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STUDY OF FIBER QUALITY TRAITS IN UPLAND COTTON USING ADDITIVE-DOMINANCE MODEL

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Abstract

Diallel analysis was studied in F_1 and F_2 hybrids by crossing six upland cotton cultivars (CIM-109, CIM-240, CIM-1100, FH-682, BH-36 and CRIS-9) following Hayman's diallel approach using Mather's concept of D, H components of variation for additive and dominance genetic variances, respectively. The objectives were to study the additive-dominance model, nature of gene action, heritability and genetic gain in F_1 and F_2 hybrids and mean performance of the selections (made in F_2 population) in advanced segregating generations (F_3, F_4 and F_5) in upland cotton. Genotypes mean values differed significantly for all the fiber quality traits. Additive-dominance model was adequate for fiber length, fiber fineness, and uniformity ratio, while showed partially adequate for fiber strength in F_1 generation. In F_2s, fiber fineness showed the adequate data, while other three traits manifested partial adequacy. Additive component (D) was found significant for all the traits in F_1 and F_2 generations. Dominance components (H_1, H_2) were also significant for all the traits in F_1s except the fiber fineness, while were insignificant for all the traits in F_2 generation. In F_1s the additive gene action was somewhat partial, while in F_2s all the traits were controlled by additive gene action as confirmed by average degree of dominance ($\sqrt{H_1}/D<$unity). Heritabilities (broad & narrow sense) were moderate to high with appreciable genetic advance. On the basis of transgressive segregation, heritability with appreciable genetic gain, selections made in F_2 population of cv. CIM-1100 surpassed the standard cultivar (CIM-446) for fiber quality traits in segregating generations.

Introduction

Cotton is a major industrial and cash crop of Pakistan, where it is grown on 12% of the total cultivated area. Cotton has a great impact on textile industry development, employment generation and foreign exchange earning of the country. Due to its importance, our economy and market channels are oriented in such a way that high fluctuations in its production and fiber quality pose a threat of economic difficulty. Stable production of quality cotton is, therefore, vital to the national interest of Pakistan. In this context, awareness among growers, millers and exporters is a must for improving and maintaining cotton standards to compete in the international market (Khan *et al*., 2003).

Conventional breeding is still having sustainable base in the present era of molecular breeding. It is well known that application of molecular markers must be certified through conventional breeding. Transgressive segregation depends upon the categorizing of genotypes having potential of transmitting desirable traits in specific genotypic combinations. Diallel analysis and additive dominance models are the established mechanisms of conventional breeders to comprehend allelic and nonallelic gene action, nature and magnitude of genetic variance used by genotypes in specific combinations. Gene action is described in statistical terms as additive, dominant and epistatic effects and their interactions with environmental factors.

In quantitative genetics, genetic mating designs are often used to estimate genetic variance components i.e. A (additive) and D (dominance). The widely used designs are additive-dominance additive x additive (ADAA) model (McCarty *et al*., 2004a & b; Wu *et al*., 2006), tested mating design (North Carolina I) and factorial mating design (North Carolina II) and variance components i.e., D (additive) and H (H_1 & H_2 for dominance) used by Hayman (1954), Griffing (1965) and Mather & Jinks (1982) in diallel mating designs. Verhalen *et al*., (1971), Tang *et al*., (1993), McCarty *et al*., (1996), Khan (2003), Khan *et al*., (2005), Aguiar *et al*., (2007) and Khan *et al*., (2007) used Hayman's approach and reported additive and dominant type of gene action influencing different fiber quality traits. Diallel cross is widely used in all the crops including cotton, and the analyses and assumptions of this method have been reviewed by Verhalen & Murray (1969) and Mather & Jinks (1982). Heritability and genetic gain also provide useful information with regard to improving a trait (Iqbal *et al*., 2005; Khan *et al*., 2005; Khan *et al*., 2007). Heritability of fiber quality traits is generally higher than that of yield and its components. Desirable heritabilities and genetic advance under guided selection for different fiber quality traits were reported (McCarty *et al*., 1996; Tang *et al*., 1996; Yingxin & Xiangming, 1998; Yunkun *et al*., 1998; Hussain *et al*., 1998; Hussain *et al*., 1999; Khan *et al*., 2007).

Present research work was carried out by using Hayman's approach with the objectives to study the additive-dominance model to see the data adequacy for said traits, genetic variance components, heritability, genetic gain in population mean and inheritance patterns (additive vs. dominance) of different fiber quality traits in a 6x6 complete diallel cross in F_1 and F_2 generations in upland cotton. In F_2 population, the selections has been made in the promising hybrids on the basis of genetic variability and phenotypic performance and the segregating populations were further studied in F_3, F_4 and F_5 generations for their mean performance and comparison with existing standard cultivar.

