differential (S) x narrowsense heritability (Falconer & Mackey, 1996). Selection differential for fibre fineness was estimated as the

difference between the overall mean of the F_1 and the mean of superior F_1 hybrids. The value of the response (R) in the F_2 genetic material is 0.242, and genetic gain is 3.716 (overall mean - R), because while screening the material for fineness, lower mic values are considered. Similarly selection differential in the F_2 population was calculated as 0.246, and R=0.246. The genetic gain is 3.470. The values of response to selection are given in Table I. Although there are greater chances of improving fibre fineness in the present material, there exist limitations in the use of the information derived because the eight parents crossed were specifically chosen and did not truly represent a random sample of all cotton germplasm. The extent to which these results apply to whole of the germplasm is uncertain, and therefore, may be confirmed by conducting another experiment involving a large number of genotypes.

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