

## Studies of Genetic Variation for Yield Related Traits in Upland Cotton

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**Abstract:** Selection of suitable parents is a crucial step in successful breeding program, owing to this a full diallel experiment was conducted involving five *Gossypium hirsutum* L. varieties SLH-41, F-281, COKER-3113, LA-85-52-1 and H-88-8-J.69-j.70 to evaluate genetic effects of various plant traits. Genetic analysis of Plant height (PH), number of bolls per plant (BPP), average boll weight (BW), yield per plant (Y), ginning out turn (GOT), fiber length (FL), strength (FS) and fiber fineness (FF) was conducted. Preliminary statistical analysis revealed significant genetic difference ( $p \leq 0.01$ ) among the genotypes for all of the above mentioned traits. Graphical as well as Numerical studies revealed that almost all of the traits exhibited additive type of gene action with partial dominance except the Ginning out turn percentage and average boll weight. These two traits showed dominant gene action with additive effects. The extremely low narrow sense heritability of Ginning out Turn percentage and average boll weight exhibited chances of delayed response to selection there by suggesting the material suitable for heterosis breeding.

**Key words:** Diallel analysis • Genetic studies • Yield traits • Upland cotton • *Gossypium hirsutum* L

### INTRODUCTION

Cotton occupies a unique position in Pakistan's agrarian economy. Efforts on various aspects of the crop have been under way to increase overall production of the country. Cotton is principal component of Pakistan's economy owing to its 69% share in foreign exchange earning, 7.5% value added in agriculture and 1.6% in GDP. It contributes about 78% in domestic oil production. The economy of Pakistan mainly depends upon cotton production, exportable surplus of cotton fiber and fiber made products. The crop not only meets the need of local industry but also provides edible oil for cooking purpose and low grade oil for the soap manufacturing industries. Residual seed cake is a valuable protein concentrate that is used for livestock feed [1]. Development of genetically

superior genotypes remained the utmost objective of cotton improvement program and cotton breeders have managed to generate several high yielding, good quality varieties through various genetic manipulations and breeding approaches consequently leading to a significant progress in raw fiber production. As the improvement in yield and quality in agricultural crops is a consistent objective therefore, the breeders remain busy all the time to develop genotype with high yield and good fibre traits in cotton.

To achieve desirable results, parents to be utilized in any breeding program, must be genetically diverse and physiologically efficient. Keeping this in view, an experiment was conducted at research farm of Breeding Department of The Islamia University of Bahawalpur, to study the gene action in  $F_1$  hybrids for the selection of

suitable parents for the evolution of high yielding, widely adaptive and better quality varieties. Current research work was launched to analyze some important cotton cultivars to ascertain the relative performance regarding genetic control for yield and its components. Diallel analysis technique devised by [2,3] reviewed and studied by [4] is a valuable approach to obtain precise information about knowing the genetic control of various yield related characters. Diallel analysis is valuable technique in order to elucidate outstanding parents and diligent cross combinations for the genetic improvement of traits under consideration. Therefore present research work was designed to obtain the genetic information for economic traits by using diallel technique, devised by [2,3].

## MATERIALS AND METHODS

The present experiment was conducted at research farm of PBG department, College of Agriculture and Environmental Sciences, The Islamia University of Bahawalpur during 2009-10. The genetic material comprised of SLH-41, F-281, COKER-3113, LA-85-52-1 and H-88-8-J.69-j. 70 representing a range of yield and fibre quality traits sown in earthen pots during November 2009. In order to attain maximum germination and growth recommended agronomic practices were followed. Five self and 20 direct & indirect crosses of parental lines were accomplished at flowering stage. Seed cotton for each self and crossed boll was collected in separate paper bags to avoid mixing. After ginning at roller ginning machine  $F_0$  seed along with their parents was sown in the field during June-2010 in triplicate Randomized Complete Block Design. Every repeat comprised of 25 genotypes planted in 5 rows of single genotype having 10 plants having row to row and plant to plant distance of 75 cm and 30cm respectively. Optimum field practices were conducted from sowing to harvesting in-order to maintain a healthy crop. Data were recorded for Plant height (PH), number of bolls per plant (BPP), average boll weight (BW), yield per plant (Y), ginning out turn percentage (GOT%), fiber length (FL), strength (FS) and fiber fineness (FF) on five guarded plants from every genotype, both in field as well as in laboratory on single plant basis.

