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**STUDY OF GENE EFFECTS FOR BOLL NUMBER, BOLL WEIGHT, AND SEED INDEX IN COTTON****Naveed MURTAZA**

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**ABSTRACT**

Sixty four cross combinations were produced by a complete diallel-mating system with eight varieties (Laokra5.5, DPL-7340-424, Fregobract, Glandless 4195-220, SA100, Stoneville-857, S-14 and B-557). The results showed that non-additive over dominance type of gene action governed the inheritance of number of bolls per plant ( $W_r + V_r$ ) 30.31<sup>ns</sup> and boll weight ( $W_r + V_r$ ) 0.063<sup>ns</sup> in  $F_1$  generation. Additive with partial dominance was operative in the inheritance of seed index ( $W_r + V_r$ ) 1.30\*\* in  $F_1$  generation. Estimates of narrow sense heritability for boll number (0.373  $F_1$  and 0.751  $F_2$ ), boll weight (0.238  $F_1$ , 0.230  $F_2$ ) & seed index (0.695  $F_1$ , 1.042  $F_2$ ) along with expected genetic gain because of selection, a potentially useful advance in these characters seems possible to achieve by selecting individual plants showing better qualities. Biparental mating in early generation among the selected lines, or diallel selective mating can be adopted in breeding programs for the improvement of the characters studied.

**KEY WORDS:** Additive and non-additive effects, Cotton, Diallel analysis, Gene action.

## INTRODUCTION

Crop improvement requires the ability to select higher-performing individuals from a population. Identification of superior individuals requires variation in the population. This is usually overcome by crossing unrelated strains to create variation followed by phenotypic screening. Parental selection for creating genetic variability for crop improvement requires knowledge of the likelihood of improving traits of interest. This likelihood is based on the amount and type of genetic control of the trait. The amount of genetic control is influential because improvement of a trait with very small genetic control relative to environmental influences will be difficult.

Several genetic mating designs exist to facilitate dissection of environmental and genetic control underlying quantitative traits in plants. Among the most common mating designs in crop, "improvement" is the diallel analysis. This involves mating a set of parents in all possible combinations, to produce a set of  $F_1$  progeny.

The present study was planned to investigate the inheritance pattern of boll number, boll weight and seed index in the Upland cotton cultivars. Diallel mating design has been used to create variability and to know the genetic parameters controlling the inheritance of the characters under study. Diallel crossing technique in cotton has been used by other cotton breeders also to get the desired results i.e. Baloch [1], Basal and Ismail [2], Chandio et al [3], Deshmukh et al [4], Deshpande et al [5] and Mehetre et al [22].

## MATERIAL AND METHODS

This study was initiated in year 2000 in the department of Plant Breeding and Genetics, University College of Agriculture, Bahauddin Zakaryia University, Multan, (30.2°N, 71.4°E) Pakistan by making all possible crosses, with reciprocals, among the eight parents (Table 1).

**Glasshouse Cultivation:** Seeds of the parental cultivars were grown in 30 x 30 cm earthen pots containing a mixture of equivalent volumes of sand, soil and farm yard manure from November 15, 2000 to March 15, 2001 in the glasshouse. 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. Seedlings were thinned to one plant per pot after two weeks of planting and after every 14 days 0.25 g of Urea (46% Nitrogen) was added to each pot, plants were provided water daily. Crosses were attempted among eight parental cultivars to obtain 56  $F_1$  (direct and reciprocal) crosses. Parental cultivars were

maintained through self-pollination.

**Field evaluation:** The eight parent varieties and their 56  $F_1$ 's were planted on a clay loam soil on June 1, 2001. Every effort was taken to reduce the environmental effect by using randomized complete block design with three replications along with keeping the growth protocol identical for all the genotypes. The experimental plots were a 3.3-meter single row with intra and inter row distances of 30 and 75cm, respectively. The  $F_1$  hybrid and parents were self-pollinated to raise  $F_2$  progeny.  $F_2$  progeny was sown in the same field also in a triplicate randomized complete block design (RCBD) on June 1, 2002. The plot size for each cross in each replication was 3.3 x 6 meters. Ten plants in  $F_1$  generation, in each replication, were randomly selected for data recording. Sample size for  $F_2$  generation was sixty competitive plants in each replication. The matured bolls were hand picked after every two weeks as soon as bolls started to open  $F_1$  and  $F_2$  for both the generations 150 days after planting (DAP) for three harvests and seed cotton was collected in Kraft paper bags. Picking was done when the dew had evaporated.

**Collection of data:**

**Bolls number per plant:** The numbers of matured bolls from all the three picks were counted and cumulative record was maintained for each plant separately. Then the average number of bolls per plant for each genotype per replication was computed.

