

Genetic Analysis of Morphological Characteristics and Seed Oil Content of Cotton (*Gossypium hirsutum* L.)

Saghir Ahmad, Muhammad Zaffar Iqbal, Saeed Ahmad,
Muhammad Attique Sadiq and Noor-ul-Islam Khan
Cotton Research Station, Old Shujabad Road, Multan, Pakistan

Abstract: Inheritance pattern of sympodia per plant, plant height, bolls per plant, seed cotton yield and seed oil content of cotton was assessed using diallel crossing model in which six genotypes B-557, Culture 728-4, MNH156, B-1850 (ne), Culture-604-4 and MNH147 were crossed in all possible combinations. The results from scaling tests for the adequacy of additive-dominance model indicated that sympodia per plant, plant height, bolls per plant, seed cotton yield and seed oil content were partially adequate for further genetic analysis. Sympodia per plant, plant height, bolls per plant and seed cotton yield were controlled by additive genes, whereas over-dominance was prevalent in seed oil content characteristics. Narrow sense heritability for plant height, bolls per plant and seed cotton yield suggested that these parameters could effectively be improved through selection in the early segregating generations.

Key words: Gene action, additive, over-dominance, heritability, cotton

Introduction

Thorough knowledge and complete understanding of inheritance pattern of economic traits is a pre-requisite for enhanced progress in breeding new varieties of cotton. The diallel analysis technique (Mather and Jinks, 1982) is a useful tool to obtain precise information about the type of gene action involved for the expression of various morpho-genetic characters and to predict the performance of the progenies in the latter segregating generations.

Sanyasi (1991) reported additive and dominant effects of genes for seed cotton yield of and number of boll per plant. Additive type of gene action with partial dominance for plant height, number of bolls per plant, seed cotton yield per plant have been investigated by Shah *et al.* (1992). The findings of Tariq *et al.* (1992) revealed over dominance for seed cotton yield and low narrow sense heritability for the same character. Both additive and non-additive gene actions were found equally important in the expression of boll number with high heritability whereas seed cotton yield showed non-additive gene action (Tiwari *et al.*, 1992). Ikram *et al.* (1993) found non-additive type of genetic behavior for yield and plant height while boll number and sympodial branches were predominantly controlled by additive gene action. Azhar and Rana (1993) reported genetic effects to be predominantly non-additive for seed cotton and number of bolls per plant. Additive effects for sympodial branches have been given by Azhar *et al.* (1994). Khan *et al.* (1999) computed additive with partial dominance for plant height and over dominance was found to be

operative for bolls per plant and seed cotton yield. Estimates of narrow sense heritability were low to moderate. The results of gene action in intra specific hybrids of *G. hirsutum L* by Saeed *et al.* (1996) showed that plant height, number of bolls per plant, seed cotton yield were controlled by additive type of gene action. Ahmad *et al.* (1996) found additive gene action for bolls per plant. Paxasia *et al.* (1998) calculated additive gene action for number of sympodia per plant and plant height. In another study, Yingxin and Xiangming (1998) found that bolls per plant and seed cotton yield were controlled by additive and non-additive gene actions respectively. Broad sense heritability was high and narrow sense heritability was medium for these traits. Jagtap and Mehtari (1998) reported high heritability for sympodia per plant. Kalwar and Babar (1999) indicated the non-additive type of gene action for sympodia per plant bolls per plant seed cotton yield per plant. Hussain *et al.* (1999) analyzed gene action in upland cotton for seed cotton yield and reported additive type of gene action with partial dominance. From the study of quantitative inheritance in cotton for oil percentage, Hussain *et al.* (1999) found additive with partial dominance type of gene action. Non-additive type of gene action for plant height sympodia per plant, bolls per plant and seed cotton yield per plant have been found by Puntha *et al.* (1999). In gene action study of height of the main stem and bolls per plant in cotton (*G. hirsutum L*) both characters were controlled by additive type of gene action with partial dominance (Khan *et al.*, 1999). Esmail *et al.* (1999) reported additive dominance gene action for boll number and seed cotton yield. Both broad and narrow sense heritability estimates were high. Rady *et al.* (1999) computed both additive and non additive genetic effects for seed cotton yield and number of bolls per plant. The findings of Kumaresan (2000) indicated additive dominant gene action for seed cotton yield and bolls per plant in cotton (*G. hirsutum L*) high estimates of broad sense heritability for these traits. Hassain *et al.* (1999) estimated non-additive genetic effects for boll number, seed cotton yield and plant height. Predominance of additive effects in inheritance of seed cotton yield has been reported by Baloch *et al.* (2000). Similarly Subhan *et al.* (2001) observed additive type of gene influence for number of bolls per plant and over-dominance for seed cotton yield per plant. The present studies were aimed to investigate the genetic basis for some economic cotton traits, e.g. monopodia per plant, sympodia per plant, plant height, bolls per plant, seed cotton yield per plant and seed oil content to lay basis for the development of high yielding with high oil content of cotton varieties.

