Australian Journal of Crop Science
2(1):10-17 (2008)
ISSN: 1835-2707

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Genetics of fibre quality traits in cotton (*Gossypium hirsutum* L.)

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Abstract

Five upland cotton varieties were crossed in a complete diallel mating system to assess the genetics of fibre length (FL), fibre strength (FS), fibre fineness (FF), fibre uniformity (FU) and fibre elongation (FE) utilizing Mather and Jinks approach. Differences were found to be significant ($P<0.01$) for all the characters. Adequacy tests revealed that data of all the characters were partially adequate for genetic interpretation except FE. Additive component (D) was significant in all the traits and was lower in magnitude than dominant components (H1 and H2) of variation for FS and FU which was firmly supported by the value of $H1/D^{0.5}$. Dominant genes were in excess than recessive genes in the parents for all the traits except for FF. Asymmetrical distribution of dominant and recessive genes in parents for all characters was confirmed, and soundly sustained by the value of $H_2/4H_1$. The h^2 value was insignificant for all the characters except FS. Moderately high narrow sense heritability ($h^2_{n.s}$) was exhibited by FF, FU and FE, while SL and FS possessed low heritability. Graphical representation demonstrated additive gene action for SL, FF, and FE whereas; FS and FU were controlled by overdominance effects. Full sib or half sib family selection, pedigree and progeny test would probably be necessary to achieve the genetic progress for SL, FF, and FE while hetrosis breeding could be fruitful for improvement of FS and FU.

Keywords: *Gossypium hirsutum* L., genetic effects, components of variation, fibre quality.

Introduction

Cotton fibre quality is no longer an afterthought; it is becoming an increasingly important issue in modern textile industry. Fibre quality of a specific cotton genotype is a composite of various characteristics including staple length, fibre strength, fineness, maturity and fibre elongation. These traits have their individual importance in spinning, weaving and dying units (Munro, 1987). Yarn strength is the processing result of greatest interest to yarn and textile manufacturers (Bradow, 1999). In addition fibre uniformity is also of tremendous value in the textile industry. It is highly correlated with the efficient spinning and weaving processes which convert the fibre into fabrics. But these traits are highly influenced by the environment with special reference to the fineness (Yuan *et al.* 2005; Percy *et al.* 2006).Therefore, it is the need of the day to improve fibre quality in the dominating hirsutum genotypes, to fulfill the requirements of growing textile industry, processing and end uses. Achievement of this objective strongly requires creation as well as quantification of genetic variability in addition to the identification of potential donor parents (Rahman *et al.*, 2005; Rahman *et al.*, 2007). Current commercial cultivars of upland cotton have limited variability for these traits. In order to introduce this genetic variability, diallel crossing techniques have been widely utilized by the breeder (Iqbal *et al.* 2003; Basal and Turgut, 2005; Murtaza *et al.* 2005).

May and Green (1994) and Haq and Azhar (2004) reported additive type of gene action for fibre length, but non-additive gene effects for fibre strength and fibre fineness. Ajmal *et al.* (2000), Khan *et al.* (2001) and Ahmad *et al.* (2003) investigated non-additive type of gene action for staple length whereas, they reported additive effects for fibre strength. Additive genes were reported to be predominant in the inheritance of fibre fineness by Ahmad *et al.* (2003), while Ajmal *et al.* (2000), Khan *et al.* (2001), and Murtaza *et al.* (2005) reported non additive type of gene action involved in the phenotypic expression of this trait. Iqbal *et al.* (2003) investigated additive genetic effects for staple length, fibre fineness and fibre strength. Khan *et al.* (2001) and Shakeel *et al.* (2001) found that non additive genes were involved in the inheritance of fibre uniformity while Hendawy *et al.* (1999) and Chen *et al.* (1999) provided dissimilar results.

The purpose of this research was to create variability, expose genetic effects and to determine appropriate parents for fibre quality characteristics in a diallel set involving among five genetically diverse *Gossypium hirsutum* L. genotypes.

