

Inheritance pattern of some polygenic fiber traits in cotton (*Gossypium hirsutum* L.)

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Abstract

Inheritance pattern of some polygenic characters was studied in five varieties of cotton. The five parents were crossed in all possible combinations. The 20 F₁ hybrids and their parents were grown in the field under randomized complete block design. Diallel analysis was used to determine the mode of gene actions and genetic components for various yield contributing and fiber traits. Results of regression coefficients showed that all the characters were fit for the genetic analysis. Both additive types of gene actions with partial dominance and over dominance were involved in the expression of the traits studied. These results suggest that these characters can be improved through appropriate selection method or by hybrid development.

Key words: Gene action, Inheritance, fiber traits, ginning outturn, *Gossypium hirsutum*.

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Introduction

Cotton (*Gossypium hirsutum* L.) is an important fiber crop and plays a vital role as a cash crop in commerce of many countries such as USA, China, India, Pakistan, Uzbekistan, Australia and Africa. Cotton crop is mainly cultivated for its fiber [1]. Cotton is of great economic importance for Pakistan as it plays a vital role in agriculture, industrial development, employment generation and earning of foreign exchange through export of its raw material as well as finished products. This crop is also of a major concern for our textile industry as it provides the basic raw material needed in its expansion. Low grade oil of cotton seeds is utilized in soap and lubricant manufacturing. The residual seed cake is a valuable protein concentrate and is used in livestock feed.

Efforts on various aspects of the crop have been under way to increase its overall production. The most important factor in the production process has always been a good variety of any crop. Therefore, cotton breeders have managed to evolve high yielding varieties with better fiber quality through different genetic manipulations and breeding practices. For this purpose, use of already existing genetic variability in breeding material and creation of new variability along with its genetic understanding is of crucial importance in a breeding program [2].

A diallel analysis technique devised by Hayman [3] is a useful tool to obtain precise information about the type of gene action and inheritance pattern of various polygenic traits of economic importance.

The genetic components of variation and heritability are also estimated from diallel analysis, which is helpful for the selection of appropriate parents and breeding procedures. The present research work was undertaken to obtain genetic information and inheritance pattern of various yield and fiber quality plant traits. This type of information may help the cotton breeders to formulate a breeding program for cotton improvement successfully.

Materials and methods

The experimental material consisting of five parental genotypes namely Stoneville-701, NIAB Krishma, LA-85-52-1, Acala-63-75 and Bt-196 representing a range of yield and fiber quality traits, were sown in earthen pots placed in a glasshouse during November. During germination and growth, environmental conditions were possibly controlled and recommended agronomic practices were adopted. In the glasshouse, the temperature was maintained at 35-40°C throughout the growth period. At flowering, the parental lines were crossed in a complete diallel fashion (5 x 5) to generate 20 F₁ crosses (including reciprocals) along with five self.

The F₀ seeds from all the crosses along with their parents were sown in the field during June following triplicate randomized complete block design. Nine seeds of each cross were shown per row with a distance of 30 cm and 75 cm within and between rows, respectively. All recommended agronomic practices and crop protection measures were carried out. At maturity, data on ginning out turn, fiber length (mm), fiber strength (g/tex) and fiber fineness (µg/inch) were recorded from 7 guarded plants on an

individual plant basis. For analyzing the data for genetic interpretation following Hayman-Jinks model, it was necessary to see whether genotypic differences for the above mentioned traits are significant or not. Therefore, the data of 20 F_1 hybrids and their parents were subjected to analysis of variance technique. From the diallel data variances of each array (V_r), covariance (W_r), variance of parental means (V_0L_0), variance of array means (V_0L_1), means of array variances (V_1L_1) and mean array covariance (W_0L_0) were calculated.

Results

Ginning outturn (%)

The genetic components of variation for ginning outturn are presented in Table 1. An additive component of variation D (0.96) was significant revealing that the ginning outturn was controlled by the dominance type of gene effects. The dominance ratio H_1/D (0.59) indicated the presence of dominance in the genetic control of this character and this was also confirmed by the position of regression line on W_r axis (Fig. 1). The difference in H_1 (0.3) and H_2 (0.06) signified unequal distribution of dominant and recessive genes in the parents for this character, verified by the ratio $H_2/4H_1$ (0.04) which was less than its maximum value of 0.25. The positive value of F (0.60) indicated the frequency of dominant alleles was higher than the frequency of recessive alleles.

Estimate of ratio $(4DH_1)^{0.5} + F / (4DH_1)^{0.5} - F$ (3.21) also supported the presence of partial dominance type of inheritance for this character. The positive value of h^2 (0.28) suggested the trend of dominance towards the higher parent. The significant value of environment component of variance E (0.52) depicted that environment did not play significant role in the phenotypic expression of this character. Narrow sense heritability was estimated moderate i.e. (34%).