Materials and Methods

Plant material and experimental design: The experiments including crossing block, F_1 and F_2 populations and study of advanced generations (F_3, F_4 and F_5) of cotton (*Gossypium hirsutum* L.) were maintained during 2000 to 2004 at Agricultural Research Institute, Dera Ismail Khan, Pakistan. Dera Ismail Khan lies between 31°, 50′ North latitude and 70°, 50′ East longitude. Six diverse genotypes of upland cotton (CIM-109, CIM-240, CIM-1100, FH-682, BH-36 and CRIS-9) having broad genetic base and varied by date of release, pedigree, seed cotton and fiber yield as well as fiber and oil quality traits, were hand sown in a non-replicated crossing block during May, 2000. Each cultivar was grown in five rows 27 m in length with plants and rows spacing of 60 and 100 cm, respectively to ensure easy crossing and to handle the breeding material carefully. All cultivars were crossed in a complete diallel fashion; unopened flower buds of the plants (to be used as female parents) were hand emasculated by removing all the stamens along with petals during late afternoon (4 pm to sunset). However, the ovary with style and stigma remained intact. Subsequently the stigmas of emasculated flowers were covered with straw tubes (tubes closed with lint on one side) by overlapping with calyx and by binding with thread to prevent entrance of unwanted stray pollens. The emasculated flowers were labeled showing name of female parent and date of emasculation. On the next day morning (8 to 11 am), the mature pollen grains from the required male parents were collected in a small Petri dish and applied to the stigma of the target emasculated flowers and covered again with the same straw tube. After pollination, the name of male parent was entered in the paper tag. At crop maturity stage, the successful and open crossed bolls were picked and ginned separately cross wise.

The F_1 and F_2 experiments of 6x6 complete diallel cross, having 30 hybrids (including reciprocals) along with 6 parents were also hand sown with randomized complete block (RCB) design during May, 2001. In F_1, each genotype was planted in a single row measuring 3.30 m, with 3 replications, while in F_2 the plant population was increased and each genotype was planted in 4 rows, each of 6.30 m length, with 4 replications. The row and plant spacing were 75 and 30 cm, respectively. The experiments comprising of advanced generations (F_3, F_4 and F_5) were also sown and maintained as above during 2002, 2003 and 2004. All the recommended cultural practices and inputs including fertilizer, hoeing, irrigation and pest control were applied same for all the entries from sowing till the harvesting and the crop was grown under uniform conditions to minimize environmental variability to the maximum possible extent. Picking was made during the months of November-December every year on single plant basis and ginning was done with 8 saw-gins.

Traits measurement and statistical analyses: The data were recorded for staple length, fiber strength, fiber fineness and uniformity ratio through High Volume Instrument (HVI). In case of F_3, F_4 and F_5 generations crop (Tables 4, 5 & 6), the 10 guarded plants were randomly selected in each family of cross and their mean values for all the fiber quality traits were compared with existing standard cultivar to formulate the percent increase / decrease over standard cultivar.

Analysis of variance: All the data were subjected to analysis of variance (ANOVA) technique using Mstatc software to test the null hypothesis of no differences between various F_1s as well as among F_2s hybrid populations along with their parental lines. In other segregating generations, the mean performance has been studied in comparison with standard cultivar.

Estimation of genetic components of variance: Diallel theory was developed by Hayman (1954) using Mather's concept of D, H components of variation for additive and dominance variances, respectively (as D used for additive variance instead of A and H_1 and H_2 for dominance components of variance instead of D). The recent developments about this technique have been described in detail by Mather & Jinks (1982) and genetic components of variation and heritabilities were estimated following that method of diallel analysis. In F_2 population the formulas were modified to calculate the components of variance as proposed by Verhalen & Murray (1969) and Verhalen *et al.,* (1971) provided in the book titled "Biometrical Methods in Quantitative Genetic Analysis" by Singh & Chaudhary (1979). After ANOVA, the data were first tested through additive dominance model which requires the computations of the variance (Vr) of the components of each array and array parent-offspring covariance (Wr). Scaling tests were made through regression analysis, arrays analysis of variance (Wr+Vr and Wr-Vr) and t^2 test. Six genetic components of variation and their ratio along with standard error were estimated as follows:

D = Additive genetic variance {D = Volo-E (Volo = Variance of the Parents)}.

H_1= Dominance variance {H_1 = Volo-4$Wolo_1$+V_1L_1-(3n-2)E/n (Wolo = Mean covariance between the parents and the arrays)}.

H_2= H_1 {$1-(u-v)^2$}, where u and v are the proportions of positive and negative genes, in the parents.