Materials and Methods

Six parental genotypes of cotton i.e. B-557, MNH-147, MNH-156 (local) Culture-728-4, B-1580 (ne) Culture 604-4 (exotic) were used to produce F₁ seed.

The parental material was grown in normal soil under natural field conditions during the month of June, 2000. At flowering, during August-September, the parental lines were crossed in a complete diallel fashion (6x6 diallel) to generate 30 F₁ crosses. At maturity, crossed bolls were picked and seed cotton was ginned with roller ginning machine. Six parents and their F₁ hybrids were grown in four replications at Cotton Research Station, Multan with plant to plant distance of 1.25 ft. and row to row distance of 2.5 ft. At maturity, data were recorded for monopodia per plant, sympodia per plant, plant height, bolls per plant, seed oil content and seed cotton yield.

Diallel technique (Mather and Jinks, 1982) was applied for determination of gene action of different traits.

Assumptions of diallel analysis and tests for the adequacy

The validity of information from a group of genotypes obtained from the diallel cross method is based on the following assumptions (Crumpacker and Allard, 1962).

- (i) Diploid segregation of chromosomes
- (ii) Homozygosity of parents
- (iii) Absence of reciprocal effects
- (iv) Absence of epistasis
- (v) No multiple allelism
- (vi) Independent distribution of genes among the parents

To fulfill the assumptions of absence of epistasis, no multiple allelism and independent gene distribution, data were subjected to three scaling tests. The first test was t^2 test. The second was the joint regression analysis of W_r and V_r . According to Mather and Jinks (1982) the regression co-efficient is expected to be significantly different from zero and not from unity. Failure of this test means the presence of epistasis or the genes are not independent. If dominance or certain types of non-allelic interaction is present, W_r+V_r must change from array to array. Similarly, if there exists epistasis, W_r-V_r will vary between arrays. Failure of these three tests completely invalidates the additive-dominance model. However, if one fulfills the assumptions, the additive-dominance model is considered to be partially adequate. Genetic components of variation were obtained using the procedures described by Hayman (1954) and adopted by Singh and Chaudhry (1985).

Genetic components of variation

Genetic components of variation were obtained using the procedures described by Hayman (1954a) and Mather and Jinks (1982) and adopted by Singh and Chaudhry (1985). Formulae for genetic components are given as under:

1. Additive variation (D).
2. Variation due dominant effect of genes (H_1).
3. Variation due to dominant effect of genes correlated for gene distribution (H_2). Relative frequency of dominant and recessive alleles (F). If F was positive dominant alleles are more than the recessive and if F is negative vice-versa is true.
4. Overall dominance of heterozygous loci (h^2).
6. Environmental variance (E)
7. Average degree of dominance $(H_1/D)^{1/2}$.
8. Proportion of genes with positive and negative effects in the parents i.e. uv over all loci u =frequency of increasing alleles and $v=1-u$ = Frequency of decreasing alleles. This ratio is equal to 0.25. When $u=v$ at all loci (Singh and Chaudhary, 1985) $H_2/4H_1$
9. Proportion of dominant and recessive genes in the parents $(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$

$$\text{Heritability} = h^2 \text{ (BS)} = \frac{0.5 D + 0.5H_1 - 0.25H_2 - 0.5F}{0.5 D + 0.5H_1 - 0.25H_2 - 0.5F + E}$$

$$h^2 \text{ (NS)} = \frac{0.5 D + 0.5H_1 - 0.5H_2 - 0.5F}{0.5 D + 0.5H_1 - 0.25H_2 - 0.5F + E}$$