Materials and Methods

Genetic material

The plant material for this study was developed by crossing five local Pakistani genotypes, namely NIAB-78, CIM-499, LSS, RH-112 and NIAB-Krishma, in a full diallel fashion. All the entries were maintained by selfing. Some of the fibre related characteristics of these genotypes are given here: ***NIAB-78*** was a reputed local cultivar, grown all over the Pakistan for many years after its approval. Although it has become susceptible to cotton leaf curl virus disease (*Gemini* group of viruses) (Arshad *et al.*, 2006), its fibre characteristics still are the standards for textile industry in Pakistan. The variety ***CIM-499*** contains great number of bolls, large boll size and good lint percentage. It also has good fibre characteristics especially fibre length and uniformity. This cultivar is still performing well in the field. ***LSS*** was a good source for fine and uniform fibre. It was released before the partition of Pakistan and India. Now it is not cultivated commercially due to its low tolerance against heat and large shattering of flowers. The genotype ***RH-112*** has good fibre strength, elongation, uniformity and fineness; it is also rich in oil content. The cultivar ***NIAB-Krishma*** displays vigorous growth habit, large boll size and good fibre qualities but it is also susceptible to cotton leaf curl virus disease (Arshad *et al*., 2006). In the experiment this genotype was utilized to transfer some of the fibre characters into other varieties.

Greenhouse experiment

The parents were grown in 30 x 30 cm earthen pots placed in greenhouse during November 2005 at the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The proper growing conditions were provided for germination and optimum growth of the plants. Temperature in the glasshouse was maintained at 30°C during the day and 25°C at night by using steam as well as electric heaters. The plants were exposed to natural sunlight and supplemented with artificial lighting, a photoperiod of 16 hours (Murtaza *et al*., 2005). Seedlings were thinned to one plant per pot two weeks after planting. Every 14 days, 0.25 g of urea (46% N) was added to each pot and plants were watered daily. At the time of flowering, all possible crosses were made among the genotypes taking all the necessary precautionary measures to avoid the contamination of the genetic material. A large number of pollinations were carried out in order to produce sufficient quantity of hybrid seed.

Field experiment

The F_0 seeds of 20 hybrids and their 5 parents were planted in the field in triplicate randomized complete block design (RCBD) during May, 2006. Each of the 25 entries, in a replication was planted in a single row having 15 plants spaced at 30 cm within and 75 cm between the rows. All the recommended agronomic and plant protection practices were followed from sowing till harvest. The matured bolls were picked from 10 guarded plants on the individual plant basis after every two weeks till the harvesting of crop in January 2007. Picking was done after the evaporation