F = Mean of Fr values over arrays = $2Volo-4Wolo_1-2(n-2)E/n$, where Fr is the covariance of additive and dominance effects in a single array. F is positive where dominant genes are more frequent than recessive.

h^2 = $(ML_1-MLo)^2-4(n-1)E/n^2$; Dominance effect (as algebraic sum over all loci in heterozygous phase in all crosses). When frequency of dominant and recessive alleles is equal, then $H_1 = H^2 = h^2$. Significance of h^2 confirms that dominance is unidirectional.

E = Expected environmental component of variation;

$$E = [\frac{Error\ S.S. + Reps.S.S.}{d.f.}] \Big/ Number\ of\ replications$$

From these estimates, the following genetic ratios were determined.

F_1 = $\sqrt{H_1/D}$, F_2 = $\sqrt{¼H_1/D}$: denotes average degree of dominance, If the value of this ratio is zero, there is no dominance; If it is greater than zero but less than 1, there is partial dominance; and if it is greater than 1, it denotes over-dominance.

$H_2/4H_1$: denotes the proportion of genes with positive and negative effects in the parents, and if the ratio is equal to 0.25, indicates symmetrical distribution of positive and negative genes.

F_1= $\sqrt{4DH_1+F}/\sqrt{4DH_1-F}$, F_2 = $¼\sqrt{4DH_1+½F}/¼\sqrt{4DH_1-½F}$: denotes the ratio of dominant and recessive genes in the parents, If the ratio is 1, the dominant and recessive genes in the parents are in equal proportion; if it is less than 1, it indicates an excess of recessive genes; but being greater than 1, it indicates excess of dominant genes.

h^2/H_2: denotes the number of gene groups/genes, which control the character and exhibit dominance.

$$Correlation\ Coefficient\ (r) = \frac{\sum XY - \frac{(\sum X)(\sum Y)}{n}}{\sqrt{\frac{(\sum X^2)-(\sum X)^2}{n} \times \frac{(\sum Y^2)-(\sum Y)^2}{n}}}$$

Negative value of correlation coefficient (r) indicates dominant genes, while if its value is positive then recessive genes are responsible for the phenotypic expression of the trait.

Heritability: The narrow sense (h^2) heritability in F_1 generation was calculated for each character according to Mather & Jinks (1982):

$$F_1\ Heritability\ (h^2) = \frac{(\frac{1}{2})D + (\frac{1}{2})H_1 - (\frac{1}{2})H_2 - (\frac{1}{2})F}{(\frac{1}{2})D + (\frac{1}{2})H_1 - (\frac{1}{4})H_2 - (\frac{1}{2})F + E}$$

The heritability (h^2) in F_2 generation was calculated for each character according to Verhalen and Murray (1969):

$$F_2\ Heritability\ (h^2) = \frac{(\frac{1}{4})D}{(\frac{1}{4})D + (\frac{1}{16})H_1 - (\frac{1}{8})F + E}$$

where

D = Variation due to additive effect.
H_1= Component of variation due to dominance effect of genes.
H_2= $H_1[1-(u-v)^2]$ [u = positive and v = negative genes].
F = The mean of "Fr" over the arrays.
E = The expected environmental component of variation.

Genetic advance: When broad sense (H^2) heritability estimates are available, progress from selection can be predicted for any breeding system, since expected gain (genetic advance) is a function of heritability. Therefore, such guided selection produces genetic advance. This change is of great interest to plant breeders, since it changes the population mean. The magnitude of genetic advance from selection for a character in a cross under 5% selection intensity (2.063) and genetic advance as a percent of the sample mean was calculated for each character in F_1 and F_2 generations according to Breese (1972).

$$Heritability\,(H^2) = \frac{\sigma^2 g}{\sigma^2 ph}$$

$$Genetic\ Advance = K.\sqrt{\sigma^2 ph}.H^2$$

$$Genetic\ Advance\ \% = \frac{G.A}{\overline{X}} \times 100$$

$$Genetic\,Variance\ (\sigma^2 g) = \frac{MSG - MSE}{r}$$

$$Phenotypic\,Variance\ (\sigma^2 ph) = \frac{MSG}{r}$$

where
MSG = Genetic mean square of ANOVA.
MSE = Phenotypic (error) mean squares of ANOVA.
r = Number replications.
H^2 = Broad sense heritability.
X = Population mean.
K = selection intensity at 5% with a value of 2.063.
σ^2ph = Standard deviation of phenotypic variation.

Results

Adequacy of the data and design: F_1 and F_2 hybrid means along with their 6 parents revealed highly significant differences ($p \leq 0.01$) for all the traits (Table 1). Diallel analysis further arbitrates the additive-dominance model, components of genetic variance, their interactions, heritability, genetic advance and correlation. In both generations, arrays analysis of variance (Wr+Vr and Wr-Vr) and t^2 test were found nonsignificant for all the traits except in F_2 fiber strength (Table 2) presenting lack of dominance with no epistasis and due to which the genes were independent in their action with random alliance among the parents. Regression coefficient (b) further confirmed the results and significantly deviated from zero and not from unity for fiber length, fiber

Table 1. Mean squares for various traits in a 6x6 F_1 and F_2 diallel cross of upland cotton.