Analysis of variance was conducted [5] to determine the genetic constitution of every genotype for the plant traits under study. Genotypes having significant difference for above mentioned traits were genetically analyzed according to additive-dominance model of genetic analysis developed by [2, 3].

## RESULTS AND DISCUSSIONS

Analysis of for the observed traits showed that genotypic differences were highly significant ( $P = 0.01, 0.05$ ) from each other illustrating the presence of genetic diversity among them (Table 1).

**Plant Height:** All of the 25 genotypes were significantly different from each other for plant height (Table 1). Results of joint regression analysis (Table 2) prove the fitness of data for additive-dominance model. Regression line intercepting the  $W_r$  axis above the origin (Figure 1) indicates that plant height is controlled by additive type of genetic effects with partial dominance. The position of the array points on the regression line indicates that Cocker 312 has maximum dominant genes as it is close to the origin while LA-85-52-1 has maximum recessive genes being away from origin.

The estimates of genetic variance components ( $D, H_1, H_2, F$ ) with their standard error were computed and shown in Table 3. Additive and non additive effects were important for plant height as the additive component ( $D = 35.59$ ) and dominance component ( $H_1 = 11.11$  and  $H_2 = 12.46$ ) were significant but the additive components were higher as compared to dominance effect ( $H_1, H_2$ ) for plant height. The value of  $H_1, H_2$  estimates were nearly equal therefore indicates equal distribution of allele at all loci. The value of  $F$  indicate that recessive genes were in equal proportion with dominant genes in parents which is also supported from the ratio  $(4DH_1)/1/2 + F / (4DH_1)/1/2 - F$  having numerical value 0.91. Degree of dominance  $(H_1/D)^{1/2}$  indicated that the greater portion of genetic variance were additive in nature and the allelic frequency of positive and negative effects of dominant genes were symmetrical as the numerical value is very close to 0.25. Broad and narrow sense heritability were higher so selection can be practiced in  $F_2$  segregating generation.

The results seemed to be compatible with those of [6, 7]. While some other scientists like [8-11] reported additive type of gene action and [12] reported both additive and non additive type of gene action for this trait.

**Number of Bolls per Plant:** Analysis of variance showed that the genotypes have highly significant differences for number of bolls per plant (Table 1) thereby allows subsequent biometrical analysis. Results of joint regression analysis (Table-2) indicated that data were quite fit for additive-dominance model.  $V_r/W_r$  graph for number of Bolls per plant depicts that the regression line

Table 1: Analysis of variation for various traits.

S.O.V	P.H	B/P	Boll Weight	Yield	GOT	F.L	F.S	F.F
Genotype	58.92**	6.83**	16.71**	1.40**	8.29**	4.10**	4.97**	0.18**
Replication	0.24	1.90	1.29	0.15	2.54	2.83	2.13	0.35
Error	1.46	1.34	1.40	0.095	0.31	0.22	0.25	0.07

Table 2: Results of joint regression analysis of eight characters of cotton plant