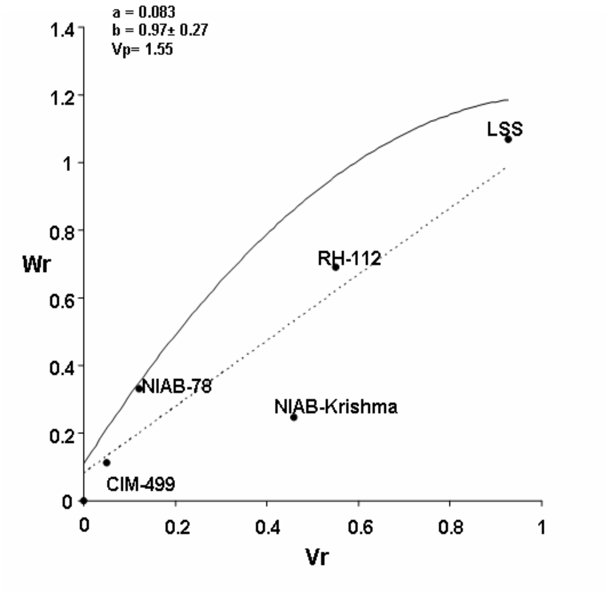

Fig 1. **Vr versus Wr graph for SL**

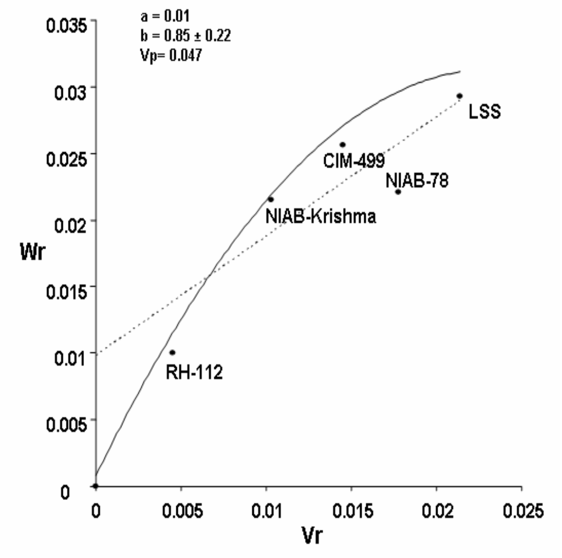

Fig 2. **Vr versus Wr graph for FF**

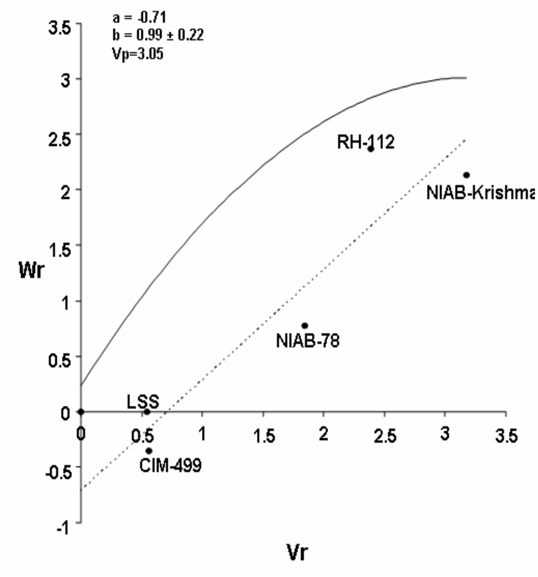

Fig 3. **Vr versus Wr graph for FS**

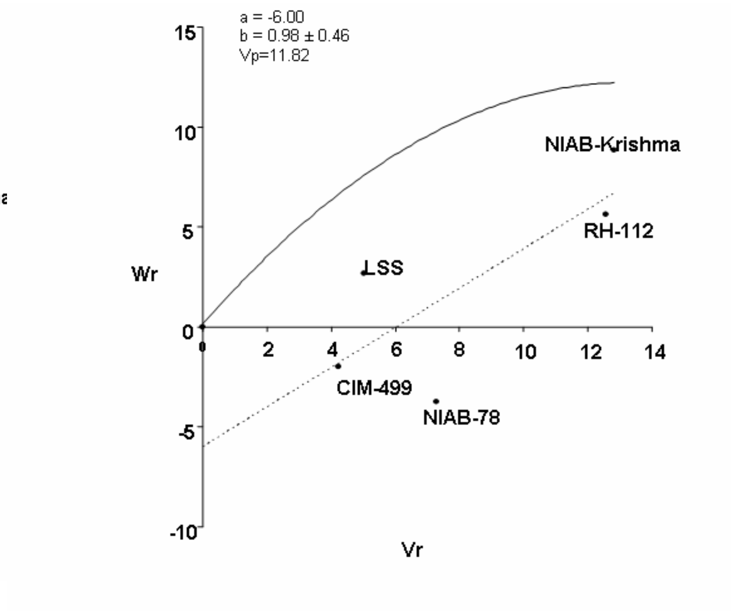

Fig 4. **Vr versus Wr graph for FU**

of dew. Seed cotton was collected in Kraft paper bags and was dried in sunlight for two days.

