



Full Length Article

Inheritance Pattern of Seed and Lint Traits in Cotton (*Gossypium hirsutum*)

MUHAMMAD AMJAD ALI¹ AND SHAHID IQBAL AWAN

Barani Agricultural Research Station, Fateh Jang, Pakistan

¹Corresponding Author: amjad.ali2001@gmail.com

ABSTRACT

A 5 x 5 diallel cross experiment was made to assess the inheritance pattern of some seed and lint traits in cotton using Mather and Jinks approach. Genotypic differences were significant ($P \leq 0.01$) for all the characters. The data of all the parameters were partially adequate for genetic analysis except seed weight per boll and lint index. Additive component of variation (D) was significant and predominant for number of seeds per boll, GOT and lint index, while dominance effects (H_1 & H_2) were main controlling agents for seed weight per boll, seed index and lint yield and it was firmly supported by the value of $H_1/D0.5$ for these parameters. Excess of dominant genes than recessive ones in the parents was revealed for seed weight per boll, seed index and lint ginning out turn (GOT). The values of h^2 and $H_2/4H_1$ demonstrated asymmetrical and un-equal distribution of dominant genes in parents for all the characters. Number of seeds per boll, GOT and lint index exhibited high narrow sense heritability (h^2 n.s.) due to the presence of additive gene action, whereas seed weight per boll, seed index and lint yield possessed low heritability. The genetic analysis suggested that number of seeds per boll, GOT and lint index could be upgraded through full-or half-sib family, pedigree and progeny selection, while exploitation of hybrid vigour would probably be the way to achieve the genetic progress in seed weight per boll, seed index and lint yield.

Key Words: Inheritance pattern; Components of variation; Seed and lint traits; Cotton

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is the most important textile fibre crop (Cherry & Leffler, 1984). Although, cotton is grown mostly for fibre, the seeds are an important source of oil (GOP, 2005-06). The cotton seed and lint yield of any cotton variety is a function of various characters including number of seeds per boll, seed weight per boll, seed index, lint yield per plant, ginning out turn (GOT) and lint index.

Seeds are the units of lint production and fibres grow from the outer cells of seed surfaces. Higher the number of seeds per boll produces more lint by increasing the surface area (Culp & Harrel, 1973). Therefore, breeding for increased bolls per unit land area, more seeds per boll, large seed surface area per unit seed weight and increased weight per unit seed surface are important (Smith & Coyle, 1999). Seed and lint indices are important in determining the seed cotton yield but they are affected by population density (Munro, 1987). Seed index is subjected to great influence by boll size and number of seeds per locule (Sikka & Joshi, 1960). Lint index, the absolute weight of lint borne by a single seed (or more often 100 seeds), is a function of mean number of hairs per seed and mean hair weight. GOT is the percentage of lint obtained from a sample of seed cotton and varies between cotton varieties (commonly ranges between 30-40%). It changes a little from year to year and from place to place (Munro, 1987).

Un-fortunately, lack of genetic variability for these characters is limiting breeding progress and gain under selection up to the final utilization of cultivars in production schemes. Diallel method of crossing is one of the reliable techniques, which enable the plant breeders to develop a source population with a lot of genetic variation for these traits. This technique not only creates variability but also permits the scientists to identify the type of genetic variation existing for the traits.

Inheritance pattern of seed and lint was focused through diallel by many scientists. The inheritance was predominantly commanded by dominant type of gene action in case of number of seeds per boll (Singh *et al.*, 1985) and seed index (Mahmoud *et al.*, 2004). However, some researchers found that additive genes were major contributors in the phenotypic manifestation of number of seeds per boll (Subhan *et al.*, 2001) and seed index (Ahmad *et al.*, 1997; Subhan *et al.*, 2002; Chandio *et al.*, 2003; Murtaza, 2005).

Studies of Tang *et al.* (1996), Ahmad *et al.* (2003), Chandio *et al.* (2003), Mehetre *et al.* (2004), Mahmoud *et al.* (2004), Basal and Turgut (2005), Murtaza *et al.* (2005) and Nadeem and Azhar (2008) revealed that the inheritance of ginning out turn, lint yield per plant and lint index was mostly controlled by dominant genes, whereas findings of Singh *et al.* (1990), Godoy and Palomo (1999), Subhan *et al.* (2001), Subhan *et al.* (2002), Iqbal *et al.* (2003),

Cheatham *et al.* (2003), Nadeem and Azhar (2004) and Mei *et al.* (2006) supported the involvement of additive genetic effects in the phenotypic expression of these traits. The objective of this research was to create variability, expose genetic effects and to establish appropriate parentage and breeding strategy for seed and lint characteristics in a complete diallel set involving five genetically diverse cotton genotypes.

