# Genetic Mechanisms Controlling Seed Cotton Yield and its Components in $F_1$ and $F_2$ Generations of *G. hirsutum* L.

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## ABSTRACT

An eight parent diallel cross data were analysed following simple additive-dominance model, in order to study genetic mechanisms controlling of seed cotton yield and its components in $F_1$ and $F_2$ generation of *Gossypium hirsutum* L. Regression analysis of $V_r$ and $W_r$ revealed that the genetic model was fully adequate for analysing the data on boll weight, ginning percentage and seed cotton yield in both the populations, whereas the model was appropriate only for $F_2$ data on number of bolls. The components of variation showed that additive genetic effects were predominant in the inheritance of all the characters, however the presence of overdominance was indicated in $F_1$ generation. The estimates of narrowsense heritabilities of the four characters were modest in $F_1$ generation, and inflated in $F_2$ generation. The presence of additive genetic effects and high estimates of heritabilities in $F_2$ generation suggests that the population is readily available for selection, and thus effective and rapid improvement in seed cotton yield is possible by making concurrent selection of the components of yield studied.

**Key Words:** Additive genes; Overdominance; *Gossypium hirsutum* L.; Heritabilities.

## INTRODUCTION

Plant yield in *hirsutum* species, as in other crops, is contributed by different components like number of bolls, average boll weight, ginning percentage, and others. Thus direct selection for these characters either separately or concurrently would increase seed cotton yield of a plant. Before the use of a selection method most appropriate for selecting the desired plants from the plant material, the availability of information about genetic components of variation, additive, non-additive and epistasis is essential.

Previous studies reveal that yield of seed cotton and its various components were controlled by the genes acting non additively (Dani & Kohel, 1989; Tariq *et al.*, 1992; Azhar & Rana, 1993; Tariq *et al.*, 1995). By contrast the studies of Singh and Singh (1981), Nadarajan and Rangaswamy (1990), Akbar *et al.* (1993) and Saeed *et al.* (1996) showed the preponderance effects of additive genes on plant yield and its contributing factors, and the estimates of heritabilities varied depending upon the magnitude of the effects of the genes. Thus the inheritance pattern of plant yield and its components differed according to the nature of the genetic material studied. The present work reports the genetic basis of variation in seed cotton yield, number of bolls, boll weight and ginning percentage in the $F_1$ and $F_2$ generations developed by crossing exotic and indigenous varieties of *G. hirsutum* L. The genetic analysis of the data was made following simple additive dominance model of Hayman (1954a,b) and Jinks (1954).

## MATERIALS AND METHODS

The plant material used in the present study was developed by crossing the eight parents in all possible combinations. The eight parents belonging to *Gossypium hirsutum* L. were selected from the gene pool maintained in the department on the basis of differences in the characters studied. The genotypes namely BJA, Reba-B50, A89/FM, Changmiah (exotics), and CIM250, S12, NIAB78 and AUH50 (local), were genetically and geographically unrelated.

The parents were planted in a glasshouse and crossed when they started to flower. During emasculation and pollination all necessary precautions were taken to avoid contamination of the genetic material. A large number of pollinations were made to produce sufficient quantity of the $F_1$ seed. The half of the seeds of 56 hybrids and their parents were field planted in single row plots during the ensuing season to develop $F_2$ seed, and the other half was kept to develop $F_1$ generation next year.

Cotton is a partially cross-pollinated crop, and therefore all the plants in $F_1$ generation were covered with glassine bags to effect complete self pollination of the $F_1$ plants. The $F_1$ and $F_2$ populations were grown together in a field during June 1993 following randomized complete block design with 3 replications. The seeds of the 56 $F_1$ hybrids and the 8 parents were planted in single rows with plants spaced at a distance of 30 cm within a row and 75 cm between the rows, and thus there were 12 plants in each row. Similarly 64 $F_2$ entries were planted in a plot measuring 3.3x6 $m^2$, having 96 plants, of each family in each