Sr. No.	Character	Regression Coefficient	Conclusion
1.	Plant height	$0.97 \pm 0.11$ b value diverge considerably from zero but not from unity	Data is fit for genetic analysis
2.	Number of bolls per plant	$0.92 \pm 0.13$ b value diverge considerably from zero but not from unity	Data is fit for genetic analysis
3.	Average boll weight (BW),	$0.89 \pm 0.92$ b value diverge considerably from zero but not from unity	Data is fit for genetic analysis
4.	Yield per plant (Y)	$1.11 \pm 0.16$ b value diverge considerably from zero but not from unity	Data is fit for genetic analysis
5.	Ginning out-turn % age	$0.98 \pm 0.22$ b value diverge considerably from zero but not from unity	Data is fit for genetic analysis
6.	Staple length	$0.96 \pm 0.23$ b value diverge considerably from zero but not from unity	Data is fit for genetic analysis
7.	Fiber fineness	$0.84 \pm 0.16$ b value diverge considerably from zero but not from unity	Data were fit for genetic analysis
8.	Fiber strength	$1.0 \pm 0.19$ b value diverge considerably from zero but not from unity	Data is fit for genetic analysis

Table 3: Components of Genetic Variation for the observed traits.

	Plant Height	Bolls/ Plant	Boll Weight	Yield	GOT	F. Length	F. Strength	F. Fineness
D	$35.59 \pm 0.99$	$3.58 \pm 0.15$	$9.89 \pm 1.71$	$0.60 \pm 0.05$	$3.34 \pm 2.07$	$2.00 \pm 0.11$	$2.27 \pm 0.18$	$0.08 \pm 0.00$
H <sub>1</sub>	$11.11 \pm 2.66$	$0.17 \pm 0.09$	$11.74 \pm 4.61$	$0.27 \pm 0.13$	$10.57 \pm 5.59$	$1.23 \pm 0.29$	$2.40 \pm 0.48$	$-0.04 \pm 0.01$
H <sub>2</sub>	$12.46 \pm 2.41$	$2.20 \pm 0.36$	$11.16 \pm 4.18$	$0.32 \pm 0.12$	$9.29 \pm 5.07$	$1.18 \pm 0.26$	$2.79 \pm 0.44$	$0.08 \pm 0.01$
F	$-1.81 \pm 2.46$	$-1.15 \pm 0.36$	$5.09 \pm 4.26$	$-0.31 \pm 0.12$	$3.08 \pm 5.17$	$-0.28 \pm 0.26$	$-0.34 \pm 0.45$	$-0.03 \pm 0.01$
E	$0.47 \pm 0.40$	$0.52 \pm 0.06$	$0.43 \pm 0.70$	$0.03 \pm 0.02$	$0.13 \pm 0.84$	$0.11 \pm 0.04$	$0.11 \pm 0.07$	$0.03 \pm 0.00$
h <sup>2</sup>	$11.95 \pm 1.63$	$0.22 \pm 0.24$	$2.06 \pm 2.82$	$0.01 \pm 0.08$	$3.01 \pm 3.42$	$0.16 \pm 0.17$	$0.25 \pm 0.29$	$-0.01 \pm 0.00$
h <sup>2</sup> ns	0.83	0.55	0.49	0.79	0.24	0.74	0.58	-0.17
H <sub>2</sub>	0.98	0.78	0.93	0.94	0.96	0.93	0.94	0.31
(H <sub>1</sub> /D) <sup>1/2</sup>	0.56	0.14	0.03	0.67	1.78	0.77	1.03	0.22
h <sup>2</sup> /H <sub>2</sub>	0.96	0.10	0.18	0.03	0.32	0.14	0.09	-0.13
H <sub>2</sub> /4H <sub>1</sub>	0.28	7.86	0.26	0.30	0.22	0.24	0.29	-0.50
(4DH <sub>1</sub> ) <sup>1/2</sup> +F								
(4DH <sub>1</sub> ) <sup>1/2</sup> -F	0.91	0.07	1.58	0.51	1.70	0.84	0.86	1.75