**Boll weight (grams):** Weight per boll was obtained by dividing the total seed cotton yield of the plants by the total number of bolls picked from that particular plant. The average boll weight per plant for each genotype was maintained for statistical analysis.

**Seed index:** Seed index is the mass of 100 linty seeds. Hundred seeds were taken at random from each genotype in each replication and weighed in grams.

**Statistical analysis:**

The data for each measurement was tabulated and analyzed by Fisher's analysis of variance, Steel and Torrie [27]. The diallel analysis was used to evaluate traits that had significant variation among the parents. Significant differences in phenotypes were assumed to imply that genetic differences were present. Simple additive – dominance model approach of Hayman [6], [7], Jinks [11], Singh and Chaudhary [26] as modified by Mather and Jinks [21] was followed for genetic analysis and for the estimation of components of genetic variation. The significance of components of variation in  $F_1$  generation

was tested by Jinks [12], Hayman [9], Mather and Jinks [19]. When the value of a parameter divided by its standard error, exceeds 1.96 then it was significant, while for  $F_2$  generation the significance of the various statistics were tested by 't' test at  $n-2$  degree of freedom as:

$$t = \text{parameter} / \text{S.E of parameter}$$

Calculation for the analysis of (Wr-Vr) and the following genetic components, ratios, and estimators were included in the program.

(Wr + Vr) = an estimator of the order of dominance of the parents as indicated by the relative values of each parent. Low values of (Wr + Vr) indicate high levels of dominance while high values indicate low dominance.

D = component of variation due to additive effects of genes.

F = an indicator of excess of dominant or recessive genes in the parent. A positive sign indicates an excess of dominant alleles of dominant effects on the parents while a negative sign indicates the same of recessive alleles. A value of  $F = 0$  indicates that either no genes exhibited dominance or that the dominant and recessive alleles of each gene are distributed equally among the parents.

$H_1$  and  $H_2$  = components of variation due to the dominance effects of genes.

$h^2$  = the summation of dominance deviation over all loci. When the 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 = environmental component as estimated by the error mean square from the analysis of variance.

$(H_1/D)^{0.5}$  = a weighted measure of the average degree of dominance at each locus with a value of zero indicating no dominance, a value of 1 indicating complete dominance and a value greater than 1 indicating over-dominance. Partial dominance results in a value between 0 and 1. The dominance component  $H_1$  is used in this ratio because it has the same coefficient as D, Hayman [6].

$H_2/4H_1$  = an estimator of the average frequency of negative versus positive alleles at loci exhibiting dominance. It has a maximum value of 0.25 when  $p = q = 0.5$ . Value less than 0.25 indicate that the additive components do not contain all dominance effects. Therefore, the above ratio of average degree of dominance would not be accurate Mather & Jinks [19].

$K_D/D_R = (4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F$ . A ratio of the total number of dominant genes to recessive genes in all the parents.

Heritability =  $(1/4D) / (1/4D + 1/4H_1 - 1/4F + F)$

The above estimators were calculated only when the genetic components in the respective ratios were significantly different from zero.

## RESULTS AND DISCUSSION

Results of the analysis of variance indicated significant differences at the 0.01 percent probability level for boll number, boll weight and seed index among genotypes (Table 2). The significance of the 'F' test indicated that the parents were diverse for all the characters under study. The results also 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 [21].

Variance of each row (Vr) and covariance between parents and their hybrids (Wr) were calculated for each member of the array for all the characters. Nevertheless, joint regression analysis of Wr and Vr and analysis of Wr-Vr, both indicated non-additive variation other than independently distributed dominance effects for boll weight and seed index in  $F_2$  generation. Thus, the data set of  $F_2$  generation of these two characters did not satisfy the simple additive dominance model of inheritance, hence, the Hayman [6] and Mather and Jinks [21] diallel analysis could not be continued on the complete data set.

Jinks [11], Jana [10] and Rood and Major [25], showed that, in certain situations selective removal of one or more of the members of a diallel array may improve fit with the simple model of inheritance. In this study, removal of SA-100 from  $F_2$  generation of boll weight and SA-100 & AC-134 from  $F_2$  generation of seed index improved the data set. Analysis of variance of resulting genotypes showed highly significant differences at 0.01 percent probability level again, and then the diallel analysis was proceed.

