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Assessment of Genetic Variation and Inheritance Mode of Some Metric Traits in Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

Five cotton cultivars were crossed in a complete diallel fashion. The resulting 20 hybrids and their five parents were studied for genetic variation involved in the inheritance of different plant traits during 2005-07. Differences were found to be highly significant (P<0.01) for all the characters i.e., number of monopodia, number of sympodia, boll weight, lint percentage and seed cotton yield. All the traits exhibited additive gene action with partial dominance. Epistasis was absent in the phenotypic expression of these characters. Estimates of narrow sense heritability were high for number of sympodia (0.74), boll weight (0.87), lint percentage (0.71) and seed cotton yield (0.86), while moderate for number of monopodia (0.66) with considerable effects. Additive gene action and high estimates of heritability advocated the utilization of selection breeding for improving these traits. The results concluded that selection based on individual plants would give rapid progress for the betterment of the traits under study.

Key Words: *Gossypium hirsutum* L.; Metric traits; Diallel analysis; Genetic variation; Inheritance pattern

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is the mainstay of both agriculture as well as economy of Pakistan. It accounts for 8.6% of the value added in agriculture and about 1.9% to GDP (Anonymous, 2006). Although a lot of research work had already been done with the objective of increasing total cotton production of the country, Pakistan is still lagging behind in production on per unit area basis as compared to some other cotton growing countries in the world (Ahmad *et al.*, 2000). This emphasizes the breeders to continue their efforts for exploiting the available genetic resources through plant improvement techniques. Both exotic and local germplasm may be evaluated advantageously for the desirable characters involved in plant improvement program. For the success of such a program, the breeders are required to collect information about the inheritance pattern governing various plant traits of economic importance in the parental plant material (Nadeem & Azhar, 2004).

Previously, many scientists remained interested to identify the inheritance pattern of metric traits like number of monopodia, number of sympodia, boll weight, lint percentage and seed cotton yield and found that these characters are controlled by the genes with both the additive and non-additive effects. For example, the investigations of Ali *et al.* (2000), Amin and Hussain (2000), Kumaresan *et al.* (2000), Subhan *et al.* (2002), Ahmad *et al.* (2003), Khan *et al.* (2003), Saghir *et al.* (2003) and Nadeem and Azhar (2004) revealed additive type of gene action with partial dominance in all the above mentioned traits, whilst some other scientists reported the presence of genes showing over-dominance for number of monopodia and sympodia (Ahmad *et al.*, 2000; Naveed *et al.*, 2005), boll weight (Murtaza *et al.*, 2005) lint percentage and seed cotton yield (Haq & Azhar, 2004; Murtaza *et al.*, 2005).

The present study envisages the analysis of plant material comprising a small sample of cotton genotypes of *Gossypium hirsutum* L. taken from the available germplasm to detect the presence of additive, dominance and epistatic types of gene action and estimate the degree of dominance and classify parents according to their breeding values and relative concentration of increaser and decreaser alleles controlling seed cotton yield and its components. These objectives were attained by exploiting diallel analysis described in detail by Mather and Jinks (1982).

MATERIALS AND METHODS

The present investigations were carried out in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the years 2005-07. The plant material for these studies was developed by crossing five local Pakistani genotypes, namely NIAB-78, CIM-499, LSS, RH-112 and NIAB-Krishma, being different from each other for the characters, in a complete diallel fashion. All the entries belonging to *Gossypium hirsutum* L. were maintained by selfing. The parents were grown in 12 x 12 inch earthen pots placed in green house during November 2005. The proper growing conditions i.e., temperature (25 to 30ºC) and light duration was possibly controlled in a way to provide favorable conditions for germination and growth of the plants. At the time of flowering, all possible crosses including self and reciprocals among the above mentioned genotypes were made following 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 F_1 hybrid seed.

The F_0 seeds of 20 hybrids and their five parents were field planted in three replications according to randomized complete block design during May, 2006. Each of the 25 entries in a replication was planted in a single row having 8 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 the time of harvesting. At maturity, data on number of monopodia, number of sympodia, boll weight, lint percentage and seed cotton yield were collected from 5 guarded plants on the individual plant basis in field and laboratory. The data collected were analyzed to determine significant genotypic differences of variance among the twenty F_1 hybrids and their parents following Steel *et al.* (1996), because the diallel analysis is valid only when significant genotypic differences exist in the data (Azhar & McNeilly, 1988).