Results

Number of sympodia per plant

Diallel analysis was carried out after obtaining highly significant genotypic differences (Table 1). When the scaling tests were applied to determine the adequacy of additive dominance model, the data were found partially adequate (Table 2).

Estimates of genetic components of variation (Table 3) depicted the additive and dominant gene effects. Gene distribution ($H_1 \neq H_2$) was observed to be asymmetrical which confirmed by the value of $H_2/4H_1$ (0.168). Lesser value for D than H_1 indicated over-dominance which was also supported by the value (1.140) of $(H_1/D)^{1/2}$. Frequency of dominant alleles for the trait under consideration was higher which was also indicated by $(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F = (1.975)$. Environment played an important role for the expression of character. Narrow sense (NS) heritability 0.528, was medium that indicated the importance of both additive and non-additive genetic variation. Similar results were found by Yingxin and Xiangming (1998) in cotton for sympodial branches, however Shanti and Raveendran (1999) reported high heritability estimates for the same trait. The intercept W_r/V_r (Fig. 1) on positive side indicated partial dominance.

Plant height

Highly significant genotypic differences (Table 1) paved way for diallel analysis. The data were found partially fit (Table 2). Table 3 showed presence of both additive and dominant effects of genes. Unequal values of H_1 and H_2 revealed asymmetrical gene distribution and this was supported by the value of $H_2/4H_1=0.209$. Pre-dominance of recessive alleles governing the expression of trait was shown by negative value of F. Proportion of dominant and recessive genes in the parents (0.476) also strengthened the results shown by the value of -F. Value of $(H_1/D)^{1/2}$, 0.682, reflected incomplete or partial dominance. Narrow-sense heritability estimate (0.837) suggested that improvement could be made through individual plant selection in the latter generations. Similar results were reported by Shanti and Raveendran (1999) in cotton for plant height.

W_r/V_r graph (Fig. 2) showed additive type of gene action. These results were in accordance with the previous studies of Saeed *et al.* (1996), Paxasia *et al.* (1998) and Khan *et al.* (1999). However non-additive gene action was observed for plant height by Puntha *et al.* (1999).