Parameters	F_1 / F_2	Mean squares		F. Ratio	CV %
		Genotypes	Error		
Fiber length	F_1	5.262	0.454	11.59**	2.47
	F_2	3.982	0.584	6.82**	2.79
Fiber strength	F_1	1.707	0.456	3.74**	3.02
	F_2	2.001	0.253	7.89**	2.19
Fiber fineness	F_1	0.459	0.099	4.64**	6.75
	F_2	0.312	0.014	22.35**	2.58
Uniformity ratio	F_1	8.082	0.578	13.98**	1.60
	F_2	7.146	1.066	6.71**	2.16

** Significant at p≤0.01.

uniformity and fiber fineness in F_1s and for fiber fineness in F_2 generation. The above three tests fully satisfy the requisites of additive-dominance model and the data of these traits showed complete adequacy (Table 2). For fiber strength in F_1s and fiber length, fiber uniformity and fiber strength in F_2s, did not satisfy the assumption about regression coefficient and makes the model partially adequate for those traits.

Fiber length: In F_1 staple length, the additive (D) and dominance (H_1 and H_2) components of genetic variation were significant, while F, h^2 and environmental variation (E) were non-significant (Table 3). The D was found greater than H_1 and H_2 and the average degree of dominance ($\sqrt{H_1}/D=0.66$) being less than 01 suggested absence of dominance and revealed that additive gene effects controlled the inheritance. Non-significant negative value of F (-0.19) indicated excess of recessive genes with increasing position due to positive value of h^2 (1.26) and was also confirmed by ratio $\sqrt{4DH_1}+F/\sqrt{4DH_1}-F$ (0.66). In F_2 staple length, D was highly significant, while other components (H_1 and H_2, h^2, F & E_2) were non-significant (Table 3). Additive component was also larger than H_1 and H_2 and the average degree of dominance (0.16) was less than unity, suggested additive gene action with partial dominance. Unequal values of H_1 and H_2 illustrated unbalanced allocation of positive and negative allele frequencies as confirmed by the ratio $H_2/4H_1$ (0.16, 0.39), respectively in both generations. High narrow (h^2) and broad sense (H^2) heritabilities (0.84, 0.91) were recorded (Table 3). Genetic advance under selection was 2.67 mm, while was 9.79% as percent mean value. In F_2s, high h^2 (0.61) and H^2 (0.85) were also noticed with appreciable genetic advance values (2.10 mm &7.67%). Negative correlation (r = -0.871) between (Wr+Vr) and mid parental (y) in F_1s indicated that parents have some dominant genes, while in F_2s correlation (r = 0.100) between (Wr+Vr) and mid parental, the recessive genes were responsible for increased staple length. CIM-1100 derivatives performed well and the selection have been made in F_2 population for further study in segregating generations.

Fiber strength: In F_1 fiber strength, except F, all other components (D, H_1, H_2, h^2 and E) were found significant (Table 3) and environmental variation also play some role in expression of the trait. The additive component (D) was smaller than H_1 but larger than H_2, and the value of $\sqrt{H_1}/D=1.17$ being greater than 01 suggested dominance type of gene action. The unequal values of dominance components ($H_1>H_2$) suggested asymmetrical distribution of positive and negative genes as confirmed by $H_2/4H_1$ (0.15). Non-significant positive value of F (0.43) also indicated excess of dominant genes with increasing ratio due to significance of h^2 (0.56) and was also confirmed by the ratio $\sqrt{4DH_1}+F/\sqrt{4DH_1}-F$ (1.71). In F_2 generation, except D, all other components (H_1, H_2, F, h^2 and E_2) were non-significant (Table 3). Average degree of dominance (0.62<01),

Table 2. Scaling test of additive-dominance model ("t", regression analysis and arrays analysis of variance) for various traits in a 6x6 F_1 and F_2 diallel cross of upland cotton.