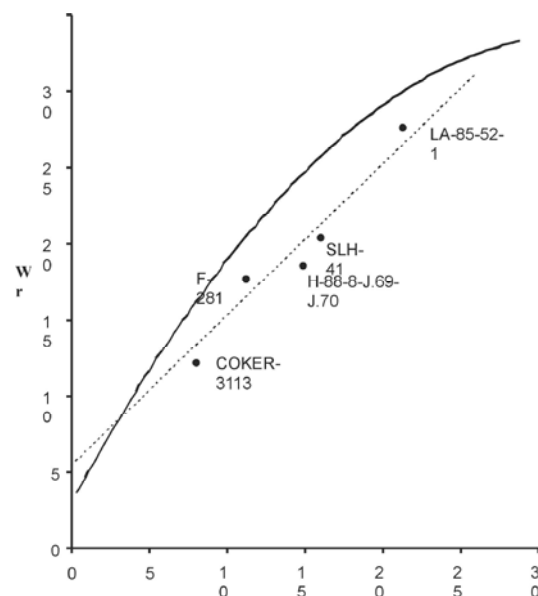


Fig. 1: Vr/Wr graph for Plant Height.

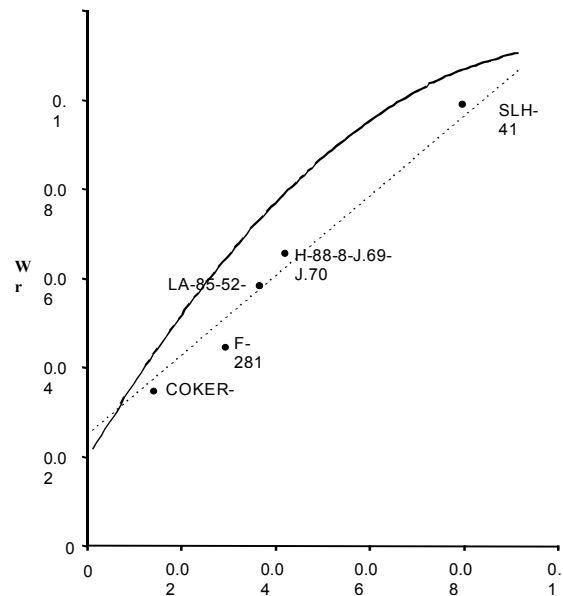


Fig. 2: Vr/Wr Graph for No. of Boll per Plant

intercepts the  $W_r$  axis above from the origin thus having predominant additive type of gene action with partial-dominance (Figure 2). Coker 312 has more dominant genes as it is close to origin and SLH-4 has more recessive genes as it is away from origin.

The estimates of components of genetic variance ( $D$ ,  $H_1$ ,  $H_2$ ,  $F$ ) with their standard error are shown in Table 3. Pronounced additive and non additive effects were observed for number of boll per plant as the additive component ( $D = 3.58$ ) and dominance effect ( $H_1 = 0.17$  and  $H_2 = 2.20$ ) were significant while additive components were higher as compared to dominance ( $H_1$ ,  $H_2$ ). Unequal  $H_1$ ,  $H_2$  estimates indicates presence of unequal genetic frequencies at various loci. The  $F$  value -1.15 indicates that recessive genes were in equal proportion with dominant genes in parents and is also supported from the ratio  $(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F$  having value -0.07. The degree of dominance  $(H_1/D)^{1/2}$  indicated that the greater portion of genetic variance were additive in nature and the allelic frequency of positive and negative effects of dominant genes were symmetrical as the value is close to 0.25. The  $h^2$  value indicates that parents can be used for hetrotic breeding. The heritability in broad (0.78) and narrow sense (0.55) indicated that selection can be practiced in  $F_2$  segregating generation. Khan [10] along with [8,9,11,13-15] found similar results whereas [16-20] reported additive type of gene action also [12,21] reported both additive and non additive type of gene action for this trait. Murtaza [22,23] reported both additive and dominance gene action.