The simple additive-dominance model suggested by Hayman (1954) and Jinks (1954) was followed for genetic analysis. Components of genetic variation viz; D (additive effects of genes), H_1 and H_2 (dominance effects of genes), F (an estimate of the relative frequency of dominant to recessive alleles in the parental lines) and h^2 (overall dominance effects of heterozygotes), narrow sense heritability (h^2n.s.) and error variance (E) were calculated according to Mather and Jinks (1982).

RESULTS AND DISCUSSION

Results of the analysis of variance indicated significant differences at the 0.01% probability level for all the traits among genotypes (Table I). The mean squares for the traits are represented in Table I. The significance of the 'F' test indicated that the parents were different for all the characters under study. Adequacy tests are given in Table II to get information about the validity of the data for additive-dominance model. The results revealed that this variability could be transmitted to the progeny, thus validated the genetic analysis of the traits following the technique of Mather and Jinks (1982). The results of different metric traits from progeny are discussed as under:

Number of monopodia. Adequacy tests (Table II) to assess the fitness of the data for number of monopodia revealed that it was fully adequate for genetic analysis. The estimates of genetic components of variation (Table III) exhibited significance of additive and dominant effects of genes. High and significant value of D over H_1 and H_2 demonstrated the presence of additive genetic effects and it is compatible with the results showed by $(H_1/D)^{1/2}$, which is less than unity (0.749). The unequal values of H_1 and H_2 revealed asymmetrical distribution of genes in the parents, which was in accordance with the value provided by $H_2/4H_1$=0.309. An estimate of the relative frequency of dominant to recessive alleles in the parental lines (F=0.004) indicated the preponderance of more dominant alleles. This was well supported by the value of $(4DH_1)^{1/2}$+F/$(4DH_1)^{1/2}$-F= 1.075, which is higher than unity. Positive value of h^2 evidenced that the direction of dominance was towards parents. The significant estimate of environmental variance (E=0.019) indicated the presence of some blocking effects.

Table I. Mean squares obtained from simple analysis of variance of F_1 hybrids and their parents for number of monopodia (NM), number of sympodia (NS), boll weight (BW), lint percentage (LP) and seed cotton yield (SCY) in *Gossypium hirsutum* L.

Source of Variation	NM (No.)	NS (No.)	BW (G)	LP (%)	SCY (G)
Replications	0.036^{NS}	0.368^{NS}	0.00016^{NS}	0.1988^{NS}	2.474^{NS}
Genotypes	1.851**	65.804**	0.7499**	2183.03**	22.448**
Error	0.052	0.395	0.0063	4.1467	0.866

*,** = Significant at 0.05 and 0.01 levels, respectively. NS = Non-significant

Moderate estimate of narrow sense heritability (0.66) suggested that improvement for this trait could be made through individual plant selection in the latter generations and this was consistent with findings of Shanti and Raveendran (1999) and Ahmad *et al.* (2003), Ahmed *et al.* (2006). Graphical representation of number of monopodia in Fig. 1 illustrated the predominance of additive gene action for this character as the regression line intersected Wr axis above the origin. These results were supported by the studies of Paxasia *et al.* (1998), Ali *et al.* (2000) and Khan *et al.* (2003). This recommended selection as an appropriate breeding method for improvement in this trait. Array points on the graph (Fig. 1) represented maximum dominant genes for RH-112 followed by NIAB-78 and LSS, whereas variety CIM-499 being farthest from the point of origin possessed maximum recessive genes.

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Number of symopodia. All the adequacy tests (Table II) recommended full fitness of the data of number of sympodia

Table II. Adequacy tests of additive-dominance model for 5×5 diallel in cotton

Characters	Y-intercept (a)	Joint regression (b)	Test for b=0	Test for b=1	Wr+Vr	Wr-Vr	Remarks
No. of monopodia	0.022	0.86± 0.10	8.09**	1.31 ^{NS}	8.037**	0.654 ^{NS}	Full adequacy for additive-dominance model
No. on sympodia	1.146	1.20± 0.055	21.80**	-3.64 ^{NS}	25.70**	2.61 ^{NS}	Full adequacy for additive-dominance model
Boll weight	0.009	0.89 ± 0.040	22.19**	2.51^{NS}	2.247 ^{NS}	3.507 ^{NS}	Partial adequacy for additive-dominance model
Lint percentage	0.379	0.92± 0.17	5.34*	0.44^{NS}	0.854 ^{NS}	0.183 ^{NS}	Partial adequacy for additive-dominance model
Seed cotton yield	69.71	0.74± 0.11	6.56*	2.30 ^{NS}	30.53**	8.37**	Partial adequacy for additive-dominance model