MATERIALS AND METHODS

Experimental material. Studies pertaining to the inheritance pattern of seed and lint traits in cotton were carried out at Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. The plant material for this study was developed by diallel crossing of five cotton genotypes, NIAB-78, CIM-499, LSS, RH-112 and NIAB-Krishma, being different from each other for seed and lint characters.

Greenhouse experiment. The parents were grown in 30 × 30 cm earthen pots placed in greenhouse. The proper growing conditions were provided for germination and optimum plant growth. Temperature in the glasshouse was maintained at 30°C during 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 to maintain photoperiod of 16 h (Murtaza *et al.*, 2005). Seedlings were thinned to one plant per pot after two weeks of planting and after every 14 days 0.25 g of urea (46% N) was added to each pot and plants were watered daily (Ali *et al.*, 2008). At the time of flowering, all possible crosses were made among the genotypes following all the necessary precautionary measures to avoid the contamination of the genetic material. A large number of pollinations were carried out in order to produce sufficient quantity of hybrid seed.

Field experiment. The F_0 seeds of 20 hybrids and their five parents were planted in field in triplicate randomized complete block design (RCBD) during May, 2006. Each of the 25 entries including 5 parents and their F_1 hybrids was planted in a single row having 15 plants spaced at 30 cm within and 75 cm between the rows. All the recommended agronomic and plant protection practices were followed throughout the experiment. The matured bolls were picked from 10 guarded plants on the individual plant basis after every two weeks till the harvesting of crop in January 2007. Picking was done after the evaporation of dew. Seed cotton was collected in Kraft paper bags and was dried in sunlight for two days. Total seed cotton of all the plants in each entry were ginned with a single roller electrical gin in the laboratory on individual plant basis. The data were collected on number of seeds per boll, seed weight per boll, seed index (100-seed weight) and lint yield per plant in each entry. From these trait ginning out turn (GOT) and lint index were calculated.

Biometrical treatment of the data. The collected data

were analyzed by Fisher's analysis of variance to determine significant varietal differences among the 25 genotypes following Steel *et al.* (1996). The simple additive-dominance (AD) model suggested by Hayman (1954) and Jinks (1954), modified by Mather and Jinks (1982) and adopted by Singh and Chaudhry (1985) was followed for genetic analysis of the data.

RESULTS AND DISCUSSION

Analysis of variance among the genotypes. Preliminary analysis of variance following Steel *et al.* (1996) indicated significant differences ($P \leq 0.01$) for all the seed and lint characters among genotypes (Table I). The mean squares for the traits described high significance of the 'F' test for all the characters under study.

The diallel analysis of variance components (Table II) indicated the significance of (a) and (b) components for seed weight per boll and seed index, which showed the presence of additive and dominance effects. However, (b) item's significance for number of seeds per boll revealed the participation of dominant genes in their genetic control. No significance of b_1 item for all the traits suggested absence of directional dominance. The (b_2) portion of the (b) item was significant for seed index, lint yield, GOT and lint index, which showed nearly symmetrical distribution of genes. The (b_3) item was non-significant for number of seeds per boll, lint yield and GOT so specific gene effects were absent, while significant value of b_3 for other three traits showed that specific gene action controlling these characters. The (c) component was non-significant for all the characters showing the absence of maternal effects, except GOT. Absence of reciprocal effects was evident by the non-significance of item (d) for all the characters except GOT.