Laboratory testing and biometrical treatment of the data

Total seed cotton of all the plants in each entry were ginned with a single roller electrical gin in the laboratory on individual plant basis. Lint was conditioned by placing at 65% humidity and 18-20°C temperature in an air conditioned room using humidifier before fibre testing. High Volume Instrument (HVI-900-SA; Zelwiger, Uster, UK) was used for fibre analysis.

Statistical Analysis

The collected data were analyzed by Fisher's analysis of variance to determine significant varietal differences among the 25 genotypes following Steel *et al.* (1996). The simple additive-dominance (AD) model suggested by Hayman (1954) and Jinks (1954) modified by Mather and Jinks (1982) and adopted by Singh and Chaudhry (1985) was followed for genetic analysis of the data.

Results and discussion

Genotypic differences among the parents

Preliminary analysis of variance indicated significant differences (P<0.01) for all the fibre traits among genotypes. The mean squares for the traits are represented in Table 1 describing high significance of the 'F' test for all the characters under study. Array means showed that five parents (e.g. NIAB-78, CIM-499, LSS, RH-112 and NIAB-Krishma) used in this study varied considerably for each component of fibre quality (Table 2). CIM-499, LSS, NIAB-78, NIAB-Krishma and RH-112 had the highest values in the order of SL, FF, FS, FU and FE. The data presented in Table 2 also revealed that the highest values of investigated characters did not follow the same pattern in every genotype.

Assessment of the data for Additive-Dominance model

The data were assessed for Additive-Dominance (AD) model by exploiting various adequacy parameters given in Table 3. According to Mather and Jinks (1982) the data will be only valid for genetic interpretation if the value of regression coefficient (b) must deviate significantly from zero but not from the unity. The value of b was significantly varying from zero but not from one for all the characters under study except FU which failed to fulfill this criterion. The test for 't' square indicated its non-significance value which proved the absence of non-allelic interactions in genetic behavior of all traits which in turn attested the data valid for AD model for all the characters. The appropriateness of the model data analysis was also verified by the analysis of variance of (Wr+Vr) and (Wr-Vr). In this test the mean squares for (Wr+Vr) should be significantly different between the arrays while the mean squares for (Wr-Vr) should be non-significant (Mather and Jinks, 1982; Singh and Chaudary, 1985). The lack of significant variation in the (Wr–Vr) arrays over replications for all the characters suggested that any kind of epistasis was not involved in the phenotypic expression of the traits. Although the value of regression coefficient (b) proved the fitness of the data of SL (0.97), FF (0.85), and FS (0.99) for AD model, mean square value of (Wr+Vr) for the traits indicated no significant deviation, thus emphasizing partial validity of these characters for further genetic analysis. On the other hand, FU exhibited non-significant value of b (0.98) at both null hypothesis (b=0, 2.12) and alternate hypothesis (b=1, 0.025), while the assessment of mean squares for Wr+Vr between arrays (230.47) exposed the data

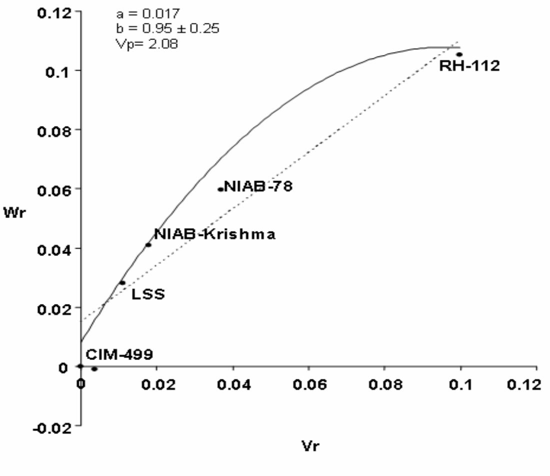

Fig 5. **Vr versus Wr graph for FE**

Table 1. Mean squares obtained from simple analysis of variance of F_1 hybrids and their parents