**Table I. Variances ($V_r$) and Co-variance ($W_r$) of eight parents for seed cotton yield and its components**

| Parents | Generations | Number of bolls | | Boll weight | | Lint percentage | | Seed cotton yield | |
|---|---|---|---|---|---|---|---|---|---|
| | | $V_r$ | $W_r$ | $V_r$ | $W_r$ | $V_r$ | $W_r$ | $V_r$ | $W_r$ |
| NIAB78 | $F_1$ | 22.64 | 8.69 | 0.17 | 0.28 | 0.82 | 0.95 | 555.60 | 555.83 |
| | $F_2$ | 20.14 | 27.81 | 0.11 | 0.20 | 0.55 | 1.28 | 688.71 | 1152.59 |
| S12 | $F_1$ | 45.07 | 23.08 | 0.32 | 0.39 | 0.93 | 1.10 | 1694.94 | 1380.51 |
| | $F_2$ | 18.91 | 31.93 | 0.10 | 0.19 | 0.97 | 1.69 | 837.38 | 1324.30 |
| AUH50 | $F_1$ | 25.57 | 5.95 | 0.05 | 0.13 | 0.83 | 1.16 | 431.36 | 391.33 |
| | $F_2$ | 18.45 | 33.66 | 0.09 | 0.19 | 0.50 | 1.16 | 498.75 | 1046.51 |
| CIM250 | $F_1$ | 23.91 | 4.66 | 0.06 | 0.15 | 1.09 | 1.27 | 486.97 | 375.41 |
| | $F_2$ | 10.67 | 17.72 | 0.10 | 0.20 | 0.87 | 1.61 | 241.82 | 661.66 |
| Changmiah | $F_1$ | 26.75 | 5.60 | 0.06 | 0.15 | 0.43 | 0.76 | 329.60 | 73.78 |
| | $F_2$ | 23.13 | 35.44 | 0.07 | 0.17 | 0.66 | 1.38 | 589.66 | 1119.31 |
| BJA | $F_1$ | 32.84 | -1.67 | 0.15 | 0.26 | 1.46 | 1.18 | 558.60 | 215.40 |
| | $F_2$ | 12.84 | 26.80 | 0.13 | 0.23 | 0.66 | 1.40 | 524.02 | 1077.40 |
| A89/FM | $F_1$ | 9.83 | -1.13 | 0.03 | 0.12 | 0.60 | 0.57 | 82.48 | -72.69 |
| | $F_2$ | 11.80 | 26.41 | 0.10 | 0.19 | 0.71 | 1.36 | 326.31 | 844.83 |
| Reba-B50 | $F_1$ | 12.70 | 6.94 | 0.06 | 0.16 | 0.85 | 1.01 | 184.58 | 268.36 |
| | $F_2$ | 11.34 | 23.31 | 0.08 | 0.18 | 0.62 | 1.33 | 343.72 | 836.39 |

replication. One plant on either end of each row of both $F_1$ and $F_2$ population was left as non experimental. At maturity, number of bolls on each of the experimental plants were counted in the field. Whole produce of each plant was weighed to record seed cotton yield (g), and was divided by number of bolls to obtain average boll weight of that plant. For calculating lint percentage, two samples of seed cotton weighing 50 g each of all the plants in a family were ginned and lint obtained was weighed and calculated on percent basis.

## STATISTICAL ANALYSIS

Before subjecting the data to diallel technique, these were analysed by analysis of variance, in order to determine whether the genotypic differences for the characters were significant. Only significant genotypic differences allow the use of simple additive-dominance model for genetic analysis.

Diallel table of the four characters was prepared, and three first degree statistics i.e. variance of the components of each array ($V_r$), co-variance of all the offspring included in each parental array with the non recurrent parent ($W_r$), and variance of the parental means ($V_0L_0$), were calculated. The second degree statistics necessary to calculate include means of array variances ($V_1L_1$), the variances of means of arrays ($V_0L_1$), and the means of array co-variances ($W_0L_0$). These statistics were used for the estimation of four genetic components of variation, D (additive effects of genes), $H_1$ and $H_2$ (dominance effects of genes), and F, which provides an estimate of the relative frequency of dominant to recessive alleles in the parental lines and the variation in dominance over the loci. Hence F will

be positive, whenever the dominant alleles are more frequent than the recessive alleles, irrespective of whether or not the dominant alleles have increasing or decreasing effects. In following the additive-dominance model, reciprocal $F_1$ families have identical expectations and are generally averaged before computing these statistics, hence halving the environmental component, E (Mather and Jinks, 1982). For calculating the genetic parameters in $F_2$ population the formulae used in $F_1$ were modified as proposed by Verhalen and Murray (1969) and Verhalen *et al.* (1971).