Assessment of data for additive-dominance model. The data were evaluated for additive-dominance (AD) model by making use of various adequacy parameters given in Table III. These parameters were the value of the regression coefficient (b) and the mean squares of $W_r + V_r$ and $W_r - V_r$. According to Mather and Jinks (1982) the data will be only valid for genetic interpretation if the value of regression coefficient (b) must deviate significantly from zero but not from the unity. The value of b varied significantly from zero

Table I. Mean squares obtained from simple analysis of variance of F_1 hybrids and their parents in cotton

Source of Variation	df	NSPB	SWPB	SI	LYPP	GOT	LI
Genotypes	24	19.59**	0.11**	0.88*	5.19**	2183.03**	1.66**
Replications	2	3.31 ^{NS}	0.04 ^{NS}	0.88 ^{NS}	2.24*	0.1988 ^{NS}	0.25 ^{NS}
Error	48	1.32	0.02	0.23	0.49	4.1467	0.11

Where;

*, ** = Significant at $P \leq 0.05$ and $P \leq 0.01$ levels, respectively. NS = Non-significant

NSPB=number of seeds per boll, SWPB=seed weight per boll, SI=seed index, LYPP= lint yield per plant, GOT= ginning out turn and LI=lint index

Table II. Mean squares from diallel analysis of variance of various seed and lint characters in cotton

Parameters	df	NSPB	SWPB	SI	LYPP	GOT	LI
a	4	22.00 ^{NS}	0.16*	5.69*	13.79 ^{NS}	78.53 ^{NS}	24.64 ^{NS}
b	10	16.12**	0.74*	3.60**	31.82*	108.19*	2.13*
b ₁	1	21.30 ^{NS}	1.97 ^{NS}	4.12 ^{NS}	58.09 ^{NS}	588.55 ^{NS}	0.94 ^{NS}
b ₂	4	25.60 ^{NS}	0.56 ^{NS}	2.89*	8.05*	6.40**	3.17*
b ₃	5	22.00 ^{NS}	0.63*	4.07*	45.58 ^{NS}	93.54 ^{NS}	1.53*
c	4	22.00 ^{NS}	0.05 ^{NS}	0.17 ^{NS}	1.23 ^{NS}	6.63*	3.23 ^{NS}
d	6	23.56 ^{NS}	0.14 ^{NS}	0.07 ^{NS}	0.32 ^{NS}	3.02**	1.20 ^{NS}
e	48	22.33	0.09	0.56	4.69	18.05	1.56

Table III. Adequacy test of additive-dominance (AD) model for 5×5 diallel in cotton

Characters	NSPB	SWPB	SI	LYPP	GOT	LI
Adequacy tests						
Joint regression coefficient (b)	0.88±0.08	0.83±0.26	0.84 ± 0.16	0.52±0.26	0.92± 0.17	0.91±0.14
t test for b=0	11.63**	3.22*	5.19*	1.98 ^{NS}	5.34*	6.52*
t test for b=1	1.55 ^{NS}	0.64 ^{NS}	1.02 ^{NS}	1.82 ^{NS}	0.44 ^{NS}	0.65 ^{NS}
Mean squares for Wr+Vr (between arrays)	16.15 ^{NS}	0.02**	0.38 ^{NS}	23.16**	0.854 ^{NS}	1.25**
Mean squares for Wr-Vr (between arrays)	1.29 ^{NS}	0.0001 ^{NS}	0.01 ^{NS}	4.38 ^{NS}	0.183 ^{NS}	0.08 ^{NS}
Adequacy to AD-model	Partial	Full	Partial	Partial	Partial	Full

Table IV. Components of variation for seed and lint traits in cotton for F1 generation

Parameters	NSPB	SWPB	SI	LYPP	GOT	LI
Components of variation						
D	10.131±0.156**	0.041±0.016*	0.211±0.047*	0.959±0.912 ^{NS}	1.808±0.099*	1.150±0.066**
H ₁	5.312±0.422**	0.185±0.043*	0.488±0.128*	7.119±2.465*	-0.042±0.269 ^{NS}	0.587±0.180*
H ₂	3.364±0.398*	0.151±0.041*	0.432±0.120*	6.695±2.327*	0.077±0.244 ^{NS}	0.397±0.170*
F	-1.252±0.258 ^{NS}	0.070±0.026*	-0.103±0.078 ^{NS}	0.845±1.509 ^{NS}	- 0.140±0.249 ^{NS}	0.258±0.110*
h ²	2.463±0.258*	0.136±0.026*	0.407±0.078*	4.011±1.509*	0.304±0.164 ^{NS}	0.042±0.110 ^{NS}
E	0.468±0.063*	0.006±0.006 ^{NS}	0.086±0.019*	0.187±0.372 ^{NS}	0.352±0.040*	0.037±0.027 ^{NS}
(H ₁ /D) ^{0.5}	0.72	2.11	1.52	2.72	0.152	0.71
H ₂ /4H ₁	0.84	2.35	0.72	1.39	-0.460	1.37
(4DH ₁) ^{0.5} +F/(4DH ₁) ^{0.5} -F	0.16	0.20	0.22	0.24	0.594	0.17
h ² _(n.s)	0.84	0.20	0.49	0.13	0.71	0.80

but not from one for all the characters, except lint yield per plant, which did not fulfill this criterion.