Table 3 contains the significance levels of the diallel analysis of variance components. The significance of (a) and (b) components in both the generations for all the characters showed the presence of additive and dominance effects. While (b<sub>1</sub>) item's significance showed that directional dominance, effects were present in all the three characters for  $F_1$  generation except for  $F_2$  generation of boll number and seed index. The (b<sub>2</sub>) portion of the (b) item was significant only in  $F_1$  generation of boll weight, which showed symmetrical distribution of genes, while it was non significant for all the other characters and generations. The (b<sub>3</sub>) item was non significant for all the characters in both the generations so specific gene effects were absent except  $F_1$  in boll number. The (c) component was non significant for all the characters showing absence of maternal effects, except  $F_1$  of boll number and boll weight which showed presence of maternal effects, so (a) item was retested by (c) and after retesting (a) become non significant which means that additive effects were masked by the presence of maternal effects. Absence of reciprocal effects was evident by the non-significance of item (d) for all the characters.

The adequacy of the additive-dominance model

Table 1: Particular attributes of cotton cultivars

Sr. No.	Cultivar	Distinctive feature
1	Laokra 5.5	Okra type leaf ( $L^{\circ}L^{\circ}$ )
2	DPL - 7340-424	Nectariless ( $ne_1ne_1ne_2ne_2$ )
3	Fregobract	Fregobracts
4	Glandless 4195-220	Glandless
5	SA100	Red leaves ( $R_1R_1$ )
6	Stoneville-857	Nectariless ( $ne_1ne_1ne_2ne_2$ )
7	S-14	High ginning outturn cultivar
8	B-557	Obsolete local cultivar

Table 2. Estimates of Mean Square for Boll number, weight, and Seed index

Parameters	Mean Squares	
	Genotypic	Error
Boll number		
$F_1$	109.76**	53.57
$F_2$	29.43**	
	3.81	
Boll weight		
$F_1$	0.51**	0.16
$F_2$	0.58**	
	0.02	
Seed index		
$F_1$	4.97**	0.032
$F_2$	3.28**	0.154

\* = Indicate significant differences at  $P < 0.05$  probability level.

\*\* = Indicate significant differences at  $P < 0.01$  probability level.

ns= Non significant at  $P < 0.05$  probability level.

This convention is followed throughout this research paper

and validity of some of the assumptions were assessed by using joint regression analysis and analysis of variance of ( $W_r + V_r$ ) and ( $W_r - V_r$ ). The results of the regression analysis for both  $F_1$  and  $F_2$  generations for all the characters were presented in (Table 4). The regression coefficient ( $b = 0.475 \pm 0.195$ ) regarding number of bolls per plant  $F_1$  and boll weight  $F_1$  ( $b = 0.411 \pm 0.213$ ) depart significantly from unity but not from zero, which indicated, non-additive variation included epistasis or multiple allelism and correlated genes distribution among the parents. Therefore, the data did not fulfill the diallel assumptions; hence, additive dominance model was partially inadequate.

The regression analysis of  $F_2$  generation ( $b=1.22 \pm 0.271$ ) regarding number of bolls per plant, boll weight ( $b= 0.668 \pm 0.190$ ) and  $F_1$  ( $b = 0.779 \pm 0.300$ ) and  $F_2$  ( $b = 1.32 \pm 0.137$ ) of seed index indicated that the regression coefficient depart significantly from zero and not from unity, suggesting no non-allelic interaction and

an independence of genes distribution among the parents. Thus, the additive-dominance model did provide fair basis for interpreting the results. This property of the regression coefficient indicated intra-allelic interaction, meaning thereby, that genes were distributed independently among the parental lines, and was independent in action. The unit slope of the regression lines suggested that all the diallel assumptions have been met Mather & Jinks [21].

The appropriateness of the model data analysis was also shown by the analysis of variance of ( $W_r + V_r$ ) and ( $W_r - V_r$ ) (Table 5). Which elaborated that there was no evidence of dominance effects as the mean square between arrays for  $W_r + V_r$  was non-significant for  $F_1$  of boll number and boll weight, while the mean square between arrays for  $W_r - V_r$  was also non- significant in  $F_1$ , thus emphasizing partial adequacy of additive dominance hypothesis for both of these characters in  $F_1$  generation. While  $F_2$  generation revealed that  $W_r + V_r$

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Table 3. Diallel Analysis of Variance for Boll number, weight, and Seed index