**Boll Weight:** Analysis of variance for boll weight showed highly significant difference ( $P \leq 0.01$ ) among the genotypes evaluated (Table 1). Results of joint regression analysis (Table 2) indicated that data were fit for additive-dominance model. The  $V_r/W_r$  graph indicates that the regression line is intercepting the  $W_r$  axis near the origin which shows the dominant type of gene action with additive effects. The different positions of the array points on regression line indicates that the varieties F-281 and H-88-8-J.69-J.70 possessed maximum dominant genes as this variety is closest to origin and the variety SLH-41 possess maximum recessive genes as it is away from the origin on the regression line (Figure 3).

Components of genetic variance and their standard errors explain that the additive component ( $D = 9.89$ ) and dominance components ( $H_1 = 11.74$ ,  $H_2 = 11.16$ ) were significant but additive component was slightly higher

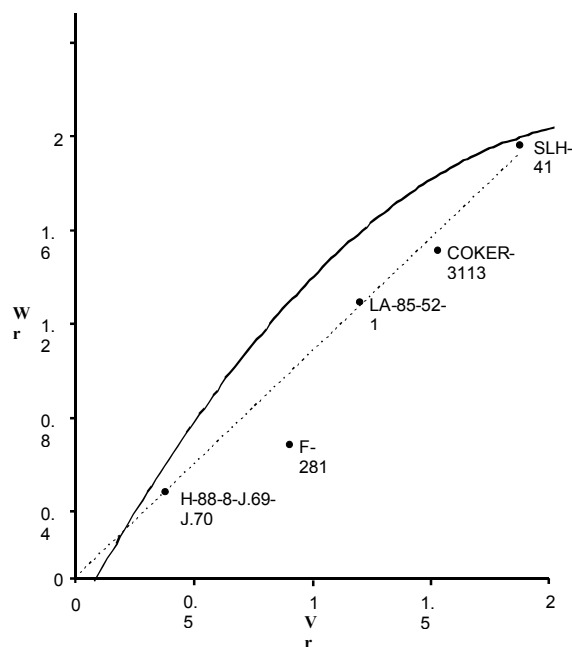


Fig. 3:  $V_r/W_r$  graph for Average Boll Weight.

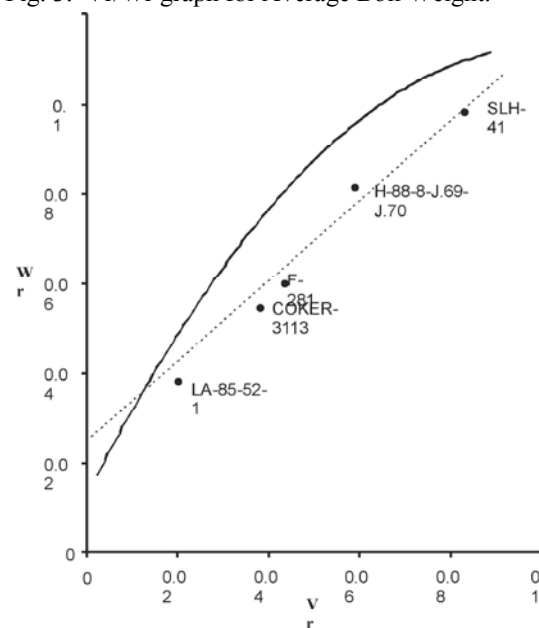


Fig. 4:  $V_r/W_r$  Graph for Yield per Plant

than dominance ( $H_1$ ) component (Table 3). The estimated values of  $H_1$  and  $H_2$  were almost a like indicating the occurrence of equal gene frequencies at all loci. The estimated value of  $F$  (2.06) suggested that the proportion of dominant and recessive genes in parents were not equal which were also supported from computed ratio  $(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F$ . The  $(H_1/D)^{1/2}$  value (0.03) however justifies additive and

dominance variation. The  $H_2/4H_1$  value (0.26) indicated that the allelic frequency of positive and negative effects of dominant gene was symmetrical. The heritability value in broad-sense (0.93) and narrow-sense (0.49) suggested that selection in segregating generation should be delayed as the heritability in narrow-sense is low and dominant gene action played important role in determining the phenotype of individual.