For the data to be valid for AD-model, the mean squares for (Wr+Vr) should be significantly different between the arrays, while the mean squares for (Wr-Vr) should be non-significant (Mather & Jinks, 1982; Singh & Chaudhry, 1985). In this study, lack of significant variation in the (Wr-Vr) arrays over replications for all the characters suggested that any kind of epistasis was not involved in the phenotypic expression of the traits. Although the value of regression coefficient (b) proved the fitness of the data of number of seeds per boll (0.83), seed index (0.84) and GOT (0.92) for AD model, the mean square value of (Wr+Vr) for the traits indicated no significance, thus rendering partial validity of these characters for further genetic analysis. The data of lint yield per plant, tested for AD-model using the analysis of variance of (Wr+Vr) and (Wr-Vr), exhibited non-significant value of regression coefficient (b) at both null hypothesis (b=0) and alternate hypothesis (b=1), while the assessment of mean squares for Wr+Vr between arrays exposed the data of these characters for genetic investigation. The data of seed weight per boll and lint index were able to meet both the adequacy criteria and expressed full fitness to AD-model.

Genetic analysis of seed and lint traits. Inheritance pattern of seed and lint traits was evaluated by the computation of

genetic components of variation D, H₁, H₂, F and h² (Table IV). All the fibre characters exhibited significant additive (D) and dominant (H₁ & H₂) components of variation except lint yield per plant and GOT, which showed significant dominance and additive components, respectively. Although both the additive and dominant components were significant for number of seeds per boll, seed weight per boll, seed index and lint index, higher magnitude of D component over H₁ and H₂ for seeds per boll and lint index revealed that additive part was more prominent in determining these characters. In case of seed weight per boll and seed index, the variability was accounted for by dominance effects, which conform to the previous studies for cotton (Singh *et al.*, 1990; Subhan *et al.*, 2001; Chandio *et al.*, 2003; Cheatham *et al.*, 2003; Mahmoud *et al.*, 2004; Mehetre *et al.*, 2004; Murtaza *et al.*, 2005).

The breeding success of a genotype is a function of the additive genes, which are directly transmitted from parents to offspring, are responsible for the resemblance between relatives and can be used to calculate inheritance (Falconer, 1989). Predominance of additive effects (D) in the genetic mechanism of number of seeds per boll, GOT and lint index advocated that the genes for the characters are fixed and the traits could be improved via selection by exploiting pedigree method right from F₂ generation. On the other hand, inheritance in seed weight per boll, seed index and lint yield

was conditioned by genes having dominant effects at most of the loci and manipulation of the parents may be useful through exploitation of heterosis for improving these quality attributes.

Degree of dominance ($H_1/D^{0.5}$) is an indicative of dominance additive ratio. Dominance additive ratio of less than unity refers to partial dominance, near one indicates complete dominance and greater than one indicates over dominance (Falconer, 1989). Degree of dominance for number of seeds per boll, GOT and lint index demonstrated the preponderance of additive genes in the genetic control of both these characters and this was well supported by higher values of D component over H_1 and H_2 for these characters (Singh *et al.*, 1990; Chandio *et al.*, 2003; Nadeem & Azhar, 2004; Murtaza, 2005). Conversely, seed weight per boll, seed index and lint yield displayed value of ($H_1/D^{0.5}$) higher than one, which indicated the effect of over-dominance in the genetics of these parameters (Mahmoud *et al.*, 2004; Basal & Turgut, 2005).

The item h^2 measures the direction of dominance. Significant value of h^2 for all the traits showed that direction of dominance was unidirectional (from parents to offspring) with the exception of GOT and lint index. This suggested that heterosis breeding could be rewarding for this trait. The value $H_2/4H_1=0.25$ imply that dominant genes ($H_1=H_2$) would be in equal proportions (Mather & Jinks, 1982; Singh & Chaudary, 1985). This value indicated asymmetrical distribution of dominant genes for all the traits. Iqbal *et al.* (2003), Basal and Turgut (2005), Murtaza (2005) and Murtaza *et al.* (2005) also reported unidirectional dominance and asymmetrical distribution of dominant genes for GOT, seed index and lint index.