Parameters	F_1/F_2	T^2 test	Regression analysis (t value of b)		Analysis of variance of arrays		Conclusions
			b/S.E	b0, b1	Wr + Vr	Wr – Vr	
Staple length	F_1	0.017^{NS}	0.993±0.100	$b0 = 9.975^{**}$ $b1 = 0.069^{NS}$	NS	NS	Model was adequate shown by all the three tests.
	F_2	4.905^{NS}	0.604±0.129	$b0 = 4.698^{**}$ $b1 = 3.082^{*}$	NS	NS	Model was partially adequate due to regression analysis.
Fiber strength	F_1	2.477^{NS}	0.456±0.201	$b0 = 2.272^{NS}$ $b1 = 2.713^{NS}$	NS	NS	Model was partially adequate due to regression analysis.
	F_2	15.865^{*}	-1.967±0.472	$b0 = -4.169^{NS}$ $b1 = 6.289^{**}$	NS	NS	Model was partially adequate due to regression and "t".
Fiber fineness	F_1	0.164^{NS}	0.835±0.192	$b0 = 4.358^{*}$ $b1 = 0.860^{NS}$	NS	NS	Model was adequate shown by all the three tests.
	F_2	2.219^{NS}	0.785±0.112	$b0 = 7.010^{**}$ $b1 = 1.920^{NS}$	NS	NS	Model was adequate shown by all the three tests.
Uniformity ratio	F_1	0.128^{NS}	0.942±0.100	$b0 = 9.384^{**}$ $b1 = 0.575^{NS}$	NS	NS	Model was adequate shown by all the three tests.
	F_2	6.377^{NS}	0.712±0.091	$b0 = 7.816^{**}$ $b1 = 3.163^{*}$	NS	NS	Model was partially adequate due to regression analysis.

Table 3. Genetic components of variance for various traits in a 6x6 F_1 and F_2 diallel cross of upland cotton.

enetic components of variance	Fiber length		Fiber strength		Fiber fineness		Uniformity ratio	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
D	2.35± 0.08*	1.34±0.08**	0.70±0.12*	0.43±0.11*	0.20±0.01*	0.11±0.002**	3.95±0.10	1.66±0.11**
H_1	1.03±0.19*	0.14±0.80	0.96±0.30*	0.66±1.15	0.02±0.04	0.02±0.02	0.57±0.27*	0.31±1.12
H_2	0.64±0.17*	0.22±0.54	0.57±0.27*	0.63±1.03	0.006±0.03	0.01±0.02	0.41±0.24	0.20±1.00
F	-0.64±0.19	-0.41±0.29	0.43±0.29	0.06±0.55	-0.02±0.03	-0.03±0.01	-1.34±0.26	-1.21±0.54
h^2	1.26±0.12	-0.05±0.36	0.56±0.18*	0.19±0.69	-0.01±0.02	-0.0002±0.01	1.05±0.16*	0.05±0.68
E	0.16±0.03	0.15±0.02	0.16±0.04*	0.06±0.04	0.03±0.01	0.003±0.001*	0.22±0.04*	0.29±0.04**
$\sqrt{H_1}/D$	0.66	0.16	1.17	0.62	0.32	0.21	0.38	0.22
$H_2/4H_1$	0.16	0.39	0.15	0.24	0.08	0.13	0.18	0.16
$4DH_1+F/\sqrt{4DH_1-F}$	0.66	0.03	1.71	1.25	0.73	0.22	0.38	-0.26
h^2/H_2	1.97	-0.23	0.98	0.30	-1.67	-0.03	2.56	0.25
Heritability (h^2)	0.84	0.61	0.52	0.53	0.78	0.77	0.89	0.47
Heritability (H^2)	0.91	0.85	0.73	0.87	0.78	0.96	0.93	0.85
Genetic advance	2.67 mm (9.79%)	2.10 mm (7.67%)	1.41 g/tex (6.31%)	1.48 g/tex (6.44%)	0.75 µg (16.11%)	0.58 µg (12.65%)	3.36 % (7.07%)	2.83 % (5.91%)
r (Wr+Vr/VP)	-0.87	0.100	-0.479	-0.587	0.366	0.536	0.977	0.352

F_1 parameter value is significant when it exceeds 1.96 after dividing it with its standard error.

F_2 parameter value is tested by "t" test at n-2 d.f. after dividing it with its standard error.

suggested additive type of gene action. H_1, H_2 were having nearly equal values revealed balanced distribution of positive and negative gene frequencies as confirmed by $H_2/4H_1$ (0.24) which was closest to 0.25. Medium h^2 and H^2 (0.52, 0.73) were observed (Table 3) with genetic gain of 1.41 g/tex and its value as percent mean was 6.31%. In F_2s, medium h^2 and H^2 (0.53, 0.87) were recorded with genetic advance of 1.48 g/tex and was 6.44% as percent mean value of genetic gain. Negative but non-significant correlation in F_1s and F_2s (r = -0.479, r = -0.587) between the (Wr+Vr) and parental mean revealed that parents containing both dominant and recessive genes and were responsible for increased fiber strength. CIM-1100 hybrids viz; CIM-240 x CIM-1100, CIM-1100 x BH-36, CIM-1100 x FH-682 and CIM-1100 x CRIS-9 and their reciprocals performed well and their selected plant families have been studied in segregating generations which have shown valuable performance.