Epistasis was absent as the regression line did not deviate significantly from unit slope (b) (Fig 1). From the distribution of variety positions on the regression line, it was observed that Stoneville-701 being closest to the point of origin possessed maximum number of dominant genes, while NIAB Krishma being farthest to the point of origin possessed maximum number of recessive genes.

Fiber length (mm)

The genetic components of variation for fiber length are presented in Table 1. Additive component

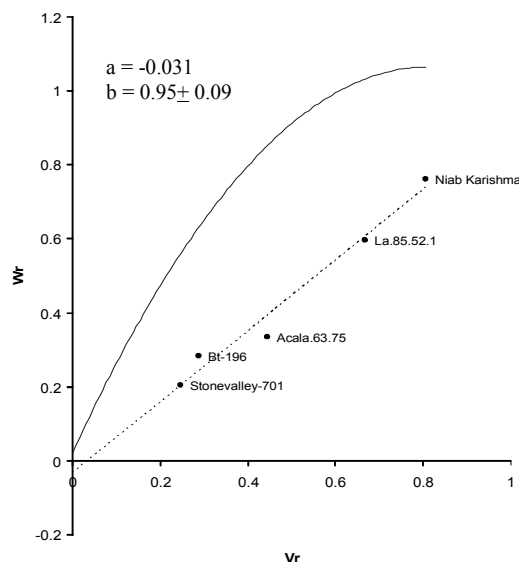


Fig. 1 Variance (V_r) and covariance (W_r) graph for ginning outturn

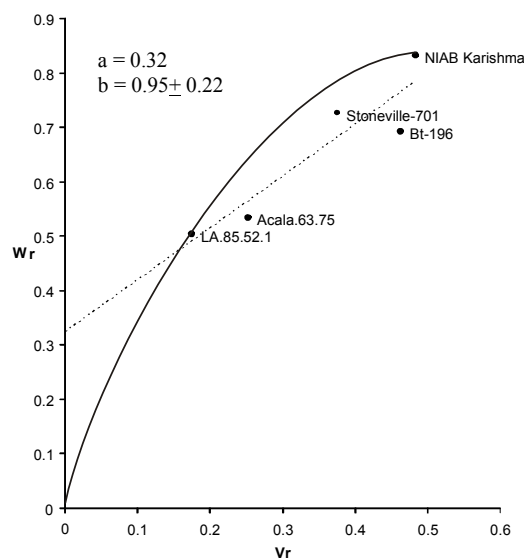


Fig. 2 Variance (V_r) and covariance (W_r) graph for fiber length

of variation D (1.17) was higher and significant than non additive components. H_1 (-0.60) and H_2 (-0.46) showed that fiber length was controlled by additive type of gene effects. Dominance ratio H_1/D (0.72) indicated the presence of partial dominance in the genetic control of this character and this was also confirmed by the position of regression line on W_r axis (Fig. 2). The difference in H_1 (-0.60) and H_2 (-0.50) signified unequal distribution of dominant and recessive genes in the parents for this character, verified by the ratio $H_2/4H_1$ (0.19) which was more than its maximum value of 0.25. The negative value

of F (-0.03) indicated that the frequency of dominant alleles was lower than the frequency of recessive alleles.

Estimate of ratio $(4DH_1)^{0.5} + F / (4DH_1)^{0.5} - F$ (0.96) also supported the presence of partial dominance type of inheritance for this character. The negative value of h^2 (-0.21) suggested the trend of dominance towards lower parent. The significant value of environment component of the variance E (0.34) depicted that the environment played significant role in the phenotypic expression of this character. Narrow sense heritability was estimated moderate i.e. 49%.

Epistasis was absent as the regression line did not deviate significantly from unit slope (b) (Fig. 2). From the distribution of variety positions on the regression line, it was observed that the variety LA-85-52-1 being closest to the point of origin possessed maximum number of dominant genes while the variety NIAB Krishma being farthest from the point of origin possessed maximum number of recessive genes.

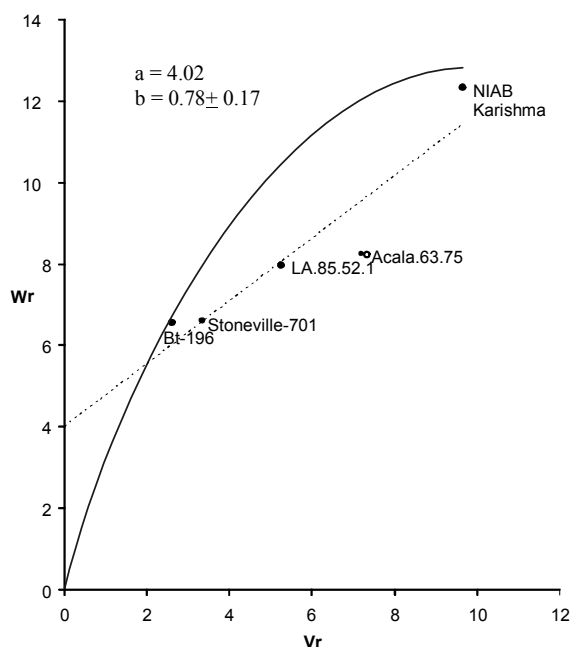


Fig. 3 Variance (V_r) and covariance (W_r) graph for fiber strength

Fiber strength (g/tex)

