Genetic Analysis of Fibre Length and Strength of *Gossypium hirsutum* L.

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ABSTRACT

A complete diallel cross experiment was conducted to obtain genetic information on fibre length and strength of *Gossypium hirsutum* L. Joint regression analysis showed the full adequacy of data for fibre length and strength. The V_r/W_r graphs showed that fibre length and fibre strength were influenced by additive type of gene action with partial dominance. The unit slope of regression lines for fibre length (b = 1.06±0.24) and fibre strength (b = 1.13±0.20) suggested the absence of epistasis. It was revealed that GFS had maximum number of dominant genes for fibre length and NIAB-999 for fibre strength, as these varieties are present near to the origin. Tashkant-7 contained maximum number of recessive genes for fibre length and S-12 for fibre strength, as these are present farthest from the origin. The estimates of narrow-sense heritability ($h^2_{n.s}$) suggest that both pedigree and recurrent selection method may be useful to effect improvement in fibre length and fibre strength.

Key Words: Genetic analysis; Partial dominance; Additive gene action; Epistasis; Heritability

INTRODUCTION

Amongst the major crops grown in Pakistan cotton crop is the main source of foreign exchange earning. According to the reports about 65% of total foreign exchange earned annually is fetched through the export of cotton fibre and cotton clothes, and thus it is the mainstay of the economy of Pakistan. Keeping in view the changing circumstances around, the breeders are necessitated to exploit the genetic resources at greater pace than ever before. Apart from bringing improvement in seed cotton yield, the progress in fibre characteristics is also essential. For exploiting variability in various fibre attributes successfully, the use of genetic information in the development of an efficient breeding programme has been advocated by several research workers (Sayal & Sulemani, 1996; Ahmad *et al*., 1997; Khan *et al*., 1997; Babar & Khan, 1999; Ahmad & Azhar, 2000; Ajmal *et al*., 2000; Subhan *et al*., 2000). In the present investigation, the inheritance pattern of fibre length and fibre strength was studied using F_1 generation developed by crossing local and indigenous material of *Gossypium hirsutum* L. The information derived from the study may help the cotton breeders for bringing improvement in fibre quality characters.

MATERIALS AND METHODS

The plant material was developed by crossing four cotton varieties namely, GFS, Tashkant-7, S-12 and NIAB-999 according to diallel fashion in the glasshouse under controlled temperature (60 to 90°F) and light conditions during December, 2001-02. All necessary precautions were made in order to avoid the foreign pollen contamination. The seeds of 12 F_1 hybrids along with their parents were planted in the field in a randomized complete block design with three replications. Each row contained eight guarded plants spaced 30 cm within and 75 cm between the rows. Normal agronomic practices and plant protection measures were adopted to obtain healthy plants. Whole plant produce was ginned, and lint samples were tested for fibre length and fibre strength, using Spin lab high volume instrument (HVI-900). The data on each of the characters were analyzed statistically in order to see differences among the 16 families, following simple analysis of variance technique (Steel & Torrie, 1980). Only significant genotypic differences allow the use of Hayman-Jinks model of genetic analysis. Adequacy of the genetic model to the data set was determined using a scaling test, known as regression coefficient (b) analysis. According to Hayman (1954a) regression coefficient (b) must deviate significantly from zero, but not from unity if all the assumptions underlying the genetic model are fulfilled. For genetic analysis of F_1 data, all the crosses were arranged into arrays. Variance (V_r) of the family mean within an array and covariance (W_r) of these means with non-recurrent parental values were calculated from each diallel table. The V_r and W_r of each variety were used to carryout regression coefficient analysis, which is one of the scaling tests of determining adequacy of the genetic model to the data set. Other statistics necessary to estimate are variance of the parental means (V_oL_o), the means of array variance (V_1L_1), the variance of means of arrays (V_oL_1), and the means of array co-variances (W_oL_o). These statistics were used to estimate four genetic components of variation, D (additive effects of genes), H_1 and H_2 (dominance effects of genes), F, which provides an

estimate of the relative frequency of dominant to recessive alleles in the parental lines, and the variation in the dominance over the loci. Heritability estimate of each character was calculated following Mather and Jinks (1982).

RESULTS AND DISCUSSION

Mean squares obtained from analysis of variance indicated significant differences among the parents and their F_1 progenies for fibre length and fibre strength (Table I), and this validated the use of Hayman-Jinks model for genetic analysis. The array means of the characters, and variance (V_r) and covariance of the parents (W_r) are given in Table II. The regression coefficient for fibre length (b = 1.06 ± 0.24) and fibre strength (b = 1.13 ± 0.20) are given in Fig. 1, and these deviated significantly from zero and were equal to unity, suggesting that the data were fit for genetic interpretation as suggested by Hayman (1954b). The unit slope of regression lines provided no evidence of the presence of epistatic interaction.

Table I. Analysis of variance of fibre length and fibre strength of *Gossypium hirsutum* L.