The results seemed to be compatible with those of [8-11] while differed from [24] as they revealed the additive type of gene action. Nadeem and Azhar [23] reported additive dominance type of gene action for this character.

**Yield:** The analysis of variance for yield indicated highly significant ( $P \leq 0.01$ ) differences among the genotypes (Table 1). Results of joint regression analysis (Table 2) indicated that 'b' value ( $0.99 \pm 0.10$ ) deviated significantly from zero but not from unity showing that the data were adequate for additive-dominance model as suggested by [2,3]. The  $V_r/W_r$  Graph indicates that this character is controlled by additive type of gene action with partial dominance, as the regression line is intercepting the  $W_r$  axis above the origin and is close to Parabolla line (Figure 4). The different array points on the regression line indicates that the variety LA-85-52-1, H-88-8-J.69-J.70 has maximum dominant genes because this variety has closest position from the origin while the varieties SLH-41 has maximum recessive genes as this variety is away from the origin (Figure 4).

The genetic component of variance and their standard error were estimated and presented in Table 3. The value of  $D$  (0.60),  $H_1$  (0.27) and  $H_2$  (0.32) indicated that additive component were more important than dominance component as the value of  $D$  is higher than  $H_1$  and  $H_2$ . The estimated value of  $H_1$  and  $H_2$  are nearly equal that indicated the gene frequency were equal at all loci. The estimated value of  $F$  is negative (-0.31) and non significant that indicated the equal proportion of distribution recessive and dominant genes in parents, which was also supported from the estimated value of  $(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F$  value is (0.51) less than one. The degree of dominance of  $(H_1/D)^{1/2}$  demonstrated that the most of genetic variation was additive in nature. The  $H_2/4H_1$  value (0.30) showed that allelic frequency of positive and negative effects of dominant genes was not symmetrical. The  $h^2$  value (0.01) is non-significant that suggested the hetrotic breeding

would not be effective for this particular trait. The heritability values in broad and narrow sense were higher which suggested that selection in early segregating generations should be practiced. The results are in accordance with the findings of [11,25-29] while [8,10,16, 30] and [7] reported additive type of gene action in phenotypic manifestation of this character.

**Ginning Out-Turn Percentage (GOT%):** Highly significant differences were observed among the genotypes for Lint % (Table 1) and thus permitting the data for further analysis. The  $V_r/W_r$  graph for GOT% indicates dominance type of gene action as the regression line intercepts the  $W_r$  and close from the origin. Different positions of the array points on the regression line indicates that the variety F-281 have maximum dominant genes as it is close to the origin while variety H-88-8-J has maximum recessive genes as it is away from the origin on the regression line (Figure 5).

The components of genetic variance and their standard errors was computed and presented in Table 3. GOT analysis indicated that the additive component ( $D = 3.34$ ) and dominance components ( $H_1 = 10.57$ ,  $H_2 = 9.29$ ) were significant. The additive component was lower than dominance ( $H_1$ ) components for GOT. The estimated values of  $H_1$  and  $H_2$  were close to each other that indicates the occurrence of equal gene frequencies at all loci. The estimated value of  $F$  (3.08) suggested that the proportion of dominant and recessive genes in parents were not equal which were also supported from computed ratio  $(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F$ . The  $(H_1/D)^{1/2}$  value (1.78) showed dominance and additive variation in nature as the value was nearly zero. The  $H_2/4H_1$  value (0.22) indicated that the allelic frequency of positive and negative effects of dominant gene was symmetrical. The heritability value in broad-sense (0.96) and narrow-sense (0.24) suggested that selection in segregating generation should be delayed as the heritability in narrow-sense is low and dominant gene action played important role in determining the phenotype of individual. Similar findings have been reported by [31] while [17] reported additive type of gene action and [18] reported non additive type of gene action for this character.

