Full Length Article

Genetic Basis of Fiber Quality Attributes in Upland Cotton (*Gossypium hirsutum*) Germplasm

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ABSTRACT

Eight diverse cotton varieties were hybridized following diallel crossing system in order to investigate the genetic mechanism controlling variation in staple length, fiber strength and its fineness in varieties of cotton (*Gossypium hirsutum*) Simple additive-dominance model was fond adequate for analyzing the F_1 data sets. Non-significant deviation of regression coefficient from unity revealed that epistatic component was absent in the inheritance of the characters studied. Degree of dominance $(H_1/D)^{1/2}$ for staple length was almost complete, whilst it was partial for fiber strength and its fineness. A greater magnitude of 'D' item for all the characters revealed the importance of the genes acting additively, and consequently estimation of h^2_{ns} for staple length (0.52), Fiber strength (0.83) and fiber fineness (0.57) were encouraging. A moderate to high narrow-sense heritability for the fiber characteristics suggest that there is potential in the plant material for improving the characters through single plant selection.

Key Words: Genetic variation; Fiber length; Fiber strength; Fiber fineness; Heritabilities

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is the biggest source of natural fiber of global importance. In Pakistan cotton is being cultivated on an area of about three million hectare (Mha) with production of 13 million bales (Anonymous, 2007). It is mainly grown in Sindh and Punjab provinces of the country. In addition to feeding local textile industry, considerable proportion of foreign exchange reserves i.e., 65% is earned through export of raw cotton, cotton yarn and textile products.

Keeping in veiw the importance of cotton crop in the economy of Pakistan, cotton breeders always focused their attention on increasing yield of seed cotton on unit area basis and also on improving fiber characteristics of commercial varieties. Although remarkable progress has been made in both quantity and quality of the varieties developed during the past three decades, demand of lint having longer staple length, more fiber fineness and fiber strength is increasing due to the introduction of high speed spinners in the local textile industry. Thus, in order to meet the increasing demand of fine cotton in local and international market, the cotton breeders are obliged to further exploit the potential of available germplasm through hybridization and selection. In order to bring genetic improvement in fiber quality parameters, it is important to investigate the mode of inheritance of variation in staple length, fiber fineness and fiber strength before developing an appropriate selection protocol.

Previous studies on this aspect of cotton plant showed that variation in staple length, fiber strength and fiber fineness was effected by the genes acting both cumulatively and non-cumulatively. The studies of Green and Culp (1990) and Nadarajan and Rangasamy (1992) revealed that fiber length, uniformity and fineness were controlled by additive gene effects, whilst in other studies fiber fineness and staple length were governed by the genes acting non-additively (Azhar & Rana, 1993; Haq & Azhar, 2005). Nadeem and Azhar (2005) reported that fiber strength and fiber length were influenced by additive gene action with partial dominance and there was no evidence of non-allelic interaction. However, in studies by Haq and Azhar (2005) additive gene effects were non-significant for these characters. Thus, before developing an appropriate breeding program it is essential that genetic mechanism controlling fiber characteristics using available germplasm must be studied. Therefore, in order to collect such information the F_1 data on staple length, fiber strength and fiber fineness measured in the genetic material were analyzed following simple additive-dominance model of Hayman (1954 a, b) and Jinks (1954).

MATERIALS AND METHODS

Development of genetic materials. For conducting the genetic investigations eight parents, all belonging to

Gossypium hirsutum were hybridized according to diallel crossing system. Out of these eight varieties, six (MNH-552, FH-1000, VH-144, CIM-496, NIAB-111, 4F) were local and two namely, LRA-5166 and Cedix S-362-T-362 (GL) were exotic. Eight parents were distinguishable on the basis of fiber properties measured in the present investigations. The parents were grown in earthen pots, with 30 cm diameter, in glasshouse during mid of October, 2004. Temperature, light and humidity in glasshouse were controlled artificially. When eight parents started to flower, they were crossed in all possible combinations to develop F_0 seed of 56 crosses. At maturity, seed cotton from crossed bolls was collected and ginned to obtain hybrid seeds.

Evaluation of the genetic material. For the assessment of genetic material 56 F_1 hybrids along with the eight parents were field-planted under normal growing conditions. Randomized complete block design in triplicate was followed. Each genotype was grown in a 450 cm long row having 16 hills spaced 30 cm apart within the row in each replication, whilst rows were 75 cm apart from each other. Two seeds of each entry were dibbled 5-6 cm deep at one hill, which were later thinned to one healthy seedling. The experiment was monitored daily for growth and attack of insect pests and sprayed with recommended pesticides when required. All recommended cotton production practices were adopted identically for the entire experiment. At maturity seed cotton of middle 10 plants was collected in each of the 64 entries in each replication, and lint was separated using single roller electric gin. A 40 g mixed sample of lint in each family in each replication was measured for staple length, fiber strength and fiber fineness using HVI (High Volume Instrument) available in fiber testing laboratory in the department of Fiber Technology. Mean values of the characters in each family were obtained for further analysis.