Table III. Components of variation for different traits in *Gossypium hirsutum* L. in F1 generation

Components of variation	NM (No.)	NS (No.)	BW (G)	LP (%)	SCY (G)
D	0.120 ± 0.008*	12.145 ± 0.463*	0.041 ± 0.0007*	1.808 ± 0.099*	296.78± 9.23*
H_1	0.027 ± 0.021	5.040 ± 1.252*	0.0056± 0.002*	-0.042 ± 0.269	70.56 ± 24.94*
H_2	0.034 ± 0.019	4.164 ± 1.135*	0.0056± 0.002*	0.077 ± 0.244	67.39 ± 22.62*
F	0.004 ± 0.019	6.197 ± 1.158*	-0.0103 ±0.002	-0.140 ± 0.249	27.77 ± 23.07
h^2	0.016 ± 0.012	0.535 ± 0.766	-0.0009 ± 0.001	0.304 ± 0.164	- 0.954 ± 15.27
E	0.019 ± 0.003*	0.149 ± 0.189	0.002 ± 0.0003*	0.352 ± 0.040*	1.511 ± 3.77
$(H_1/D)^{1/2}$	0.479	0.644	0.37	0.152	0.51
$H_2/4H_1$	0.309	0.206	0.25	-0.460	0.23
$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	1.075	2.311	0.49	0.594	1.22
$h^2_{(n.s)}$	0.66	0.74	0.87	0.71	0.86

for additive-dominance model. The calculation of genetic components of variation (Table III) depicted additive as well as dominant gene control, because of the significant values of D and H_1. The value of $(H_1/D)^{1/2}$ =0.644 also revealed incomplete and partial dominance. Asymmetrical allocation of genes was confirmed due to unequal estimates of H_1 and H_2, which was supported by the value of $H_2/4H_1$=0.206. The positive value of F (6.197) and proportion of dominant to recessive alleles (2.311) exhibited more frequency of dominant ones. Direction of dominance towards parents was advocated by the positive value of h^2. External effects (0.149) were found to be non-significant.

Moderately high value of narrow sense heritability (0.74) was an indicative of additive gene action suggesting the feasibility of selection in the early generation Shah *et al.* (1992) reported similar results. A view of Fig. 2 gave the expression of additive gene action for number of sympodia, which was in accordance with the discoveries of Ali *et al.* (2000), Ahmad *et al.* (2003) and Khan *et al.* (2003) who also investigated additive genetic effects for the character. These results rendered importance to selection procedure for improvement in the character. The position of the array points on regression line (Fig. 2) showed that variety NIAB-Krishma had maximum dominant genes, while variety LSS possessed maximum recessive genes, which confirmed the genetic variability of the parents for number of sympodia.

Boll weight. The scaling tests of the data for boll weight (Table II) indicated partial adequacy for additive-dominant model. Significant and higher magnitude of H_1 and H_2 than D for this trait (Table III) provided evidence for the presence of both dominance and additive type of gene

Fig. 1. Wr/Vr graph for number of monopodia

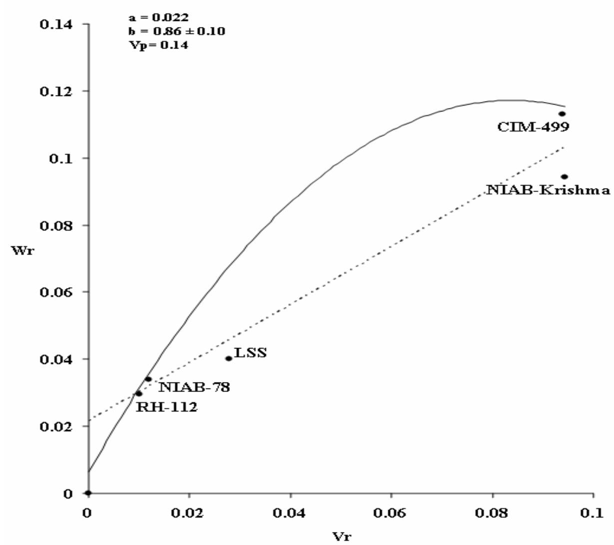
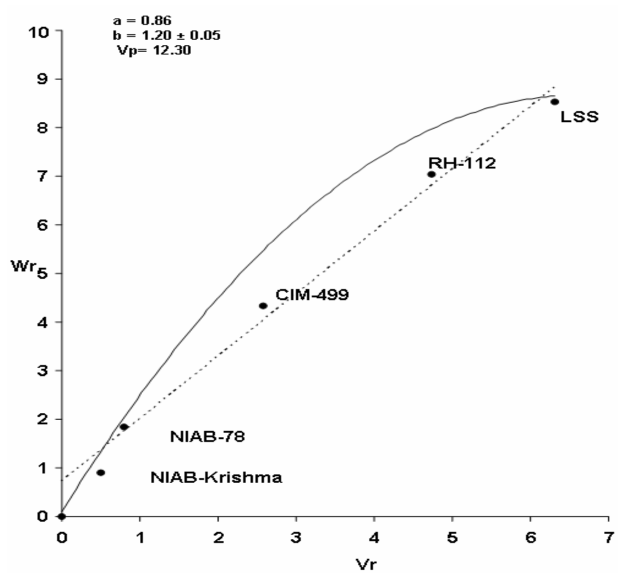