To determine the adequacy of the simple additive-dominance model to account for the analysis of the data, joint regression analysis, one of the two scaling tests, of variance ($V_r$) and co-variance ($W_r$) was carried out. According to Hayman (1954b), the regression co-efficient (b) must deviate significantly from zero, but not from unity, if all the assumptions underlying the genetic model were met. Narrowsense heritabilities of the number of bolls, boll weight, ginning percentage and seed cotton yield were calculated following the formula given by Mather and Jinks (1982).

## RESULTS

The mean squares obtained from analysis of variance of all the characters in both the populations were significant (P≤0.01), revealing that the hybrids and their parents differed for these characters. The significant genotypic differences allowed the use of simple additive-dominance model for analysing the data (the results of analysis of variance are not given here). The variances ($V_r$) and co-variances ($W_r$) of the

**Table II. Estimation of components of variation in number of bolls and boll weight in $F_1$ and $F_2$ generations of *G. hirsutum* L.**

| Components | No. of bolls | Boll weight | |
|---|---|---|---|
| | $F_2$ | $F_1$ | $F_2$ |
| $V_{0L0}$ | 66.88 | 0.501 | 0.398 |
| $V_{1L1}$ | 15.91 | 0.111 | 0.097 |
| $V_{0L1}$ | 12.31 | 0.086 | 0.094 |
| $W_{0L0}$ | 27.88 | 0.205 | 0.193 |
| D | $65.55^* \pm 20286$ | $0.4997^* \pm 0.0084$ | $0.3980^* \pm 0.0016$ |
| $H_1$ | $52.84^* \pm 21.022$ | $0.1200^* \pm 0.0194$ | $0.0469^* \pm 0.0143$ |
| $H_2$ | $39.64^* \pm 18.289$ | $0.0955^* \pm 0.0169$ | $0.0412^* \pm 0.0124$ |
| F | $40.55^* \pm 10.779$ | $0.1784^* \pm 0.0199$ | $0.449^* \pm 0.0073$ |
| $h^2$ | $-16.71 \pm 12.260$ | $0.1392^* \pm 0.0113$ | $-0.0082^{NS} \pm 0.0084$ |
| E | $1.287^* \pm 0.762$ | $0.0014^{NS} \pm 0.0028$ | $0.00077 \pm 0.00052$ |
| $\sqrt{H_1/D}$ | 0.4488 | 0.4900 | 0.1716 |
| $H_2/4H_1$ | 0.1875 | 0.1990 | 0.2193 |
| $\sqrt{4DH_1} + F / \sqrt{4DH_1} - F$ | 5.430 | 2.1460 | 1.9800 |
| $\frac{1}{2}F/\sqrt{[D(H_1 - H_2)]}$ | 0.689 | 0.8069 | 4.770 |
| Narrowsense heritability | 1.027 | 0.8725 | 1.0197 |

eight parents for seed cotton yield and its three components are given in Table I.

The results of joint regression analysis showed that in $F_1$ generation regression line for number of bolls ($b=0.437\pm0.219$) did not deviate significantly from zero, whilst for boll weight ($b=0.990\pm0.047$), lint percentage ($b=0.586\pm0.201$), and seed cotton yield ($b=0.847\pm0.110$), these deviated significantly from zero, and are also of unit slope. In the $F_2$ generation, regression slope for number of bolls ($1.02\pm0.259$), boll weight ($0.985\pm0.046$), lint percentage ($1.060\pm0.091$), and seed cotton yield ($1.040\pm0.091$) deviated significantly from zero, and all of them were of unity. The coefficients of regression line for all the characters are given in the figures. The unit slope of regression lines suggests that all the assumptions underlying the additive-dominance model were met (Hayman, 1954a) and thus there was no indication of the presence of epistasis. Thus the additive-dominance model was adequate for these characters, and it was found not