Parameters	d.f	Boll number		Boll weight		Seed index	
		Squares		Mean Squares		Mean Square	
Item	F <sub>1</sub> & F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>
a	7	1160.38**	295.32**	3.05**	2.79*	76.41**	37.95**
b	28	251.29**	70.84**	1.69**	1.56*	8.29**	3.04**
b <sub>1</sub>	1	1087.54**	30.18 <sup>ns</sup>	18.25**	12.25**	54.31*	4.50 <sup>ns</sup>
b <sub>2</sub>	7	229.68 <sup>ns</sup>	100.81 <sup>ns</sup>	2.30**	1.27 <sup>ns</sup>	5.56 <sup>ns</sup>	3.89 <sup>ns</sup>
b <sub>3</sub>	20	217.05*	62.39 <sup>ns</sup>	0.65 <sup>ns</sup>	0.92 <sup>ns</sup>	6.94 <sup>ns</sup>	2.41 <sup>ns</sup>
c	7	314.06*	59.05 <sup>ns</sup>	1.99*	1.72 <sup>ns</sup>	7.88 <sup>ns</sup>	8.99 <sup>ns</sup>
d	21	161.28 <sup>ns</sup>	52.27 <sup>ns</sup>	0.61 <sup>ns</sup>	1.60 <sup>ns</sup>	5.54 <sup>ns</sup>	6.42 <sup>ns</sup>
e	63	112.38	51.23	0.69	1.13	9.87	6.26

Table 4. Test of Regression Coefficient for Boll number, weight, and Seed index

Parameters	Regression Coefficient (b)	Standard Error of regression SE(b)	t value for b-0	t value for 1-b
<b>Boll number</b>				
F <sub>1</sub>	0.475	0.195	2.44 <sup>ns</sup>	2.70*
F <sub>2</sub>	1.220	0.271	4.50*	-0.81 <sup>ns</sup>
<b>Boll weight</b>				
F <sub>1</sub>	0.411	0.213	1.92 <sup>ns</sup>	2.76*
F <sub>2</sub>	0.668	0.190	3.52*	1.75 <sup>ns</sup>
<b>Seed index</b>				
F <sub>1</sub>	0.779	0.300	2.60*	0.74 <sup>ns</sup>
F <sub>2</sub>	1.32	0.137	9.66*	-2.34 <sup>ns</sup>

Table 5. Heterogeneity test for (Wr + Vr) and (Wr - Vr) Estimates

Parameters	d.f	Boll number		Boll weight		Seed index	
		Mean Squares		Mean Squares		Mean Squares	
		F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>
Wr + Vr between arrays	7	30.31 <sup>ns</sup>	2.32*	0.063 <sup>ns</sup>	0.027**	1.30**	0.94**
Wr + Vr within arrays	16	23.47	0.72	0.034	0.0021	0.93	0.09
Wr - Vr between arrays	7	5.58 <sup>ns</sup>	0.19 <sup>ns</sup>	0.017 <sup>ns</sup>	0.003**	0.22**	0.05 <sup>ns</sup>
Wr - Vr within arrays	16	3.12	0.08	0.017	0.0004	0.008	0.01

Table 6. Estimates of genetic parameters for Boll number, weight, and Seed index

Components of Variation	Boll number		Boll weight		Seed index	
	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>
D	6.98 <sup>ns</sup> ± 7.93	18.01* ± 1.8	0.08 <sup>ns</sup> ± .05	0.098* ± 0.02	2.95* ± 0.20	2.24* ± 0.08
H <sub>1</sub>	24.01 <sup>ns</sup> ± 18.2	73.7* ± 16.51	0.41* ± 0.11	1.674* ± 0.21	2.28* ± 0.47	2.97* ± 0.81
H <sub>2</sub>	18.8 <sup>ns</sup> ± 15.9	45.17* ± 14.36	0.27* ± 0.09	1.297* ± 0.19	1.82* ± 0.41	2.02* ± 0.72
H <sup>2</sup>	44.8* ± 10.63	-11.9 <sup>ns</sup> ± 9.63	0.86* ± 0.06	2.580* ± 0.13	2.64* ± 0.27	0.4 <sup>ns</sup> ± 0.49
F	15.4 <sup>ns</sup> ± 18.7	35.42* ± 8.50	0.16 <sup>ns</sup> ± 0.11	0.22 <sup>ns</sup> ± 0.11	1.29* ± 0.48	2.24* ± 0.39
E <sub>2</sub>	18.53* ± 2.64	1.27 <sup>ns</sup> ± 0.60	0.05* ± 0.02	0.01 <sup>ns</sup> ± 0.01	0.01 <sup>ns</sup> ± 0.07	0.05 <sup>ns</sup> ± 0.03
(H <sub>1</sub> /D) <sup>0.5</sup>	1.854	1.019	2.327	2.066	0.880	0.580
(H <sub>2</sub> /4H <sub>1</sub> )	0.196	0.150	0.160	0.194	0.200	0.170
K <sub>D</sub> /K <sub>R</sub>	0.255	65.330	2.537	3.270	1.660	14.420
K=h <sup>2</sup> /H <sub>2</sub>	2.390	-0.264	3.254	1.988	1.450	0.212
H <sup>2</sup> (ns)	0.373	0.751	0.238	0.230	0.695	1.042