Biometrical analysis. The ordinary analysis of variance technique was performed in order to see whether the genotypic differences are significant (Steel *et al.*, 1997). Only significant genotypic differences allowed the use of Hayman-Jinke additive-dominance model for analyzing the data.

RESULTS

Adequacy of additive-dominance model to the F_1 data sets. In order to test the adequacy of the additive-dominance model to the data sets, one of the scaling tests i.e., joint regression analysis was carried out. 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. In the present case, the regression coefficient for staple length (b= 0.79) fiber strength (0.61) and fiber fineness (b=0.93) deviated significantly from zero, and were of unit slope. Therefore, the data on these characters were found fit for genetic analysis.

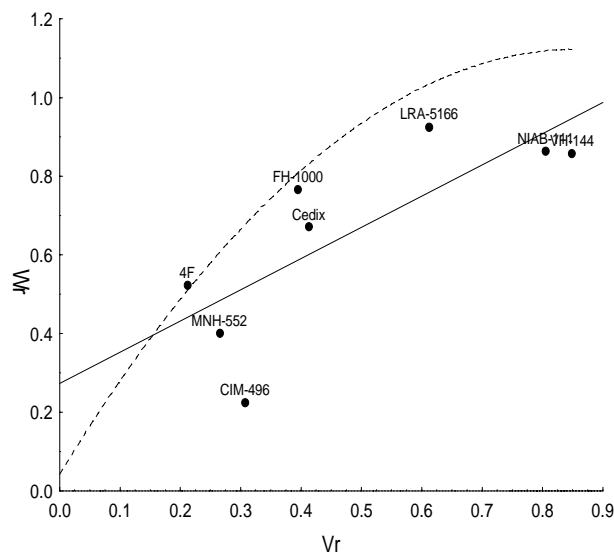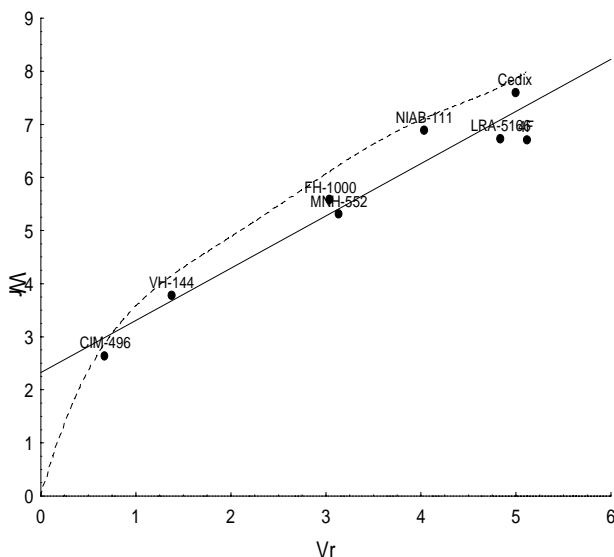**Fig. 1. Wr/Vr graph for fiber length**

Fig. 2. Wr/Vr graph for fiber strength of *G. hirsutum*

Estimation of components of variation in fiber characteristics. Estimation of components of variation in the three characters was made (Table I). The results revealed that only D was positive (P ≤ 0.05) for three fiber quality attributes. Although H_1 and H_2 were positive, they were non-significant (P > 0.05) for fiber strength and fineness, for fiber length they were negative (P ≤ 0.05). The magnitude of D was exceedingly higher than those of H_1 and H_2 suggesting the pronounced effect of additive genes in the inheritance of fiber length, strength and fineness. The degree of dominance $\sqrt{H_1/D}$ was less than unity, thus showing partial dominance of genes and this claim was verified by the slope of regression line, which intercepted Wr-axis above the origin (Fig. 1, 2 & 3). For fiber strength and fineness, magnitude of H_1 and H_2 was almost equal, and