**Table III. Estimation of components of variation in lint per centage and seed cotton yield in $F_1$ and $F_2$ generations of *G. hirsutum* L.**

| Components | Lint percentage | | Seed cotton yield | |
|---|---|---|---|---|
| | $F_1$ | $F_2$ | $F_1$ | $F_2$ |
| $V_{0L0}$ | 1.69 | 3.00 | 1412.60 | 2293.50 |
| $V_{1L1}$ | 0.63 | 0.69 | 540.50 | 506.20 |
| $V_{0L1}$ | 0.63 | 0.65 | 203.80 | 456.10 |
| $W_{0L0}$ | 1.0 | 1.41 | 398.49 | 1007.80 |
| D | $1.6664^* \pm 0.0497$ | $3.00^* \pm 0.0275$ | $1391.14^* \pm 115.45$ | $2272.50^* \pm 33.88$ |
| $H_1$ | $1.1193^* \pm 0.3428$ | $0.6157^* \pm 0.2528$ | $1921.68^* \pm 0.265.40$ | $785.08^* \pm 311.58$ |
| $H_2$ | $0.9263^* \pm 0.2983$ | $0.5017^* \pm 0.2200$ | $1303.90^* \pm 230.90$ | $519.14^{NS} \pm 271.07$ |
| F | $-0.6633NS \pm 0.3524$ | $0.7910^* \pm 0.1296$ | $1199.04^* \pm 272.80$ | $1050.49^* \pm 159.77$ |
| $h^2$ | $0.1916^* \pm 0.2000$ | $0.0617NS \pm 0.1475$ | $1069.56^* \pm 154.85$ | $-275.13NS \pm 181.79$ |
| E | $0.0272NS \pm 0.0497$ | $0.0058NS \pm 0.0092$ | $21.47NS \pm 38.48$ | $20.21NS \pm 11.29$ |
| $\sqrt{H_1/D}$ | 0.8196 | 0.2265 | 1.1753 | 0.2938 |
| $H_2/4H_1$ | 0.2069 | 0.2037 | 0.1696 | 0.1653 |
| $\sqrt{4DH_1} + F / \sqrt{4DH_1} - F$ | 0.6092 | 3.7845 | 2.1579 | 8.3660 |
| $\frac{1}{2}F/\sqrt{[D(H_1 - H_2)]}$ | **-0.5848** | **0.6763** | **0.6467** | **0.6756** |
| Narrowsense heritability | 0.8298 | 1.0780 | 0.5382 | 1.1200 |

suitable for the data on number of bolls in the $F_1$. Estimation of genetic components of variation in all the characters are given in the respective table.

**Estimation of genetic components of variation**

**Number of bolls.** The genetic components of variation, D and $H_1$ and $H_2$ presented in Table II were significant, indicating the presence of additive and non additive genes effects controlling the inheritance of number of bolls in the $F_2$, but relatively greater size of D than $H_1$ and $H_2$ suggests that additive gene effects were important in affecting the character variation. The greater magnitude of $H_1$ than $H_2$, and the low ratio of $H_2/4H_1=0.188$ indicated the presence of unequal distribution of the genes in the parents. The degree of dominance was partial ($\sqrt{H_1/D}$ =0.449), and it occurred towards the parents with low number of bolls, because sign of $h^2$ is minus. The positive and significant value of F suggests that dominant genes were more frequent than recessive genes, a suggestion substantiated by the ratio $[\sqrt{4DH_1} + F/\sqrt{(4DH_1)} - F]$. The level of dominance varied from one loci to another, as the ratio of $\frac{1}{2}F/\sqrt{[D(H_1 - H_2)]}$ appeared to be 0.69.

The distribution of array points along the regression line (Fig.1) suggests that the maximum number of dominant genes for number of bolls were present in CIM250 and Reba-B50, as these varieties occupied the nearest position to point of origin. By contrast, Changmiah, S12, NIAB78, AUH50, being farther from the origin contained the maximum number of recessive genes for the character.

**Fig. 1. $W_r/V_r$ graph for number of bolls per plant ($F_2$)**
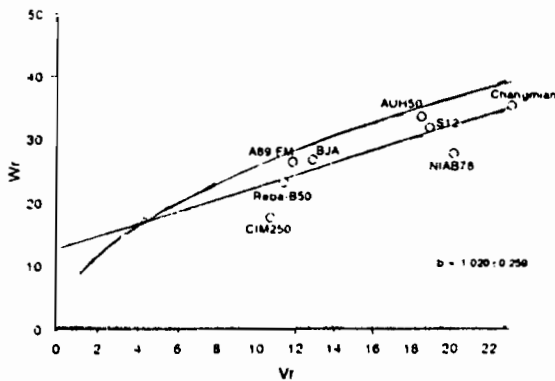


**Boll weight.** The relative sizes of D, $H_1$ and $H_2$, reveal that effects of additive genes were important in affecting variations in boll weight, because magnitude of D is greater than those of $H_1$ and $H_2$ (Table II). In both $F_1$ and $F_2$ generations the degree of dominance was partial as