Fiber fineness: In F_1 fiber fineness, except D which was significant, the H_1, H_2 F, h^2 and E were non-significant (Table 3). The additive component was greater than dominance (H_1 & H_2) and mean degree of dominance (0.32<01) also suggested additive type of gene action with partial dominance. Unequal values of dominance (H_1>H_2) indicated asymmetrical distribution of positive and negative gene frequencies as confirmed by $H_2/4H_1$ (0.08). The value of F (-0.02) indicated excess of recessive genes with increasing ratio due to negative value of h^2 (-0.01). Additive effects control the inheritance of micronaire as also confirmed by ratio $\sqrt{4DH_1}+F/\sqrt{4DH_1}-F$ (0.73). In F_2s, the D was highly significant, E_2 was only significant, while other components (H_1, H_2, F and h^2) were non-significant (Table 3). The additive component was larger (D>H_1 & H_2) and the genetic ratio ($\sqrt{¼H_1}/D$ = 0.21<unity) indicated absence of dominance. Unbalanced dominance values (H_1>H_2) showing uneven distribution of positive and negative genes as confirmed by $H_2/4H_1$ (0.13). The F value (-0.03) indicated excess of recessive genes with increasing position due to h^2 (-0.0002). Additive gene effects were also confirmed by ratio $¼\sqrt{4DH_1}+F/¼\sqrt{4DH_1}-F$ (0.22) as less than unity. High and at par h^2 and H^2 (0.78) heritabilities were recorded for F_1s (Table 3), revealed that genetic variation was controlled by additive gene action with partial dominance. Genetic advance and as percent population mean were 0.75 µg and 16.11%. In F_2s, high h^2 (0.77) and H^2 (0.96) exhibited that the genetic variation was also on account of additive gene effects having partial dominance with genetic advance of 0.58 µg and 12.65% as percent mean. Positive correlation coefficient in F_1s and F_2s (r = 0.366, r = 0.536), respectively between the (Wr+Vr) and mid parental established that parents having recessive genes and were responsible for desirable fiber fineness in both generations. Some of the CIM-1100 hybrids revealed prominent heritability along with genetic advance and the selection in the said cross families can stabilize the fiber fineness to the desired level.

Uniformity ratio: In F_1s, the D, H_1, h^2 and E were significant, while the values of H_2 and F were non-significant (Table 3). Environmental variation also play role in phenotypic expression of the trait. The additive component was greater (D>H_1 & H_2) and the genetic parameter ($\sqrt{H_1}/D$ = 0.38) also being less than unity, hence, absence of dominance. The F_2 population exhibited highly significant values for D and E_2, while H_1, H_2, h^2 and F were non-significant (Table 3). The D was also larger than H_1 and H_2 and average degree of dominance (0.22<01) suggested additive gene action with partial dominance. In both generations, the unequal values of H_1 and H_2 represented unbalanced distribution of positive and negative genes as confirmed by $H_2/4H_1$ (0.18, 0.16). The F values in F_1s and

F_2s (-1.34, -1.21) indicated excess of recessive genes with increasing position due to positive value of h^2 (1.05, 0.05). High h^2 (0.89) and H^2 (0.93) heritabilities were noticed for F_1s (Table 3), elucidates that 96% genetic variation was controlled by additive genes with partial dominance. Genetic advance was 3.36%, and as percent mean the value was 7.07%. In F_2s, moderate h^2 and H^2 (0.47, 0.85) were recorded, which clarified that the genetic variation was controlled by additive gene effects. Genetic advance values were 2.83% and 5.91% as percent mean (Table 3). Positive significant and non-significant correlation in F_1s and F_2s (r = 0.977, r = 0.352), respectively between the (Wr+Vr) and parental mean (y) indicated that parents containing recessive genes that were responsible for increased uniformity ratio. Desirable F_2 hybrids like CIM-1100 x BH-36, CIM-1100 x CRIS-9 and their reciprocals have shown best performance and these genotypes could be advanced through simple selection.

Performance of F_3, F_4 and F_5 population: In F_3 generation (Table 4), 10 out of 11 plant families means of four promising crosses viz., CIM-109 x CIM-1100, CIM-240 x CIM-100, CIM-1100 x CIM-240 and CIM-1100 x CIM-109 surpassed the standard cultivar (CIM-446) with percent increase for staple length (+5.06 to +14.01%) and fibre strength (+0.50 to +5.03%), respectively. For fiber fineness, 10 plant families of selected F_3 population showed negative values for increase over standard (-4.35 to -17.39%), which were also desirable from breeding point of view by having fine fibers. On the said phenotypic performance, selection was made and was taken to F_4 generation (Table 5) for further study. In F_4 population for staple length and fiber strength, the 25 and 17 plant families showed increase over standard ranged from +4.37 to +17.86% and +1.01 to +13.57%, respectively. For fiber fineness, 24 plant families have manifested decreasing values as compared to standard (-4.35 to -29.06%) except one plant family of CIM-109 x CIM-1100 having positive value (+4.35%) in F_4 generation. In F_5 (Table 6), the families were reduced and almost all the nine plant families have shown increased values over standard for staple length (+0.78 to +7.39%) and fiber strength (+8.54 to +15.08%), respectively. In case of fiber fineness, four out of nine plant families showed negative values for increase over standard (-2.17 to -10.87%), which were desirable from textile point of view by having fine fibers.