Source of Variation	**S L** (mm)	**F F** (µg/inch)	**F S** (g/tex)	**F U** (Ratio)	**F E** (%age)
Replications	0.388	0.020	1.082	0.058	0.007
Genotypes	7.0537**	0.376**	6.687**	8.21**	0.295**
Error	0.7547	0.300	1.094	0.73	0.021

** Significance at P<0.01, Where SL=Staple Length, FF=Fibre Fineness, FS=Fibre Strength, FU=Fibre Uniformity and FE=Fibre Elongation

Table 2. Array means for various fibre traits in 5×5 diallel cross in cotton

Parants	**S L**	**F F**	**F S**	**F U**	**F E**
NIAB-78	27.63	5.18	27.36	49.40	6.100
CIM-499	28.09	5.09	25.73	48.39	6.633
LSS	27.12	4.95	26.37	49.81	6.200
RH-112	27.85	4.95	26.96	50.71	7.267
NIAB- KRISHMA	27.18	4.98	26.72	51.03	6.733

Where SL=Staple Length, FF=Fibre Fineness, FS=Fibre Strength, FU=Fibre Uniformity and FE=Fibre Elongation

of this character for genetic investigation. The character FE was the only to fulfill all the adequacy tests. The value of b (0.95 ± 0.25) in case of FE was significantly differed from zero and not from one, non-significant value of t square (0.040), highly significant value of mean squares for (Wr+Vr) between the arrays (0.030) and non-significant character of (Wr-Vr) mean squares (0.002) revealed full fitness of the data for further genetic elaboration.

Genetic analysis of fibre quality traits

Genetics of fibre quality traits was evaluated by the calculation of genetic components of variation D, H1, H2 and F (Table 4). All the fibre characters exhibited significant additive variation (D) at P<0.05 such as SL, FF, FS, FU and FE. This proved that additive genetic effects are prominent in determination of these characters. May and Green (1994), Hendway *et al.* (1999), Ahmad *et al.* (2003), Iqbal *et al.* (2003), Haq and Azhar (2004), Basal and Turgut (2005), Murtaza *et al.* (2005) also investigated significant value of additive component of variation (D) for these characters. Dominance components (H1 and H2) were significant for FS, FU and FE, while SL and FF demonstrated no significance value of both H_1 and H_2 (Table 4). These results showed that inheritance of SL and FF was completely dominated by additive gene action whereas, the expression of FS, FU and FE was determined by additive genetic effects with partial dominance (Ahmad *et al.*, 2003; Iqbal *et al.*, 2003; Basal and Turgut, 2005; Murtaza *et al.*, 2005). The breeding value of a line is a function of the additive gene action. The additive genes are directly transported from the parents to the offspring, are responsible for the resemblance between relatives and can be used to calculate inheritance (Falconer, 1989). Predominance of additive effects (D) in the genetic mechanism SL and FF advocated that the genes for the characters are fixed and the traits could be improved via selection by exploiting pedigree method right from F_2 generation. Although D and H_1&H_2 components were significant for FE, the greater magnitude of D item for the character suggested that additive genetic effects were more pronounced than dominance effects in the genetic mechanism controlling this character. On the other hand, higher values of H1 and H2 over D suggested the

***Table 3.** Adequacy test of additive-dominance model for 5×5 diallel in cotton*

Parameters	S L	F F	F S	F U	F E
Joint regression (b)	0.97± 0.27	0.85± 0.22	0.99± 0.22	0.98± 0.46	0.95 ± 0.25
Test for b=0	3.50*	3.87*	4.49*	2.12^{NS}	3.80*
Test for b=1	0.087^{NS}	0.662^{NS}	0.018^{NS}	0.025^{NS}	0.181^{NS}
Test for t^2	0.116^{NS}	0.080^{NS}	0.098^{NS}	0.450^{NS}	0.040^{NS}
Mean squares of Wr+Vr between arrays	1.085^{NS}	0.002^{NS}	17.40^{NS}	230.47*	0.030**
Mean square of Wr-Vr between arrays	0.074^{NS}	0.0002^{NS}	0.580^{NS}	31.80^{NS}	0.002^{NS}
Fitness of the data to Additive-Dominance Model	Partial	Partial	Partial	Partial	Full