the ratio of $\sqrt{H_1/D}$ is lesser than 1. The estimate of $H_1>H_2$, therefore the genes for boll weight were distributed unequally in the parents, and this conclusion was strengthened by the low ratio of $H_2/4H_1=0.20$ in $F_1$ and 0.22 in $F_2$ populations. The positive value of F is significant, showing that there were more dominant genes than recessive genes in the parents, and is supported by $[\sqrt{4DH_1} + F/\sqrt{(4DH_1)} - F]$. The positive sign of $h^2$ in $F_1$ indicates that dominance was directional towards the parent with higher boll weight, and by contrast the negative sign of $h^2$ in $F_2$ suggested that direction of dominance was towards the parent with low boll weight. The estimate of $\frac{1}{2}F/\sqrt{[D(H_1-H_2)]}$ is relatively high which indicates that level of dominance at all the loci was constant in $F_1$ and $F_2$ generations. Since the magnitude of additive component is greater than that of non additive, therefore estimates of narrowsense heritabilities in both the populations are high i.e. 87% and 100% respectively.

**Fig. 2. $W_r/V_r$ graph for boll weight**
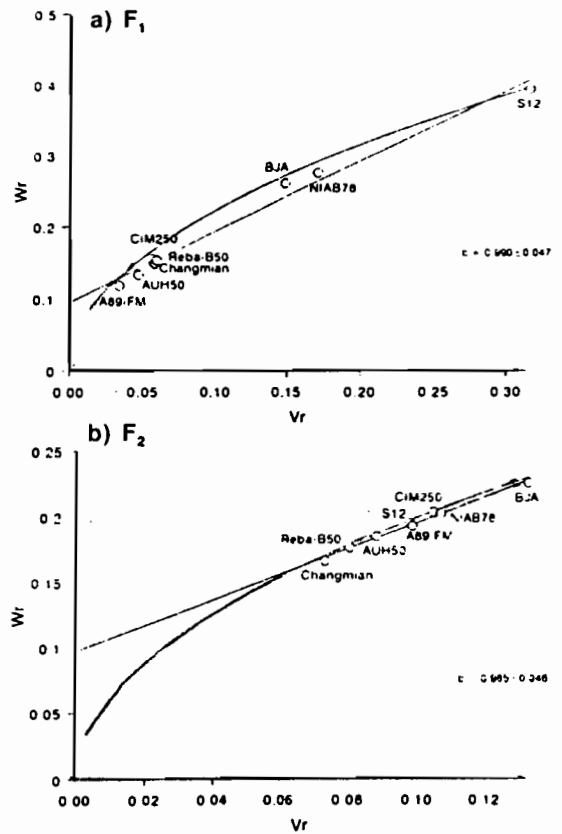


The distribution of varietal points in Fig. 2a reveals that line A89/FM and AUH50 being closer to point of origin contained the maximum number of