Estimate of the relative frequency of dominant to recessive alleles in the parental lines (F) was negative for number of seeds per boll, seed index and GOT. This revealed the excess of recessive alleles present in genetic material in which these characters were evaluated. This claim was strengthened by values of $(4DH_1)^{0.5}+F/(4DH_1)^{0.5}-F$ which were lower than one. However, the positive F value for remaining three parameters disclosed the excess of dominant genes in the parents. Significant blocking component (E) for seeds per boll, seed index and GOT indicated that these characters were affected by environment.

Narrow sense heritability is a measure of breeding values and articulates the magnitude of genotypic variance in the population, which is mainly responsible for changing the genetic composition of the population via selection (Falconer, 1989). Estimates of narrow sense heritability ($h^2_{n.s.}$) showed high heritability for number of seeds per boll, GOT and lint index. This implied that this was the function additive genes was involved in the heritage of these traits, which indicated that selection response could be rapid for these characters. Ahmad *et al.* (2003), Nadeem and Azhar (2004), Naem and Azhar (2008) and Basal and Turgut (2005) also reported high narrow sense heritability for GOT,

however, Murtaza *et al.* (2005) found high $h^2_{n.s.}$ for lint index. Thus selection could be an appropriate method for improvement in these parameters. However, seed weight per boll, seed index and lint yield demonstrated lower heritability estimates due to the involvement of dominance effects in their inheritance (Tang *et al.*, 1996; Ahmad *et al.*, 1997; Iqbal *et al.* 2003).

CONCLUSION

The data showed significant genetic variation to allow the diallel analysis to work on. Additive genes coupled with high narrow sense heritability were involved in the inheritance of number of seeds per boll, GOT and lint index, while the heritage of seed weight per boll, seed index and lint yield per plant was determined by dominant genetic effects. Furthermore, number of seeds per boll, GOT and lint index could be improved via selection, whereas hybrid vigour might be fruitful for progress in case of seed weight per boll, seed index and lint yield.

REFERENCES

- Ahmad, R.T., I.A. Khan and M. Zubair, 1997. Diallel analysis for seed-cotton yield and its contributing traits in upland cotton (*Gossypium hirsutum*). *Indian J. Agric. Sci.*, 67: 583–585
- Ahmad, S., M.Z. Iqbal, A. Hussain, M.A. Sadiq and A. Jabbar, 2003. Gene action and heritability studies in cotton (*Gossypium hirsutum* L.). *Online J. Biol. Sci.*, 4: 443–450
- Ali, M.A., I.A. Khan and S.I. Awan, S. Ali and S. Niaz, 2008. Genetics of fibre quality traits in Cotton (*Gossypium hirsutum* L.). *Australian J. Crop Sci.*, 1: 10–17
- Basal, H. and I. Turgut, 2005. Genetic analysis of yield components and fibre strength in upland cotton (*Gossypium hirsutum* L.). *Asian J. Plant Sci.*, 27: 207–212
- Chandio, M.A., M.S. Kalwar and G.M. Baloch, 2003. Gene action for some quantitative characters in upland cotton (*Gossypium hirsutum* L.). *Pakistan J. Sci. Indus Res.*, 46: 295–299
- Cheatham, C.L., J.N. Jenkins, Jr. J.C. McCarty, C.L. Watson and J. Wu, 2003. Genetic variances and combining ability of crosses of American cultivars, Australian cultivars and wild cottons. *J. Cott. Sci.*, 7: 16–22
- Cherry, J.P. and H.R. Leffler, 1984. Seed. In: Kohel, R.J. and C.F. Lewis (eds.), *Cotton*, pp: 511–569. ASA, Madison, WI
- Culp, T.W. and D.C. Harrel, 1973. Breeding methods for improving yield and fiber quality upland cotton (*Gossypium hirsutum* L.). *Crop Sci.*, 13: 686–689
- Falconer, D.S., 1989. *Introduction to Quantitative Genetics*, 2nd edition, p: 438. Longman New York, USA
- Godoy, A.S. and G.A. Palomo, 1999. Genetic analysis of earliness in upland cotton (*Gossypium hirsutum* L.). II. Yield and lint percentage. *Euphytica*, 105: 161–166
- GOP (Government of Pakistan), 2005-06. *Agricultural Statistics of Pakistan*. Ministry of Food, Agriculture and Live Stock, Economic Wing, Islamabad, Pakistan
- Hayman, B.I., 1954. The analysis of variance of diallel crosses. *Biometrics*, 10: 235–245
- Iqbal, M., M.A. Chang and M.Z. Iqbal, 2003. Breeding behavior effects for yield, its components and fibre quality in Intraspecific crosses of cotton (*G. hirsutum* L.). *Online J. Bio Sci.*, 4: 451–459
- Jinks, J.L., 1954. The analysis of continuous variation in diallel crosses of *Nicotina rustica* L. varieties. *Genetics*, 39: 767–788
- Mahmoud, A.M., T.M. El-Ameen, A.A. Mohamed and M.A. Ali, 2004. Inheritance of some agro-economic traits in interspecific cotton cross using six parameters model under two locations. *Assiut J. Agric. Sci.*, 3: 95–106