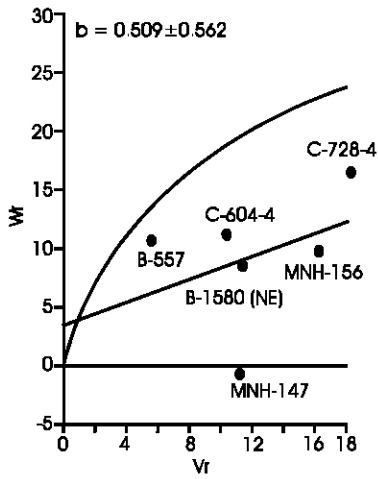


Fig. 1: W_r/V_r for sympodia per plant

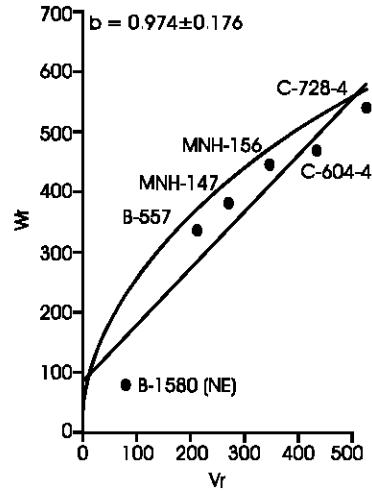


Fig. 2: W_r/V_r for plant height

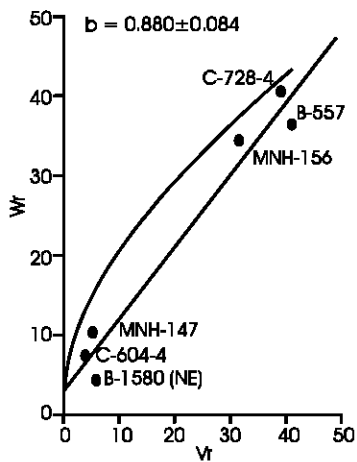


Fig. 3: W_r/V_r for bolls per plant

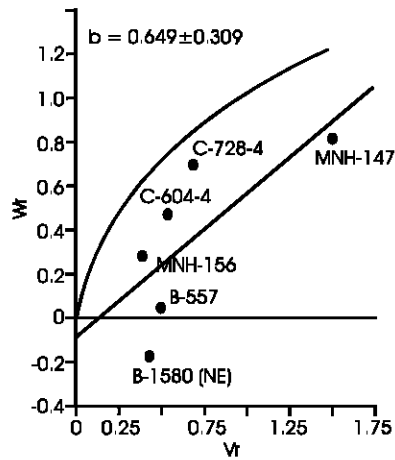


Fig. 4: W_r/V_r for seed oil content

Number of bolls per plant

Analysis of variance (Table 1) showed highly significant ($P \leq 0.01$) genotypic differences. Three scaling tests for the validity of additive-dominance model (Table 2) indicated partial adequacy of data that allowed for the computation of genetic components of variation (Table 3). The significance of D indicated the presence of additive effects among the parents, whereas H1 and H2 pointed out the absence of dominance effects of genes and symmetrical distribution of positive and negative alleles among the parents. It was supported by the value of $H_2/4H_1$, (0.248), which suggested equal proportion of genes with positive and negative effects. The higher value

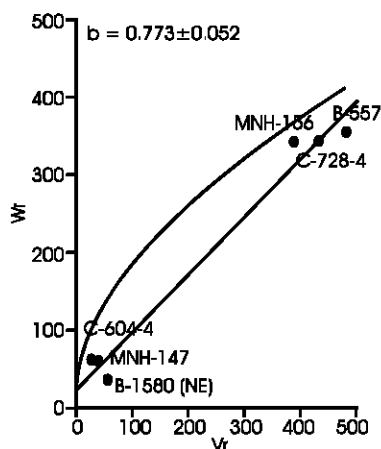


Fig. 5: W_r/V_r for seed cotton yield per plant

of D than H1 reflected the partial or incomplete dominance. The negative value of h^2 showed that direction of dominance was negative and the mean degree of dominance (0.825) revealed partial or incomplete dominance. The proportion of dominant and recessive genes in the parents (0.813) suggested that recessive genes are more frequent than dominant genes. These results were also confirmed by the value of F (-6.571). The environment played a significant role for the expression of trait under consideration. Narrow sense heritability (0.65) suggested that selection based on individual plants, in the latter generations, would give rapid progress. Similar findings were observed for number of bolls per plant by Ahmad *et al.* (1996), Esmail *et al.* (1999) and Kumaresan *et al.* (2000). The regression line (Fig. 3) expressed additive gene action. Saeed *et al.* (1996) and Kumaresan *et al.* (2000) also found similar observations. This is in contrast to the findings of Kalwar and Babar (1999) and Puntha *et al.* (1999) who reported non-additive gene action for this trait.

Seed Oil Content

The data were found partially adequate as it did not qualify all the three scaling tests. The genetic components showed (Table 3) that both additive and dominant effects were significant. Almost equal values of H_1 and H_2 indicated symmetrical gene distribution that was supported by $H_2/4H_1$ (0.251). Degree of dominance $(H_1/D)^{1/2} = 1.455$ indicated over-dominance genes effects. F value (0.371) expressed dominance genes. Significant value (0.937) of h^2 reflected that overall dominance was due to heterozygous loci. Higher values of H_1 and H_2 than h^2 indicated presence of directional dominance. The effect of environment was significant. The narrow-sense heritability (0.267) was low suggesting slow progress for individual plant selection in segregating population for the character under study. Low to high heritability estimates were found in cotton for the trait by Kohel (1987) and Dani (1989).