The genetic components of variation for fiber strength are presented in Table 1. Additive component of variation D (15.57) was higher and significant than non additive components H_1 (1.26) and H_2 (2.07), showing that fiber strength was controlled by additive type of gene effects. Dominance ratio $(H_1/D)^{0.5}$ (0.28) indicates the

presence of partial dominance in the genetic control of this character and this was also confirmed by the position of regression line on W_r axis (Fig. 3). The difference in H_1 (1.26) and H_2 (2.07) signified unequal distribution of dominant and recessive genes in the parents for this character, verified by the ratio $H_2/4H_1$ (0.41) which was more than its maximum value of 0.25. The negative value of F (-0.03) indicated the frequency of dominant alleles was lower than the frequency of recessive alleles.

Estimate of ratio $(4DH_1)^{0.5} + F / (4DH_1)^{0.5} - F$ (0.99) also supported the presence of partial dominance type of inheritance for fiber strength. The negative value of h^2 (-0.90) suggested the trend of dominance towards lower parent. The significant value of environment component of the variance E (2.25) depicted that environment played significant role in the phenotypic expression of this character. Narrow sense heritability was estimated high i.e. 63%.

Epistasis was absent as the regression line did not deviate significantly from unit slope (b) (Fig.3). From the distribution of variety position on the regression line it was observed that the variety Bt-196 being closest to the point of origin possessed maximum number of dominant genes, while the variety NIAB Krishma being away from the point of origin possessed maximum number of recessive genes.

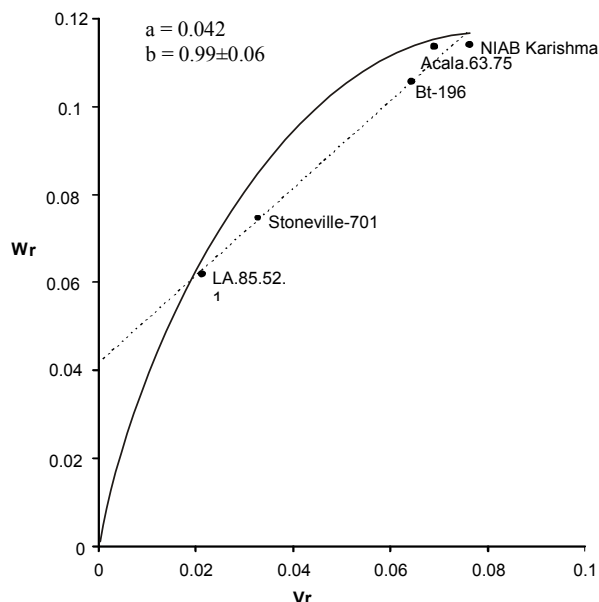


Fig. 4 Variance (V_r) and covariance (W_r) graph for fiber fineness

Fiber fineness ($\mu\text{g}/\text{inch}$)

The genetic components of variation for fiber fineness are presented in Table 1. Additive component of variation D (0.18) was higher and

significant than non additive components. H_1 (-0.002) and H_2 (0.004) showed that fiber fineness was controlled by additive type of gene effects. The dominance ratio $(H_1/D)^{0.5}$ (0.09) indicated the presence of partial dominance in the genetic control of fiber fitness and this was also confirmed by the position of regression line on Wr axis (Fig. 4). The difference in H_1 (-0.002) and H_2 (0.004) signified unequal distribution of dominant and recessive genes in the parents for fiber fitness. It was verified by the ratio $H_2/4H_1$ (-0.74) which was less than its maximum value of 0.25. The negative value of F (-0.008) indicated that the frequency of dominant alleles was lower than the frequency of recessive alleles.

Estimate of ratio $(4DH_1)^{0.5}+F/(4DH_1)^{0.5}-F$ (0.63) also supported the presence of partial dominance type of inheritance for fiber fitness. The negative value of h^2 (-0.003) suggested the trend of dominance towards lower parent. The significant value of environment component of the variance E (0.66) depicted that environment did not play significant role in the phenotypic expression of this character. Narrow sense heritability estimated was high i.e. 80%.

Epistasis was absent as the regression line did not deviate significantly from unit slope (b) (Fig.4). From the distribution of variety positions on the regression line, it was observed that the variety LA-85-52-1 being closest to the point of origin had maximum dominant genes, while NIAB Krishma and Acala-63-75 being away from the point of origin possessed maximum number of recessive genes.