**Fiber Quality:** The analysis of variance for fiber length, strength and fineness indicated highly significant differences among the genotypes (Table 1). Results of joint regression analysis (Table 2) indicated that 'b' value deviated significantly from zero for all of fiber traits

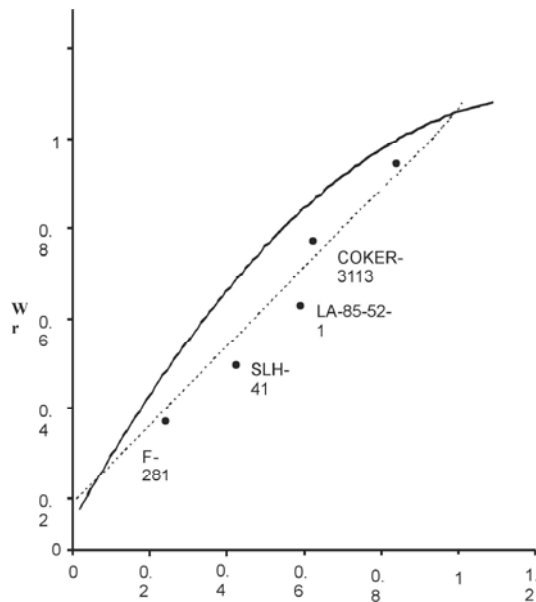


Fig. 5: Vr / Wr Graph for Ginning out turn percentage

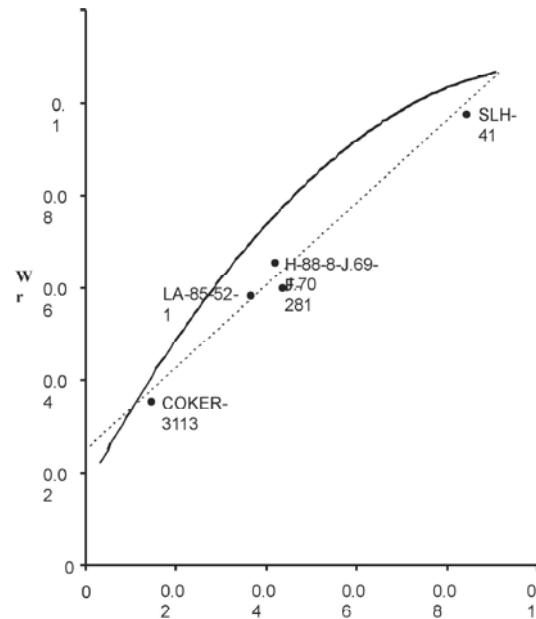


Fig. 7: Vr /Wr graph for Fibre strength.