W_r/V_r graph (Fig. 4) reflected over-dominance as the regression line passed towards negative side. In contrast to these results, Kohel (1987) and Dani (1989) observed additive genetic effects.

402

Table 1: Mean squares from analysis of variance for monopodia per plant, sympodia per plant, plant height, bolls per plant, seed oil content and seed cotton yield per plant of F_1 of cotton

Items	Monopodia/plant	Sympodia/plant	Plant height	Bolls per plant	Seed oil content	Seed cotton yield
Replication	0.037	2.71	468.72	24.98	0.57	482.92
Genotype	1.799**	88.622**	2065.02**	129.244**	3.37**	1378.1**
Error	0.540	9.538	121.96	22.32	0.74	274.98

*,** = Significant at 0.05 and 0.01 levels, respectively.

Table 2: Tests of adequacy of additive-dominance model for 6x6 diallel of cotton

Characters	Joint regression	Test for t^2	Test for $b=0$	Test for $b=1$	Wr+Vr	Wr - Vr	Remarks
Monopodia per plant	$b=-0.048 \pm 0.061$	1.648 ^{ns}	-0.299 ^{ns}	6.491*	0.429 ^{ns}	3.408**	Inadequacy of additive-dominance model
Sympodia per plant	$b=0.509 \pm 0.562$	0.216 ^{ns}	0.906 ^{ns}	0.873 ^{ns}	2.184 ^{ns}	2.567 ^{ns}	Partial adequacy of additive-dominance model
Plant height	$b=0.974 \pm 0.176$	0.043 ^{ns}	5.536**	0.146 ^{ns}	11.335**	11.905**	Full adequacy of additive-dominance model
Bolls per plant	$b=0.880 \pm 0.084$	1.354 ^{ns}	10.406**	1.148 ^{ns}	4.734 ^{ns}	2.901*	Full adequacy of additive-dominance model
Seed oil content	$b=0.649 \pm 0.309$	0.102 ^{ns}	2.103 ^{ns}	1.136 ^{ns}	7.124**	2.201 ^{ns}	Partial adequacy of additive-dominance model
Seed cotton yield/plant	$b=0.774 \pm 0.052$	14.324**	14.994**	1.121 ^{ns}	5.475**	2.681**	

Partial adequacy of additive-dominance model*,** = Significant at 0.05 and 0.01 levels, respectively^{ns} = Non-significant

Table 3: Components of genetic variation for sympodia per plant, plant height, bolls per plant, seed oil content and seed cotton yield per plant of F₁ of cotton when grown in normal soil

Components	Sympodia per plant	Plant height	Bolls per plant	Seed oil content	Seed cotton yield/plant
D	28.534±4.416**	609.077±42.46**	38.66±2.928**	0.839±0.228**	297.848±40.23**
H ₁	37.094±11.209**	283.75±107.79**	26.294±7.432**	1.776±0.579**	322.269±102.11**
H ₂	25.029±10.013**	237.281±96.28**	26.11±6.638**	1.785±0.517**	310.984±91.21**
h ²	12.197±6.714**	756.264±64.83**	-2.66±4.47ns	0.937±0.348**	-34.688±61.41ns
F	21.329±10.784**	-295.435±103.69ns	-6.57±7.15ns	0.371±0.557ns	-166.957±98.24ns
E	2.337±1.685ns	32.898±16.21**	5.598±1.12*	0.183±0.087ns	70.189±15.35**
(H ₁ /D) ^{1/2}	1.140	0.682	0.825	1.455	1.04
H ₂ /4H ₁	0.168	0.209	0.248	0.251	0.241
[(4DH ₁) ^{1/2} +F]/					
[(4DH ₂) ^{1/2} -F]	1.975	0.476	0.813	1.359	0.575
h ² /H ₂	0.487	3.187	-0.102	0.525	-0.111
h ² (NS)	0.764	0.837	0.652	0.267	0.617
h ² (BS)	0.911	0.942	0.973	0.786	0.818

Table 4: 10 outstanding combinations of F₁ of cotton.