Discussion

The present research work was carried out to investigate the genetic mechanisms of controlling ginning outturn, fiber length, fiber strength and fiber fineness in *Gossypium hirsutum*. The data showed that variation does exist for all these characters in the plant material examined. This plant material may be used advantageously by the research worker subjected to the availability of information on the genetic mechanism controlling variations. For this purpose, triple test cross [4], path coefficient analysis [5], line x tester analysis [6], generation mean analysis [7] and North Carolina Designs [8], provide valuable information on the pattern of inheritance, but diallel cross method [3] has the advantage to provide such information in F1 generation.

Present results revealed that over dominance was involved in the phenotypic expression of ginning outturn [9], and this gene action operates, when most of the progenies perform better than their parents, and

the progenies showing heterotic effects may be considered in a breeding programme. Due to over dominance gene effect and low heritability i.e. 34% this character may be improved through hybrid development, as suggested by Soomro et al [10].

Although improvement of lint yield is the main objective of plant breeders; characteristics like fiber length, fiber strength and fiber fineness cannot be sacrificed at the cost of quality. The present studies revealed the additive type of genes action with partial dominance for the inheritance of fiber length, which was in agreement with the results of Islam et al [11]. Estimate of narrow sense heritability for fiber length was moderate i.e. 49% and more fiber length is desirable so the fiber length may be improved through rigorous selection. Fiber strength and fiber fineness were also controlled by additive type of gene actions with varying degree of partial dominance. Such results were also reported by Iqbal et al [12] and Rahman and Malik [13]. The narrow sense heritability estimate for fiber strength was 63%, suggesting that selection of plants with more fiber strength may be easier. Fiber fineness is also an important factor with respect to quality, and thus fine fiber is desirable. Results showed that the fiber fineness was also controlled by additive type of gene actions with varying degree of partial dominance. Our results were not in agreement with the results of Haq and Azhar [14]. Estimate of narrow sense heritability for fiber fineness was 80%, so fiber fineness can be improved by the selection of plants with appropriate fiber fineness.

Analysis of variance revealed that the differences among the genotypes for all the traits were highly significant. Results of joint regression analysis revealed that the data for all the traits were fit for analysis using simple additive-dominance model. The F1 data were analyzed, following diallel cross method to study genetic basis of variation in various polygenic traits of upland cotton. The genetic components of variation and heritability of these characters are also estimated which may be helpful for making the selection of potential breeding material from the F2 population. The graphical representation of variance (Vr) and co-variance (Wr) suggested that all the characters were affected by the genes acting additively with varying degree of dominance except ginning outturn for which the genes showed over-dominance.

From the above discussion, it is concluded that the characters examined in the present study may be improved straight forward by selecting plants. The characters which were controlled by dominance or

Table 1 Genetic components of variation for plant height, monopodial branches, sympodial branches, number of bolls plant⁻¹, boll weight and cotton seed yield

Components	Estimates			
	Ginning outturn	Fiber length	Fiber strength	Fiber fineness
D	0.96*±0.03	1.17*±0.04	15.75*±0.82	0.18*±0.002
H ₁	0.34*±0.08	-0.60 ^{ns} ±0.11	1.26 ^{ns} ±2.23	-0.002 ^{ns} ±0.005
H ₂	0.06 ^{ns} ±0.07	-0.46 ^{ns} ±0.01	2.07 ^{ns} ±2.01	0.004 ^{ns} ±0.005
F	0.60*±0.07	-0.03 ^{ns} ±0.10	-0.03 ^{ns} ±2.05	-0.008 ^{ns} ±0.005
h ²	0.28*±0.05	-0.21 ^{ns} ±0.07	-0.90 ^{ns} ±1.36	-0.003 ^{ns} ±0.003
E	0.52 ^{ns} ± 0.01	0.34* ± 0.02	2.25* ± 0.34	0.01 ^{ns} ± 0.000
(H ₁ /D) ^{0.5}	0.59	0.72	0.28	0.09
H ₂ /4H ₁	0.04	1.94	0.41	-0.74
(4DH ₁) ^{0.5} +F/(4DH ₁) ^{0.5} -F	3.21	0.96	0.99	0.63
h ² _(ns)	0.34	0.49	0.63	0.80

over-dominance may be used for hybrid development, as suggested earlier [10].

Conclusion

In this experiment, variety Stoneville-701 carried maximum dominant genes for ginning outturn. An exotic line LA-85-52-1 possessed maximum dominant genes for fiber length and fiber fineness, while Acala-63-75 did not carry the maximum number of dominant genes for any trait studied. Cultivar Bt-196 possessed maximum dominant genes for fiber strength. From the above results it may be suggested that fiber traits could be improved by straight forward selection.

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