*, ** Significance at P<0.05 and P<0.01 levels, respectively. NS = Non-significant, Where SL=Staple Length, FF=Fibre Fineness, FS=Fibre Strength, FU=Fibre Uniformity and FE=Fibre Elongation

preponderance of dominant genes for FS and FU which revealed that the variation in these parameters was controlled by genes having dominant effects at most of the loci and manipulation of the parents may be useful through exploitation of heterosis for improving these quality attributes.

The dominance additive ratio indicates the degree of dominance ($H1/D^{0.5}$). The values of degree of dominance ($H1/D^{0.5}$) for SL (0.643), FF (0.652) and FE (0.940) were less than unity which confirmed the contribution of additive genes in the heritage of these characters (Table 4). However, the value of $H1/D^{0.5}$ for FS (1.350) and FU (1.762) demonstrated the prevalence of dominant genes in the genetic control of both these characters and this was well supported by higher values of dominant components over the additive ones for these quality characters. Dominance additive ratio of less than one refers to partial dominance, near one indicates complete dominance and greater than one indicates overdominance (Falconer, 1989). Thus the degree of dominance for FS and FE was greater than one indicating the effect of overdominance in the genetics of these parameters (Ahmad *et al.* 2003).

Asymmetrical distribution of dominant genes for all the traits was confirmed by unequal estimates of H_1 and H_2 which was soundly supported by the value of $H_2/4H_1$ for SL (0.198), FF (0.161), FS(0.221), FU (0.201) and FE (0.184) (Hendway *et al.* 1999; Ahmad *et al.* 2003; Iqbal *et al.* 2003; Basal and Turgut, 2005; Murtaza *et al.* 2005). This was due to the fact that dominant genes would be in equal proportions (H1=H2) only if $H_2/4H_1=0.25$ (Mather and Jinks, 1982; Singh and Chaudary, 1985).

The F value which is an estimate of the relative frequency of dominant to recessive alleles in the parental lines was positive for SL (1.677), FS (0.805), FU (13.32) and FE (0.022) revealing the excess of dominant alleles present in genetic material (e.g. NIAB-78, CIM-499, LSS, RH-112 and NIAB-Krishma) in which these characters were evaluated and the claim was strengthened by values of $(4DH_1)^{0.5}+F/\ (4DH_1)^{0.5}-F$ which were greater than one. However, F value for FF was negative disclosing the presence of recessive genes in the parents (Murtaza *et al*, 2005) and this was finely sustained by the value of $(4DH_1)^{0.5}+F/(4DH_1)^{0.5}$ which was less than unity (0.754). The lack of significance for component h^2 for all the fibre characteristics illustrated that dominance was not unidirectional except FS (6.960 ± 0.566) which displayed significant h^2 value resulting in unidirectional type of dominance and suggesting that heterosis breeding could be rewarding for this trait (Iqbal *et al.* 2003; Ahmad *et al.*, 2003). Significant environmental component (E) for SL (0.414), FF (0.010) and FS (0.414) indicated that the fibre quality characters were highly affected by environmental conditions (Bradow, 1999; Yuan *et al.* 2005; Percy *et al.*, 2006; Rahman *et al.*, 2006).