Crosses	Sympodia/plant	Plant height	Bolls per plant	Seed oil contents	Seed cotton yield
B557XC728-4	30.90	133.87	28.75	22.37	81.67
B557XMNH156	26.27	120.25	29.60	22.15	88.95
C728-4XB557	23.55	107.32	22.05	20.80	77.12
C728-4XC604-4	23.05	112.00	22.55	21.55	75.95
C728-4XMNH156	24.30	104.67	27.45	22.15	97.67
MNH156XB557	22.90	124.25	30.57	23.47	96.57
MNH156XC728-4	26.00	123.37	28.77	22.65	94.85
MNH156XC604-4	17.67	123.00	21.32	21.57	61.42
MNH156XMNH147	17.00	123.42	22.67	21.12	70.50
MNH147XC728-4	21.47	115.52	22.35	20.00	66.45

The cultivar MNH147 and Culture-728 had maximum recessive genes and C604 possessed both dominant and recessive genes while MNH156 and B-557 had more dominant genes than the recessive.

Seed Cotton Yield

Analysis of variance (Table 1) showed highly significant ($P \leq 0.01$) genotypic differences. Tests for the validity of the additive-dominance model (Table 2) showed partial adequacy of data. The estimates for genetic components of variation for seed cotton yield are given in Table 3. The positive and significant values of D and H suggested control of both the additive and dominant gene effects, which corresponds to the findings of Sanyasi (1991). The lesser value of D than H1 indicated over dominance. Unequal values of H1 and H2 signified asymmetrical distribution of positive and negative alleles. The negative value of F showed excess of recessive genes for the expression of the character under study. The greater values of H1 and H2 over h^2 suggested the absence of directional dominance non-significance of h^2 showed absence of overall dominance effect due to heterozygous loci. The environmental influence was significant. The positive intercept of W_r/V_r regression line (Fig. 5) reflected additive gene action. Similar results have been obtained by Saeed *et al.* (1996), Esmail *et al.* (1999), Shanti and Raveendran (1999) and Kumaresan *et al.* (2000). Narrow sense heritability (0.617) suggested that selection based on individual plant will give better progress for the character under study. Yingxin and Xiangming (1998), Esmail *et al.* (1999) and Kumaresan *et al.* (2000) also reported high heritability for seed cotton yield.

References

- Ahmad, S., M.D. Khan, M. Hassan, L. Ali and L.H. Akhtar, 1996. Exploration of varietal differences for some economic and quality characters in cotton. Pak. J. Pl. Sci., 2: 101-107.
- Azhar, F.M. and A.H. Rana, 1993. Genetic analysis of some quantitative plant characters in upland cotton. I. yield and its components. Pak. J. Agri. Sci., 30: 89-98.
- Azhar, F.M., N. Khan and S.K. Ajmal, 1994. Genetic basis of variation in upland cotton. J. Agric. Res., 32: 9-16.
- Baloch, J.M., A.R. Lakho, H. Bhutto, A.M. Memon, G.N. Panhwar and A.H. Soomro, 2000. Estimates of combining ability and genetic parameters for yield and fiber traits in upland cotton. Pak. J. Bio. Sci., 3: 1183-1186.
- Crumpacker, D.W. and R.W. Allard, 1962. A diallel cross analysis of heading data in wheat. Hilgardia, 32: 275-318.
- Dani, R.G., 1989. Heterosis and combining ability for oil content and other economic traits in cotton (*Gossypium hirsutum* L.). Ind. J. Genet. Pl. Br., 49: 47-51.
- Esmail, R.M, F.A. Hendawy, M. S. Rady and A.M. Hamid, 1999. Genetic studies on yield and yield components in one inter and two intra specific crosses of cotton. Egyptian. J. Agron., 21: 37-51.
- Hayman, B.I., 1954 a. The theory and analysis of diallel crosses. Genetics, 39: 789-809.
- Hussain, B., A.G. Ghaffari, M.A. Amin and M.A. Khan, 1999. Genetics analysis of some agronomic traits in cotton. J. Agri. Res., 37: 1-8.