Fig. 2. Wr/Vr graph for number of sympodia



effects. Greater value of H_1 over D indicated predominance of dominance effects over additive gene effects. But $(H_1/D)^{1/2}$ ratio did not exceed unity, which proved the presence of partial dominance involved in the phenotypic expression of the trait. The value of $H_2/4H_1$ ratio (0.25) suggested equal positive and negative allelic frequencies in the parents, while proportion of $(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$ lesser than unity (0.49) indicated preponderance of recessive

Fig. 3. Wr/Vr graph for boll weight

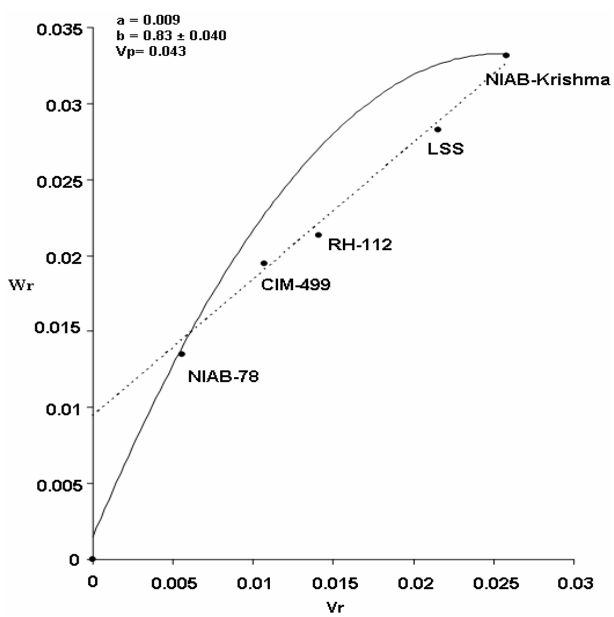
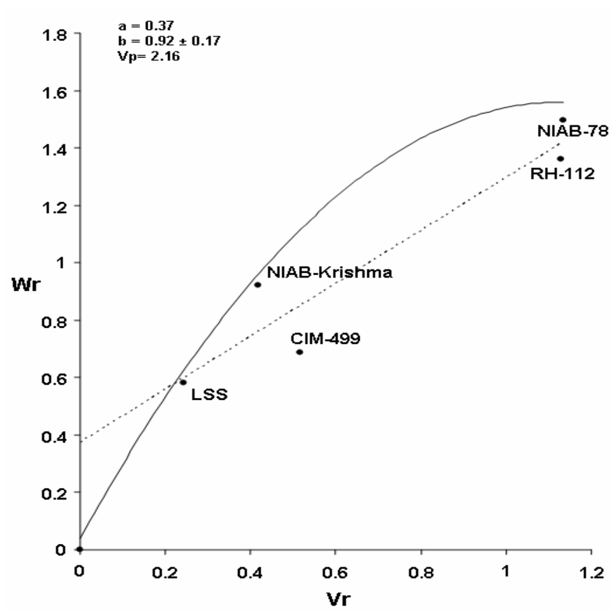