Table 4. Performance of selected F_3 population for fiber length, strength and fineness of upland cotton.

F_3 Hybrids	Plant families	Fiber length (mm)		Fiber strength (g/tex)		Fiber fineness (µg)	
		Mean	% +/-	Mean	% +/-	Mean	% +/-*
CIM-109 x CIM-1100	1	29.3	+14.01	20.2	+1.51	3.8	-17.39
”	2	27.7	+7.78	20.4	+2.51	3.9	-15.22
CIM-240 x CIM-1100	1	27.9	+8.56	19.8	-0.50	4.2	-8.70
”	2	25.5	-0.78	20.3	+2.01	4.1	-10.87
”	3	27.3	+6.23	20.2	+1.51	4.0	-13.04
”	4	27.7	+7.78	20.0	+0.50	4.7	+2.17
”	5	27.0	+5.06	20.8	+4.52	3.9	-15.22
CIM-1100 x CIM-240	1	27.0	+5.06	20.5	+3.02	4.0	-13.04
”	2	27.6	+7.39	20.4	+2.51	4.1	-10.87
”	3	28.3	+10.12	20.7	+4.02	4.2	-8.70
CIM-1100 x CIM-109	1	27.9	+8.56	20.9	+5.03	4.4	-4.35
Standard (CIM-446)	-	25.7	-	19.9	-	4.6	-

% Increase (+) and decrease (-) over standard cultivar (CIM-446).

Table 5. Performance of selected F_4 population for fiber length, strength and fineness of upland cotton.

F_4 Hybrids	Plant families	Fiber length (mm)		Fiber strength (g/tex)		Fiber fineness (µg)	
		Mean	% +/-	Mean	% +/-	Mean	% +/-*
CIM-109 x CIM-1100	1	28.3	+12.30	21.50	+8.04	3.4	-26.09
”	2	28.7	+13.89	22.30	+12.06	3.5	-23.91
”	3	26.4	+4.76	19.00	-4.52	4.8	+4.35
”	4	26.7	+5.95	20.10	+1.01	3.9	-15.22
”	5	27.2	+7.94	22.20	+11.56	3.5	-23.91
CIM-240 x CIM-1100	1	27.1	+7.54	19.50	-2.01	4.0	-13.04
”	2	27.4	+8.73	19.80	-0.50	3.8	-17.39
”	3	27.6	+9.52	21.10	+6.03	4.4	-4.35
”	4	26.9	+6.75	20.30	+2.01	4.4	-4.35
`”	5	27.3	+8.33	20.90	+5.03	3.9	-15.22
”	6	26.3	+4.37	20.30	+2.01	3.5	-23.91
”	7	27.6	+9.52	23.90	+20.10	3.4	-26.09
”	8	26.9	+6.75	22.00	+10.55	3.7	-19.57
”	9	26.7	+5.95	19.80	-0.50	4.1	-10.87
”	10	26.9	+6.75	19.80	-0.50	3.9	-15.22
”	11	27.1	+7.54	19.50	-2.01	4.4	-4.35
CIM-1100 x CIM-240	1	27.1	+7.54	20.50	+3.02	3.6	-21.74
”	2	27.2	+7.94	20.50	+3.02	3.7	-19.57
”	3	29.7	+17.86	22.50	+13.07	3.7	-19.57
”	4	28.8	+14.29	22.60	+13.57	3.7	-19.57
”	57	26.7	+5.95	21.90	+10.05	4.3	-6.52
”	6	27.3	+8.33	22.00	+10.55	4.0	-13.04
”	7	26.9	+6.75	19.10	-4.02	4.0	-13.04
CIM-1100 x CIM-109	1	27.2	+7.94	21.20	+6.53	4.2	-8.70
”	2	28.0	+11.11	20.40	+2.51	4.2	-8.70
Standard (CIM-446)	-	25.2	-	19.90	-	4.6	-

* % Increase (+) and decrease (-) over standard cultivar (CIM-446).

Table 6. Performance of selected F_5 population for fiber length, strength and fineness of upland cotton.