varied significantly from array to array, while  $W_r - V_r$  did not except for boll weight. It showed that not only there was no evidence of interaction between non-allelic genes in producing their effects, but also that there was no evidence of the genes being associated in a non-random way in their distribution between the parents, Mather and Jinks [20]. Evidently, the additive dominance model was adequate to account for the behavior of this diallel. The additive-dominance model was also shown to be adequate by both the tests for number of bolls per plant in  $F_2$  generation. The similar type of findings were also reported by Khan et al [14], Khan et al [14], Khan and Khan [15] and Murtaza et al [23], who advocated the presence of over dominance type of genetic mechanism for number of bolls per plant and boll weight in their cotton genotypes.

Significant differences at 0.01 percent probability level for  $(W_r + V_r)$  of seed index in both the generations revealed the presence of dominance, while the  $W_r - V_r$  for  $F_1$  also highly significant, and this significance was the result of the presence of non-allelic interactions thus invalidate the additive dominance model and did not permit for further analysis of diallel data. While in  $F_2$  generation, the non-significance of  $(W_r - V_r)$  suggested the absence of non-allelic interaction. This discrepancy was due to different environmental conditions. The foregoing results of  $F_2$  population suggested, that the additive-dominance model appeared to be adequate for this set of data. The additive with partial dominance type of gene action for seed index had been reported by Latif et al [17], Wang and Li [28], Murtaza et al [24] and Khan et al [13]. Cotton is an international agricultural commodity of which the quantity and quality are subject to various whims of nature.

Genetic components: With regard to the genetic components estimated by the diallel analysis (Table 6), the additive component (D) was significant at the 0.01 level only for  $F_2$  generation of boll number and boll weight and for both the generations of seed index. This confirmed the additive effects of the genes for these generations. Dominance components ( $H_1$  and  $H_2$ ) were significant for all the characters, which showed dominance effects of genes. The positive values of the F component for all the characters indicated excess of dominant alleles were present in the genetic material.

The significance for the component  $h^2$  in all the characters confirmed that dominance was unidirectional. The ratio  $(H_1/D)^{0.5}$  measured the overall degree of dominance, which was in the range of over dominance for both boll number and boll weight, while it was in the range of partial dominance in seed index.

The ratio  $H_2/4H_1$ , estimated the frequency of negative

versus positive alleles at loci exhibiting dominance, it was less than 0.25, which indicated that the additive components did not contain all the dominance effects in all the characters.

Estimates for the ratio of dominance to recessive genes in the parents ( $K_D/K_R$ ) for all the characters were more than 1.0, which indicated the presence of an excess of dominant genes for each trait in the parents. While only  $F_1$  of boll number showed lower than 1.0 value, indicated the presence of an excess of recessive genes for this trait in the parents.

Heritability values were in the range of low to high. In boll weight low additive effect decreases heritability values ( $F_1 = 0.24$ ,  $F_2 = 0.23$ ). While boll number  $F_1$ ,  $F_2$  (0.37, 0.75), and Seed index  $F_1$  and  $F_2$  (0.70, 1.04) showed moderate to high estimates of heritability. High estimates of heritability in narrow sense represents fixable, additive heritable variation, which indicated that response to selection, should be rapid for these characters. This offers a lot of scope for improvement of the characters through individual plant selection. According to Hayman [8], epistasis can decrease or increase degree of dominance, which also effect on heritability estimates.

## CONCLUSION

The inheritance pattern of variation, for different quantitative characters in the eight genotypes of *Gossypium hirsutum* L., revealed by the diallel data appeared to be complex. Although genetic variation for the characters appeared to be influenced predominantly by genes with additive or dominance effects, the presence of a significant additive component is encouraging. Based on narrow sense heritability and expected genetic gain because of selection, a potentially useful advance in high yielding, with better seed qualities, seems possible to achieve by selecting individual plants showing better qualities.

Although the diallel analysis revealed the importance of both additive and non-additive gene effects in controlling the observed variation for these components, the effects of the former appeared to be less pronounced. Lawrence [18] has argued that populations subjected to strong directional selection pressure show reduced additive component for the character under selection. There is much information in the literature, which may indicate that cotton has previously been subjected to directional selection pressures in the wild and in cultivated material for high yield and improved fiber characters. It would seem likely that additively based variation in the characters under study should be

exploited through selection in early generations while those with over dominance should be delayed.

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