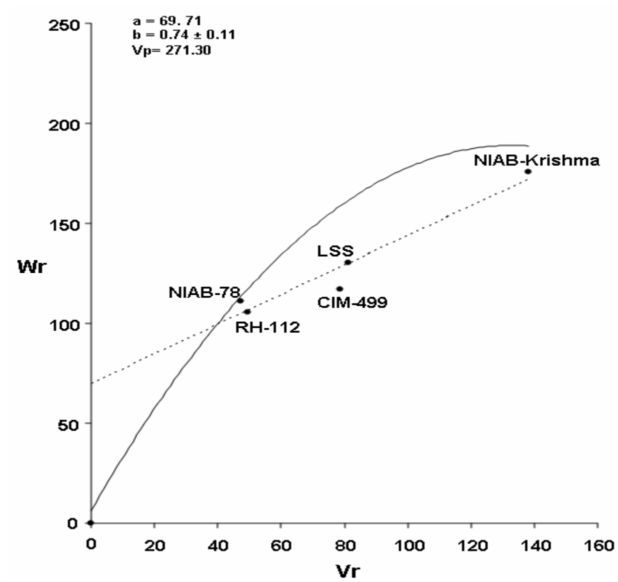
Fig. 4. Wr/Vr graph for lint percentage



alleles in the parents. The negative value of h^2 suggested that dominance is towards offspring. The negative value of F for boll weight revealed that the parents had more recessive alleles. High estimate of narrow sense heritability (0.87) in Table III was an indicator for the presence of additive gene action. Within replication effects (E) were also found to be considerable.

A study of Fig. 3 illustrated additive type of gene action controlling the inheritance of this trait as the regression line intercepted the Wr-axis above the point of origin. As the regression line is of a unit slope, it confirmed the absence of epistasis. Ahmad *et al.* (2000) and Nadeem

Fig. 5. Wr/Vr graph for yield of seed cotton



and Azhar (2004) too provided the same results, which revealed the importance of high heritability and additive genetic control for the improvement of the character and suggested that this trait could be made better through individual plant selection.

Lint percentage. Tests of validity (Table II) for lint percentage confirmed the partial adequacy of for additive-dominance model. The components of variation (Table III) exhibited preponderance of D over H_1 and H_2, which demonstrated the presence of additive genetic effects and it is well-matched with the result of $(H_1/D)^{1/2}$, which is less than unity (0.152). Evidance for unequal gene frequencies in the parents was suggested by the data as H_2/4H1 ratio (-0.46) provided the same results. An estimate of F (-0.14) showed that more recessive alleles are involved and this was verified by the value of $(4DH_1)^{1/2}$+F/$(4DH_1)^{1/2}$-F= 0.594. Positive h^2 value proved that the direction of dominance was towards parents. The significant estimate of environmental variance (E=0.019) indicated the presence of some external effects.

Graphical representation of the data for lint percentage (Fig. 4) showed the predominance of additive genetic effects in the manifestation of this character. The results were supported by those of Amin and Hussain (2000), Subhan *et al.* (2002), Saghir *et al.* (2003). Array points on the graph (Fig. 4) indicated maximum dominant genes for LSS, whereas variety NIAB-78 secured maximum recessive genes. Moderate estimate of narrow sense heritability (0.71) and preponderance of additive gene control advocated the utilization of individual plant selection for improvement of this trait.

Seed cotton yield. Tests of fitness for the additive-dominance model (Table II) showed partial adequacy of seed cotton yield data for the analysis. The estimates for genetic components of variation for this character are given in Table III. The positive and significant values of D and H suggested control of both the additive and dominant gene effects, which corresponded to the findings of Sanyasi (1991) and Ahmad *et al.* (2003). The higher value of D than H1 indicated additive control, which was also revealed by the value of $(H_1/D)^{1/2}$ =0.51. Unequal values of H1 and H2 signified asymmetrical distribution of positive and negative alleles. The estimate of $H_2/4H_1$ ratio (0.23) provided the same consequences. The positive value of F (27.77) showed excess of dominant genes for the expression of the character under study. This was soundly supplemented by the ratio of $(4DH_1)^{1/2}$+F/$(4DH_1)^{1/2}$-F which was (1.22). Negative h^2 advocated that the direction of dominance is towards hybrids. The environmental influence was non-significant. Narrowsense heritability (0.86) with the predominance of additive gene action suggested that selection based on single plant will give better progress for the character under study. Kumaresan *et al.* (2000) and Murtaza (2005) also reported high heritability for seed cotton yield and conferred the same suggestion.

The positive intercept of Wr/Vr regression line (Fig. 5) reflected additive gene action. Similar results were obtained by Kumaresan *et al.* (2000), Subhan *et al.* (2002) and Ahmad *et al.* (2003). Position of array points on regression line expressed that variety RH-112 and NIAB-Krishma secured maximum dominant and recessive genes respectively. This showed the genetic diversity of the parents for this trait.

The results concluded that the estimates of h^2 n.s. for all the characters, within the limits of present study were overgenerous. The high estimates might be expected since the genetic mechanism of all the characters appeared to be predominantly influenced by additive genetic effects. The presence of additive gene action and high heritability of seed cotton yield and its components suggest 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.

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