F_5 Hybrids	Plant families	Fiber length (mm)		Fiber strength (g/tex)		Fiber fineness (µg)	
		Mean	% +/-	Mean	% +/-	Mean	% +/-*
CIM-109 x CIM-1100	1	27.6	+7.39	22.40	+12.56	4.5	-2.17
-do-	2	27.1	+5.45	21.60	+8.54	4.4	-4.35
CIM-240 x CIM-1100	1	27.5	+7.00	22.20	+11.56	4.1	-10.87
-do-	2	27.0	+5.06	19.80	-0.50	4.7	+2.17
-do-	3	26.3	+2.33	22.90	+15.08	4.9	+6.52
CIM-1100 x CIM-240	1	26.9	+4.67	22.50	+13.07	4.4	-4.34
-do-	2	27.5	+7.00	22.80	+14.57	5.0	+8.70
CIM-1100 x CIM-109	1	25.9	+0.78	21.60	+8.54	4.9	+6.52
-do-	2	27.2	+5.84	21.80	+9.55	5.2	+13.04
Standard (CIM-446)	-	25.7	-	19.90	-	4.6	-

* % Increase (+) and decrease (-) over standard cultivar (CIM-446).

Discussion

The scaling tests (Table 2), revealed no epistasis with lack of dominance and showed that genes were independent in their action with random association among the parents. Verhalen *et al*. (1971) and Khan *et al*., (2003) also detected no epistasis for fiber quality traits. Results indicated that fiber length, fiber fineness and fiber uniformity ratio were found additive in both generations. Verhalen & Murray (1969), Khan *et al*., (2003), McCarty *et al*., (2004 a), Wu *et al*., (2006) and Aguiar *et al*., (2007) have also recorded additive type of variance for fiber quality traits. High heritabilities (h^2 and H^2) and genetic gain in promising F_2 hybrids were also encouraging. Same heritability and genetic advance have also been recorded by Tang *et al*., (1993), McCarty *et al*., (1996), Tang *et al*., (1996), Hussain *et al*., (1998) and Yingxin & Xiangming (1998). With

stability in additive variance, the fibre length and fiber uniformity can be improved through simple selection in segregating generations. In case of micronaire, additive inheritance was also encouraging because the over dominance responsible for increased values of micronaire which is undesirable and not effectively operative, as high values of fiber fineness exhibits coarse fibers. So, through simple selection the fiber fineness can be maintained in desirable hybrids. McCarty *et al*., (2004a & b) and Wu *et al*., (2006) have mentioned additive variance for micronaire. However, Ahmad *et al*., (1997) and Iqbal *et al*., (2005) noticed nonadditive type of gene action for fiber quality traits. The contradictory findings may be due to different factors like breeding material used and the climatic conditions under which the experiments were conducted.

Fiber strength was nonadditive on the basis of genetic components and degree of dominance value was also more than unity in F_1 generation, which further confirms over dominance. Yingxin & Xiangming (1998) and Iqbal *et al*., (2005) also reported same type of inheritance for fiber strength. High ratio of heritability and genetic advance were also seen in the findings (Tang *et al*., 1996; Yingxin & Xiangming, 1998; Yunkun *et al*., 1998; Hussain *et al*., 1999; Khan *et al*., 2003). In F_2s, the fiber strength was found additive as verified by components of variance and mean degree of dominance. Verhalen & Murray (1969) Tang *et al*., (1993), McCarty *et al*., (1996) and Hussain *et al*., (1999), McCarty *et al*., (2004a & b), Wu *et al*., (2006) and Aguiar *et al*., (2007) also recorded same type of variances for fiber strength. Hence, after selection in promising F_2 hybrids, improvement can be made in this trait through segregating generations.

On the basis of the above mentioned performance, the selections was made in F_2 population of cv. CIM-1100 on a single plant basis and were studied by plant to row method for further improvement. In advanced generations (F_3, F_4 and F_5) almost all the plant family means of the four promising derivatives of CIM-1100 (CIM-109 x CIM-1100, CIM-240 x CIM-1100, CIM-1100 x CIM-240 and CIM-1100 x CIM-109) superseded the standard cultivar (CIM-446) for staple length, fiber strength and manifested desirable negative values for micronaire. Same findings were also reported by Khan *et al*., (2003). This improvement may be due to transgressive segregation and homozygosity obtained in generation after generation. Some of the plant families have not shown the valuable performance as compared to standard, which were discarded.

Conclusion

Additive components were significantly higher than dominance components for all the parameters under study in both generations except fiber strength in F_1s and that also diverted to additive in F_2 generation. Mostly additive components were significant and dominance was nonsignificant. Heritabilities were moderate to high with appreciable genetic gain. Hence, with the stability of additiveness, the selection which was made in F_2 promising population revealed remarkable performance for fiber quality traits as compared to existing standard cultivar (CIM-446). It is aimed that the breeding material could provide the strong basis for sustainable development in fiber quality properties and to stabilize them up to the desired level in some new strains.

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