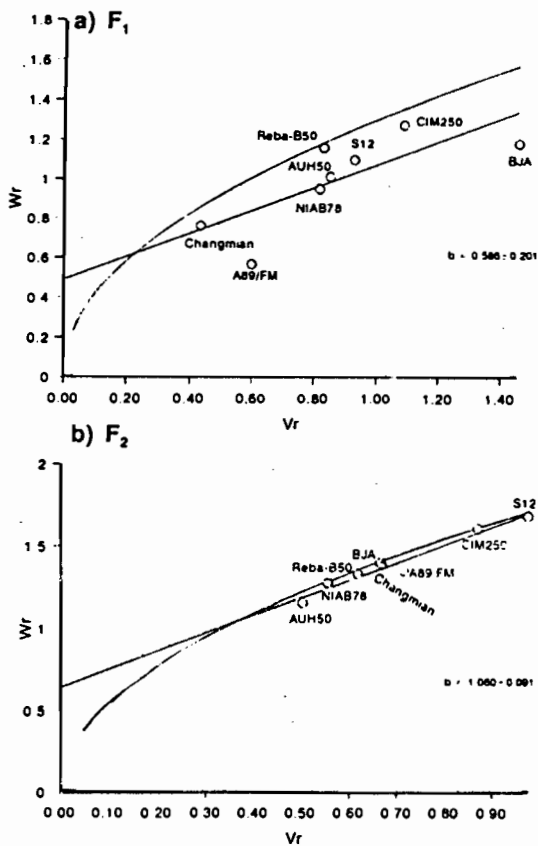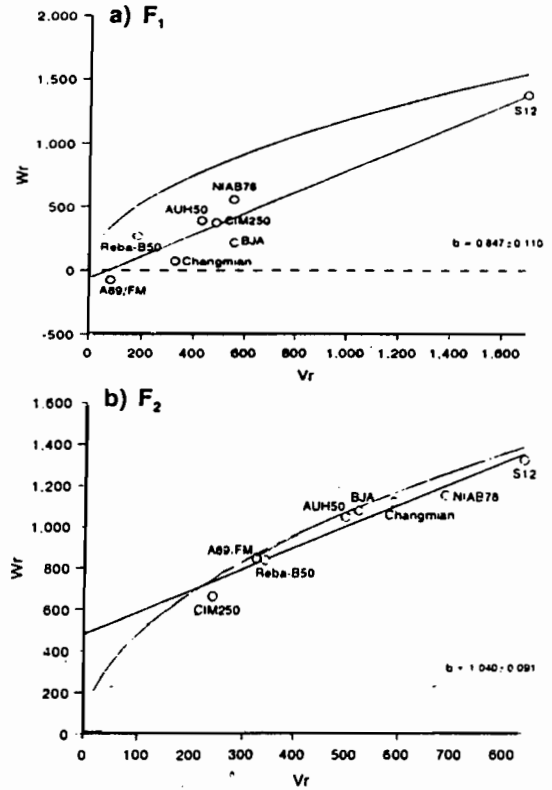**Fig. 3. $W_r/V_r$ graph for lint per centage**



**Fig. 4. $W_r/V_r$ graph for seed cotton yield**



dominant genes, and S12, BJA and NIAB78 being away from the origin carried maximum number of recessive genes for boll weight. The remaining varieties BJA and NIAB78 formed another group intermediate between the two. In $F_2$ population Changmiah, Reba-B50 and AUH50 were found to carry maximum number of dominant genes, and BJA contained the most recessive genes for boll weight (Fig. 2b).

**Lint percentage.** The relative sizes of D, $H_1$ and $H_2$ components, given in Table III, indicate that the extent of D item is greater than that of $H_1$ and $H_2$, and therefore the genes with additive effects controlled variation in lint percentage in $F_1$ and $F_2$ populations. Because $H_1 > H_2$, therefore frequency of gene distribution in the parents was unequal, and the low ratio of $H_2/4H_1$ i.e. 0.20 also provided further evidence of unequal gene distribution in the parents in both the populations. The negative value of F and low ratio of $[\sqrt{4DH_1} + F/\sqrt{(4DH_1)} - F]$ (0.61) indicate that recessive genes were more frequent in $F_1$, whilst in $F_2$, the high positive sign of F (3.78) reveals that dominant genes were more frequent than recessive genes. The degree of dominance is partial ($\sqrt{H_1/D}$ =0.82, 0.23) in $F_1$ and $F_2$ population

respectively. The positive sign of $h^2$ showed that dominance of the genes was directional to the parents with high lint percentage in both the generations. The estimate of narrowsense heritabilities of lint percentage in $F_1$ is 83% and 100% in $F_2$ population.

An examination of Fig.3a reveals that Changmiah and A89/FM being closer than BJA and CIM250 to the point of origin contained the maximum number of dominant genes for lint percentage, and BJA and CIM250 carried the maximum number of recessive genes. In $F_2$, AUH50 and NIAB78 were closer to the origin than S12 and CIM250, and thus were shown to possess the maximum number of dominant genes for lint percentage (Fig. 3b).