- Ikram, M.A., A. Masood and A. Naveed, 1993. Manipulation of combining ability and its significance in cotton (*G. hirsutum* L.). J. Agri. Res., 31: 145-159.
- Jagtap. D.R. and S.S. Mehtari, 1998. Genetic variability in intervarietal crosses of upland cotton (*G. hirsutum* L.). Annual Agri. Res. Rep. Ind., 19: 130-132.
- Kalwar, M.S. and S.B. Babar, 1999. Estimates of combining ability in upland cotton. The Pak Cottons, 43 : 25-30.
- Khan, M.A., M.A Khan and T.E. Lodhi, 1999. Genetic study of yield and yield related components in cotton (*G. hirsutum* L.). JAPS, Uni. Agri. Faisalabad, 9: 73-75.
- Kohel, R.J., 1987. Seed oil content of glanded and glandless cottons. J.Amer. Oil Chem. Soc., 64: 1337-1340.
- Kumaresan, D.J. Ganesan and S. Ashok, 2000. Genetic analysis of quantitative characters in cotton (*G. hirsutum* L.). Crop Res. Ind., 19: 481-484.
- Mather, K. and J.L. Jinks, 1982. Biometrical genetics (3rd Ed.) Chapman and Hall Ltd. London, U.K.
- Paxasia, M.J., P.J Shukla and V.K. Poshiya, 1998. Combining ability for vegetative characters over environments in upland cotton (*G. hirsutum* L.). Gujarat Agri. Uni. Res. J. Ind., 23: 28-32.
- Puntha, D., T.S Raveendran and M. Kavitha, 1999. Heterosis and combining ability studies for quantitative characters in coloured cotton genotype (*G. hirsutum* L. × *G. barbedense* L.). PKV. Res. J., 23: 17-20.
- Rady, M.S., F.A. Hndendawy, A.M. Hamid and R.M. Esmail, 1999. Combining ability of yield and yield components in cotton. Egyptian. J. Agron., 21: 53-66.
- Saeed, F., T. Salam and M. Ikram, 1996. Gene action in intraspecific hybrids of *G. hirsutum* L. for yield parameters. J. Agri. Res., 34: 63-71.
- Sanyasi I.P.S., 1991. Genetic analysis of yield and number of bolls in upland cotton (*G. hirsutum* L.). Ind. J. Agric. Res., 25: 167-172.
- Shah, M.K, M.A. Khan, S.N. Chohan and R.A. Kainth, 1992. Genetic analysis of different parameters of cotton plant in different cross combinations of *G. hirsutum* L. J. Agric. Res., 30: 7-6.
- Shanti, P. and T.A. Raveendran, 1999. Genetic variability in F₂ populations in Cotton (*G. hirsutum* L.). PKV. Res. J., 23: 9-13.
- Singh, R.K. and B.D. Chaudhry, 1985. Biometrical methods in Quantitative Genetic analysis. Kalyani Pub. Ludhiana, New Delhi, Revised ed., pp: 102-118.
- Subhan, M., H.U. Khan and R.O. Ahmad, 2001. Population analysis of some agronomic and technological characteristics of upland cotton (*G. hirsutum* L.). Pak. J. Bio. Sci., 1: 120-123.
- Tariq, M., M.A. Khan and G. Idrees, 1992. Correlation and path coefficient analysis in upland cotton. Sarhad J. Agric., 8: 335-341.
- Tiwari, V.N., K.C. Mandloi and V.N. Acharya, 1992. Breeding behavior effects for yield and its components in intraspecific crosses of cotton (*G. hirsutum* L.). Ind. J. Agric. Res., 26: 173-178.
- Yingxin, Liu. and H. Xiangming, 1998. Research on the combining ability and inheritance of 12 economic characters in upland cotton. China Cotton, 25: 9-11.