Table I. Components of variation in fiber length, strength and fineness in *G. hirsutum*
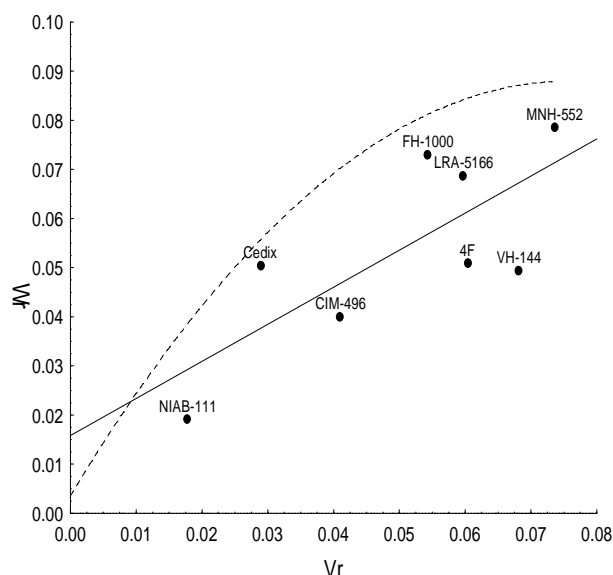
Components	Fiber length	Fiber strength	Fiber fineness
D = additive variance	0.91 ± 0.12	11.55 ± 0.31	0.085 ± 0.010
H_1 = dominance variance	-0.91 ± 0.29	0.99 ± 0.72	0.022 ± 0.023
H_2 = proportion of positive and negative genes in the parents	-0.60 ± 0.25	0.99 ± 0.63	0.037 ± 0.020
F =	-0.47 ± 0.29	0.86 ± 0.74	-0.031 ± 0.024
E = environmental variance	0.647 ± 0.041	0.85 ± 0.10	0.0282 ± 0.0034
$\sqrt{H_1/D}$ = mean degree of dominance	0.99	0.29	0.51
$H_2 / 4H_1$ = proportion of genes with positive and negative effects in the parents	0.16	0.25	0.22
$\sqrt{4DH_1} + F / \sqrt{4DH_1} - F$ = proportion of dominant and recessive genes in the parents	0.59	1.29	0.47
Heritability (ns)	0.52	0.83	0.57

thus ratio of H_2/H_1 for the two characters was 0.25 and 0.22, respectively being almost equal to maximum value of 0.25. This suggest that there was equal distribution of the genes among the parents, whilst the genes for fiber length were unequally distributed among the parents as H_1 was greater than H_2; thus ratio of $H_2/4H_1$ was low (0.16). A negative F-value and low ratio of $[\sqrt{4DH_1} + F]/[\sqrt{4DH_1} - F]$ for fiber length (0.59) and fineness (0.47) indicated the presence of recessive genes in the parents. Non-significant positive F-value and high ratio of $[\sqrt{4DH_1} + F]/[\sqrt{4DH_1} - F]$ for fiber strength (1.29) indicated the involvement of more dominant genes than recessive ones in the parents. Due to the presence of additive genetic component in the genetic control, estimates of narrow-sense heritabilities for fiber length, strength and fineness were 0.52, 0.83 and 0.57, respectively.

The pattern of variety distribution showed a greater variation in the parents for staple length. Data revealed that 4F, MNH-552 and CIM-496 being closer to the point of origin possessed maximum number of dominant genes, and by contrast NIAB-111, LRA-5166 and VH-144 contained maximum number of recessive genes, whilst Cedix and FH-1000 carried both dominant and recessive genes for staple length (Fig. 1). The scatter of array points along the regression line depicts that CIM-496 and VH-144 contained the greatest number of dominant genes, whilst 4F, LRA-5166, NIAB-111 and Cedix carried the greatest number of recessive genes for fiber strength (Fig. 2). However, varieties FH-1000 and MNH-552 carried both dominant and recessive genes for fiber strength. The parents for fiber fineness differed widely from each other for the presence of dominant and recessive genes (Fig. 3). Variety NIAB-111 being closer to the origin contained more dominant, and MNH-552 more recessive genes for fiber fineness, whilst the remaining varieties contained both dominant and recessive genes for the character.

DISCUSSION

The preliminary analysis of the F_1 data on staple length, fiber strength and fiber fineness revealed significant variation in these characters, suggesting that use of simple additive dominance model was valid for genetic interpretation of the plant material used in the present investigations. The significant deviation of regression coefficients for fiber length, fiber strength and fiber fineness

Fig. 3. Wr/Vr graph for fiber fineness

from zero and non-significant deviation from unity suggested that non-allelic interaction was absent in the genetic control of these characters. Furthermore, all the assumptions underlying the genetic model were fulfilled as suggested by Hayman (1954a).

Regression coefficient analysis of the data revealed that simple genetic model was adequate for analyzing the data sets on the three characters. The relative estimates of genetic components of variation in the three fiber quality characteristics showed that additive genetic component, D, item was higher and significant for three characters, which revealed that additive gene effects were much important in the inheritance of these characters and there was no evidence of the presence of epistatic component in the inheritance of variation in the three characters. Thus, the nature of gene action reported previously by Green and Culp (1990), Nadarajan and Rangasamy (1992) and Nadeem and Azhar (2005) for these characters supported the present data, which is encouraging for making selection of desired plants from the segregating population. Due to the greater influence of additive gene effects in the genetic mechanisms controlling the fiber characteristics, moderate to high estimates of h^2_{ns} for the characters appeared to be

useful. These results suggest that single plant selection may be made for bringing genetic improvement in these characters. However, it is suggested that before making selection for the desired plants, based upon the estimates of h^2_{ns}, this information must be substantiated by studying larger number of varieties from the available germplasm under different environmental conditions.

In conclusion, from the distribution pattern of the genes in the parents and wider variation in the parents for the characters, it seems that there is potential in the breeding material for making effective improvement in these characters.

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