**Seed cotton yield.** The relative magnitudes of components of variation indicate that both additive and dominance genetic effects were important in affecting variation in seed cotton yield in $F_1$ and $F_2$ (Table III). In $F_1$ the extent of $H_1 > D$, therefore dominance properties of the genes appeared to be pronounced. In $F_2$, $H_2$ is non significant and $D > H_1$, hence the genes with cumulative action controlled variation in seed cotton yield. The high ratio of $\sqrt{H_1/D}$ =1.17 showed overdominance in $F_1$, and low estimate in $F_2$ (0.29) indicated partial

dominance. As $H_1 > H_2$ in both the populations, the occurrence of unequal gene frequencies was indicated, and this conclusion was substantiated by the ratio of $H_2/4H_1$, which are 0.169 and 0.165 respectively, and are lower than the maximum value of 0.25. The positive and significant value of F reveal that there were more dominant genes than recessive genes in the parents, a conclusion supported by the estimate of ratio of $[(4DH_1)+F/(4DH_1)-F]$. The positive sign of $h^2$ in $F_1$ indicates that dominance was directional towards the parents with high seed cotton yield, and reverse was true for $F_2$ generation. The estimates of $1/2F/\sqrt{[D(H_1-H_2)]}$ were lower in $F_1$ and $F_2$ population, which suggest that level of dominance was not constant at all the loci. The estimate of narrowsense heritability of seed cotton yield in $F_1$ is about 54%, and in $F_2$ 100%.

The distribution of array points along with the regression line (Fig. 4a) indicates that line A89/FM, Changmiah and Reba-B50 being nearer to the point of origin than others contained the carried the maximum number of recessive genes, and NIAB78, AUH50, CIM250 and BJA were intermediate between the two groups. In $F_2$ cultivars CIM250, Reba-B50 and A89/FM contained maximum number of dominant genes, and S12 and NIAB78 possessed maximum number of recessive genes for seed cotton yield (Fig. 4b).

## DISCUSSION

From evolutionary point of view whether it may be occurring under natural conditions or in the experimental laboratory, the availability of variation affected by a significant genetic component is essential for rapid response to selection. The preliminary analysis of variance of $F_1$ and $F_2$ data revealed that there was significant variation in seed cotton yield, number of bolls, boll weight and lint percentage. Analysis of diallel cross data provided useful information about the genetic mechanism controlling the variation observed in the four characters.

Yield of seed cotton is a polygenic character and is the product of an interplay between many genetic and non genetic components, and thus inheritance and manifestation of plant yield is very complex (Poehlman and Sleper, 1995). In $F_1$ generation the genes controlling seed cotton yield showed overdominance (Fig. 4a), and the direction of dominance was towards the parents having higher seed-cotton yield. In $F_2$ population seed cotton yield was controlled by the genes acting additively with varying degree of dominance (Fig. 4b). Similarly for number of bolls, boll weight, lint percentage, the genes were additive in nature. Although the previous investigations showed the presence of non-

additive genes controlling yield of seed cotton and its components (Dani and Kohel, 1989; Tariq et al., 1992; Akbar et al., 1993; Tariq et al., 1995), there is ample evidences available in the literature which support the present information on the genetic controlling system of these characters (Singh & Singh, 1981; Nadarajan & Rangaswamy, 1990; Saeed et al., 1996). The preponderance effects of additive genes on yield of seed cotton and its various components suggest that the inheritance of these characters is not very complex (Liang and Walter, 1968), and thus seems to be advantageous from breeding point of view. Although the presence of additive gene effects suggest that concurrent improvement in all the characters studied here may be made, the possible occurrence of negative correlation between some of the characters may complicate the process of selection. Therefore it is suggested that the nature and strength of correlation between these characters may be studied before subjecting the segregating population to selection. Modest estimates of heritabilities of all the characters in $F_1$ population and higher in $F_2$ population are justified in view of the inheritance pattern of the characters. Saranga et al. (1992) stated that higher magnitude of heritabilities in $F_2$ may have been due to greater recombination of genes or low environmental component. However Falconor and Mackey (1996) stated that the estimates of heritabilities are subject to environmental variation, and therefore these must be reported and used with great care while making selection of desirable combinations. Nonetheless the high estimates are encouraging to a research worker while screening the $F_2$ material to effect improvement in seed cotton yield and other characters.

However, there exists limitation to a general interpretation of the results obtained in the present investigations. Since the eight genotypes were specifically chosen and did not truly represent a random sample of all cotton germplasm, inferences drawn from the present data apply only to the eight parental lines and their hybrids. The extent to which the information derived here applicable to whole of the germplasm of *hirsutum* species is uncertain. Therefore it is suggested that further experiments involving large number of genotypes may be conducted to substantiate the present information on the genetics of seed cotton yield, and its components, under local conditions.

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