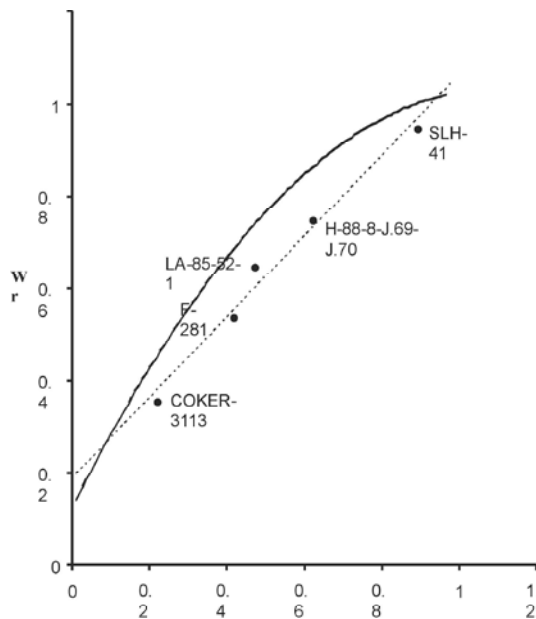


Fig. 6: Vr / Wr Graph for Fibre length

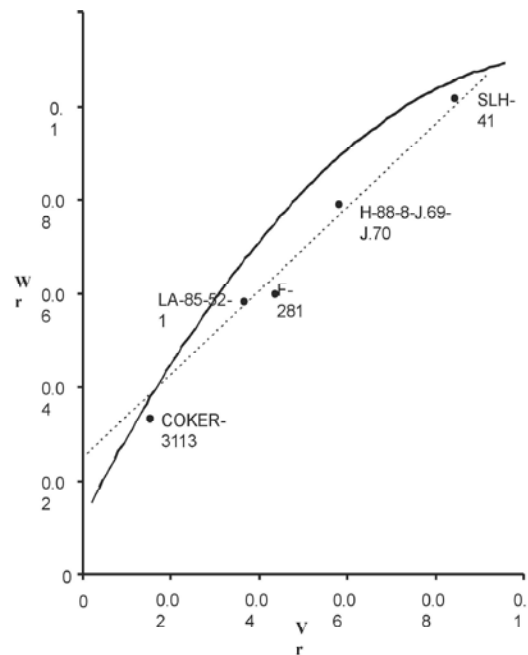


Fig. 8: Vr/Wr graph for fibre fineness.

showing that the data were valid for additive-dominance model as suggested by [2,3]. In Vr/Wr graph for fiber length, fiber fineness and fiber strength it is evident that the regression line intercepts the Wr-axis above origin and close to parabola thus indicating additive type of gene action with partial dominance (Figure 6, 7, 8). The array point on regression line showed that Cooker 312 has maximum of dominant genes for Fiber length,

fineness and strength. The genotype SLH-41 has maximum recessive genes for fiber length, strength and fineness as this genotype is away from the origin at regression line (Figure 6, 7, 8). The results are in accordance with the findings of [10,30,31] who reported over dominance type of gene action while [23,32,33] reported additive type of gene action in phenotypic manifestation of this character.

Estimates of components of genetic variance for fiber quality traits fiber length, fiber strength and fiber fineness were computed and presented in Table 3. The additive and non additive components were significant for fiber length, fiber strength and fiber fineness. However the additive component D is higher than  $H_1$  and  $H_2$  for these traits. The values of  $H_1$  and  $H_2$  were close to each other for fiber length and fiber fineness which indicated the occurrence of equal gene frequency at all loci but for fiber strength  $H_1$ ,  $H_2$  values were not equal which indicated that the gene frequency at all loci are not equal. Value of F was negative for all these three traits which indicated that the recessive genes were in equal proportion with dominant genes in the parents for these three quality traits. The  $H_1/D$  value for these traits indicated that the greater portion of genetic variance was additive in nature. The allelic frequency of positive and negative effects of dominant genes ( $H_2/4H_1$ ) was symmetrical as the value was 0.24, 0.27 and 0.23 for fiber length, fiber strength and fiber fineness respectively. The heritability value in broad and narrow sense was higher for these traits which indicated that the selection should start from early segregating generation. Nadeem and Azhar [23,34,35] obtained genetic information on fibre strength of *Gossypium hirsutum* L. and it showed that it was influenced by additive type of gene action with partial dominance. While other results according to the findings of [30,36] said that it is under control of over dominance type of gene action and some scientist [23,37,38] reported additive type of gene action for this character.

On an overall basis, it was observed that the characters i.e Plant height (PH), number of bolls per plant (BPP), average boll weight (BW), yield per plant (Y), fiber length (FL), strength (FS) and fiber fineness (FF) were controlled by additive type of gene action with partial dominance. While, GOT was observed to be under control of pronounced effect of dominance as compared to additive component.

## DISCUSSION AND CONCLUSION

Under a situation when there is additive type of gene action without the involvement of any epistatic effects, the breeder can improve such characters through simple selection procedures. While over dominance occurs when most of the progenies perform better than their parents. This in other words means heterosis. Therefore, the progenies showing heterotic effects may be considered in a breeding programme for developing hybrid cotton. Although the results of the parents studies are in agreement with a number of previous researchers but

disagree with many others. This situation may be due to the different experimental materials and environmental conditions.

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