- Mather, K. and J.L. Jinks, 1982. *Biometrical Genetics*, 3rd edition. London Chapman and Hall
- Mehetre, S.S., G.C. Shinde, H.J. Rajput and B.D. Solunke, 2004. Genetic studies of seed cotton yield and its components in cotton. *Ann. Agric. Res.*, 4: 529–531
- Mei, Y., Z. Ye and L. Zhang, 2006. Genetic Analysis for F₁ Yield Traits with Conditional Approach in Island Cotton (*Gossypium barbadense* L.). *Acta Genet. Sin.*, 33: 841–850
- Munro, J.M., 1987. *Cotton: Tropical Agriculture Series*, 2nd edition, p: 161. Longman Scientific and technical John Willey Sons Inc, New York
- Murtaza, N., 2005. Study of gene effects for boll number, boll weight and seed index in cotton. *J. Cent. European Agric.*, 6: 255–262
- Murtaza, N., G.M. Ali and H. Rahman, 2005. Inheritance of fiber quality characters in upland cotton genotypes having non-preference traits for insect pests. *J. Food Agric. Environ.*, 3: 180–184
- Naeem, M. and F.M. Azhar, 2008. Identification of superior parents and hybrids for yield and its components in cotton (*Gossypium hirsutum*). *Int. J. Agric. Biol.*, 10: 447–450
- Nadeem, K. and F.M. Azhar, 2004. Genetic analysis of seed cotton yield and its components in *Gossypium hirsutum* L. *Int. J. Agric. Biol.*, 6: 865–8
- Sikka, S.M. and A.B. Joshi, 1960. *Problems of Cotton Improvement*, pp: 137–335. Cotton, India Monograph
- Singh, M., T.H. Singh and G.S. Chahal, 1985. Genetic analysis of some seed quality characters in upland cotton (*Gossypium hirsutum* L.). *Theor. Appl. Genet.*, 71: 126–128
- Singh, M., T.H. Singh, G.S. Chahal and L.S. Randhawa, 1990. Genetic analysis of lint yield and its components in cotton. *Crop Improvement*, 17: 64–67
- Singh, R.K. and B.D. Chaudhary, 1985. *Biometrical Methods in Quantitative Genetics*, pp: 102–127. Kalyani Publishers, New Dehli
- Smith, C.W. and S.G. Coyle, 1999. Association of fiber quality parameters and within boll yield components in upland cotton. *Crop Sci.*, 37: 1775–1779
- Steel, R.G.D., J.H. Torrie and D.A. Deekey, 1996. *Principles and Procedures of Statistics: A Biometrical Approach*, 3rd edition. McGraw Hill Book Co., New York
- Subhan, M., H.U. Khan and R. Ahmad, 2001. Population analysis of some agronomic and technological characteristics of upland cotton (*Gossypium hirsutum* L.), using diallel analysis. *Online J. Biol. Sci.*, 1: 120–123
- Subhan, M., M. Qasim, K. Ahmad and H. Niazi, 2002. Genetics of yield and its components in Upland cotton. *Asian J. Plant Sci.*, 1: 250–253
- Tang, B., J.N. Jenkins, J.C. McCarty, C.E. Watson and R.G. Creech, 1996. Evaluation of genetic variances, heritabilities and correlations for yield and fiber traits among cotton F₂ hybrid populations. *Euphytica*, 91: 315–322

(Received 08 April 2008; Accepted 29 August 2008)