Narrow sense heritability measures the extent of correspondence between breeding values and phenotypic values and expresses the magnitude of genotypic variance in the population, which is mainly responsible for changing the genetic composition of

Table 4. Components of variation for different traits in *Gossypium hirsutum* L. in F_1 generation

Components of variation	**S L**	**F F**	**F S**	**F U**	**F E**
D	1.276 ± 0.132*	0.036 ± 0.002*	2.446 ± 0.342*	10.844 ± 2.554*	0.158 ± 0.02*
H_1	0.536 ± 0.358	-0.015 ± 0.006	4.850 ± 0.925*	33.70 ± 6.90*	0.140 ± 0.048*
H_2	0.415 ± 0.324	-0.010 ± 0.005	4.455 ± 0.839*	27.15 ± 6.25*	0.103 ± 0.043*
F	0.805 ± 0.330*	-0.006 ± 0.006	1.677 ± 0.855	13.32 ± 6.38*	0.022 ± 0.044
h^2	0.328 ± 0.219	-0.003 ± 0.003	6.960 ± 0.566*	1.026 ± 4.22	0.005 ± 0.030
E	0.414 ± 0.054*	0.010 ± 0.0009*	0.414 ± 0.139*	0.980 ± 1.043	0.007 ± 0.007
$(H_1/D)^{0.5}$	0.643	0.652	1.350	1.762	0.940
$H_2/4H_1$	0.198	0.161	0.221	0.201	0.184
$(4DH_1)^{0.5}+F/(4DH_1)^{0.5}-F$	2.890	0.754	1.612	2.070	1.160
$h^2_{(n.s)}$	0.43	0.69	0.30	0.65	0.71

the population via selection (Falconer, 1989; Dabholkar, 1992). Estimates of narrow sense heritability ($h^2_{n.s}$) showed low heritability for SL (0.43) and FS (0.30), whereas, heritability was moderately high for FF (0.69), FU (0.65) and FE (0.71). High estimates of heritability in narrow sense represented fixable and additively heritable variation, which indicated that selection response should be rapid for these characters. These results were in correspondence with those of Tang *et al.* (1996), Ahmad *et al.* (1997), Hendway *et al.* (1999), Ahmad *et al.* (2003), Iqbal *et al.* (2003), Basal and Turgut (2005) and Murtaza *et al.* (2005).

Graphical representation of the data

On the basis of simple Hayman-Jinks model, the Vr versus Wr graphs (Fig. 1 to 5) were plotted which showed unit slope of regression line indicating no concern of epistasis. These graphs revealed that the genes controlling the inheritance of SL, FF and FE were additive in nature as the regression line intercepted vertical axis above the origin and these results were firmly supported by larger values of D component over H1 and H2 for these traits. In contrast the traits FS and FU were in command of over dominant gene as the regression line crossed theY-axis below the origin and this was superbly maintained by results provided by the higher values of dominance components H1 and H2 over the additive one D (Shah *et al.* 1993; May and Green, 1994; Khan *et al.,* 2001; and Shakeel *et al.*, 2001; Ahmad *et al,* 2003; Haq and Azhar, 2004; Murtaza *et -al.*, 2005; Basal and Turgut, 2005). However these results are not in accordance with Hendawy *et al.* (1999), Chen *et al.* (1999), Ajmal *et al.* (2000) and Ahmed *et al.* (2006) were not in accordance with those reported in this study.

The relative distribution of varieties along the regression line (Fig. 1 to 5) revealed that CIM-499 having the lower values of Vr and Wr was present closer to the origin, and has carried the most dominant genes for all the characters except FF and FS where RH-112 and LSS conceded the maximum number of dominant genes. On the other hand genotype LSS being located away contained the most recessive genes for SL and FF while the cultivar NIAB-Krishma contained maximum recessive genes for FS and FU, whilst for FE RH-12 hold the most recessive genes.

Conclusion

The results revealed that there was significant genotypic variation among the genotypes which made the diallel analysis practical. The data of all the characters were partially adequate for genetic interpretation except FE. Additive genes coupled with high narrow sense heritability were involved in the heritage of SL, FF and FE while the inheritance of FS and FU was dominated by dominant genes. The genes controlling SL, FF and FE were additive in nature and these fibre characteristics could be improved via selection while heterosis breeding might be fruitful for progress in FS and FU.

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