Source of variation	Degree of freedom	Fibre length (mm)	Fibre strength (g/tax)
Replications	2	0.259	8.788*
Genotypes	15	0.581*	4.038*
Error	30	0.232	1.853

Table II. Variance (V_r), Covariance (W_r) of the parents, and array means of fibre length and fibre strength of *Gossypium hirsutum* L.
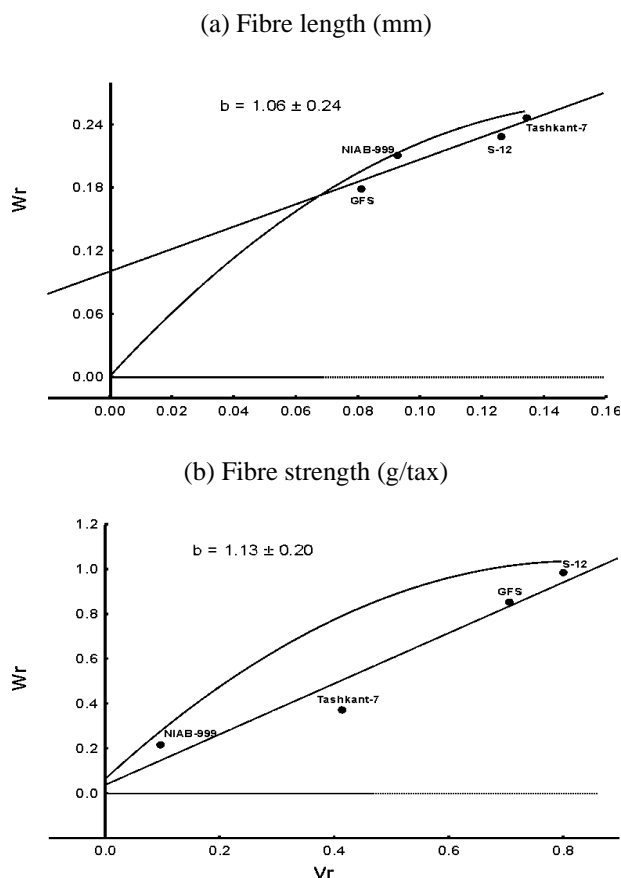
Varieties	Fibre length (mm)	Fibre strength (g/tax)
GFS	27.50	21.84
Tashkant-7	27.37	21.15
S-12	27.37	22.31
NIAB-999	28.02	22.28
V_r	0.11	0.48
W_r	0.22	0.60

Table III. Estimates of components of variation in fibre length and fibre strength of *Gossypium hirsutum* L.

Components of variation	Fibre length (mm)	Fibre strength (g/tax)
V_0L_0	0.48	1.40
W_0L_0	0.22	0.61
V_0L_1	0.10	0.29
V_1L_1	0.11	0.50
E	0.10 ± 0.003	0.94 ± 0.03
D	0.38* ± 0.007	0.46* ± 0.08
H_1	-26.53 ± 0.02	-1.68 ± 0.23
H_2	-0.15 ± 0.02	-1.02 ± 0.21
F	0.001 ± 0.02	-0.57 ± 0.20
h	0.07	-0.61
$(H_1/D)^{0.5}$		
$h^2_{(n.s)}$	0.97	0.22

Note: If the value of a parameter divided by its S.E exceeds 1.96, then it is significant.

Fig. 1. Vr/Wr graph for fibre characters

(a) Fibre length (mm)

(b) Fibre strength (g/tax)

The study of V_r and W_r graphs (Fig. 1) revealed that the genes controlling the inheritance of fibre length and fibre strength appeared to act additively, as the regression lines (b) were of unit slope. Interception of the regression lines for fibre length and fibre strength above the origin signified the importance of partial dominance. The relative distribution of varieties along the regression line (Fig. 1) revealed that for fibre length, GFS was present nearest to the origin, and has carried the most dominant genes, and Tashkant-7 being away carried the maximum number of recessive alleles. For fibre strength, NIAB-999 being located near to the origin had maximum number of dominant genes, and S-12 being located away contained the maximum number of recessive genes.

The significance of the components of variation i.e. D, H_1, H_2 and F calculated for fibre length and fibre strength (Table III) suggested that the additive component (D) being significant, revealed the presence of genes showing additive properties. H_1, H_2 and F components were non-significant for the two characters. Similar genetic control of fibre length and fibre strength had been reported by Hendawy *et al.* (1999), Ahmad and Azhar (2000), Ajmal *et al.* (2000) and Mukhtar *et al.* (2000).

The positive values of F for fibre length revealed that there were more dominant genes than recessive alleles in the

parents. The sign of h (mean F_1- parental means), which measured the direction of dominance, was positive for fibre length (Table III), suggesting that dominance acted in the direction of the parents with higher expression of the character, whilst for fibre strength, it was negative, indicating the lower expression of character from parents to offspring.

The high estimates of $h^2_{n.s}$ for fibre length (0.97) achieved since the genetic mechanism appeared to be predominantly influenced by additive genetic effects, however, this was low (0.22) for fibre strength and must be interpreted with caution, as the material has been tested under single environment, as suggested by Falconer and Mackey (1996). The presence of additive gene action suggests that the F_2 populations may be amenable to selection, and both pedigree method and recurrent selection may be successful for improving the characters studied here. The extent to which the information derived here, applies to *Gossypium hirsutum* L. as a whole is uncertain, and thus may be substantiated by conducting another genetic study using a large number of parents / lines of the species.

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