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Studies on Gene Effects of Seed Cotton Yield and its Attributes in Five American Cotton Cultivars

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ABSTRACT

A 5 X 5 full diallel cross experiment was conducted involving five cotton (*Gossypium hirsutum* L.) varieties namely CIM-443, NIAB Krishma, Cris-420, RH-112 and Coker-207 to evaluate genetic effects involved in the inheritance of various multigenic plant traits. The characters under consideration were number of monopodial branches, number of sympodial branches, boll weight, yield of seed cotton, lint percentage, staple length, fibre fineness and fibre strength. All the characters showed considerable genetic variations among the genotypes ($P < 0.01$). The data for all the characters were partially fit for additive-dominance genetic model. All the characters showed additive type of gene effects with partial dominance. Narrow sense heritability estimates were higher for all the characters studied except lint percentage and staple length. Presence of additive genetic effects and high narrow sense heritability estimates suggested that selection breeding might be progressive for genetic improvement for yield of seed cotton and its attributes.

Key Words: American cotton; Quantitative characters; Genetic effects

INTRODUCTION

Despite of substantial progress made in other sectors, agriculture, by part, still has the pivotal position in the economy of the country. Amongst the crops, upland cotton (*Gossypium hirsutum* L.) is very important. It sustains a lot of peoples in various fields such as textile mills, agriculture fields, ginning factories, small-to-large scale business and trade. Cotton accounts for 8.6% of the value added in agriculture and about 1.9% to GDP (Anonymous, 2006; Ali & Khan, 2007). Efforts on various aspects of the cotton crop have been under way to increase its production. The most important factor in the process of crop production has always been a good variety in any crop. Cotton breeders managed to produce high yielding varieties through various genetic manipulations and breeding approaches and consequently a significant progress was achieved in this connection. In order to evolve high yielding varieties of cotton, the genetic information on different traits like, number of bolls per plant, number of monopodial branches, number of sympodial branches, boll weight and yield of seed cotton may help the breeders in improving genetic architecture of the plant in particular direction for maintaining and improving the proper crop production level.

For this purpose, the use of already existing genetic variability in the breeding material as well as, the creation of new variability along with its genetic understanding is of crucial importance in a breeding program. Thus before making selection for a breeding population, it is necessary to collect information whether the desired variability is existing among the characters under interest and also to study the mode of gene action controlling the characters to be improved.

In past many scientists were interested in studies to identify the inheritance pattern of these. For example, the investigations of Malek and Shamsuddin (1998), Hussain *et al.* (1999), Deshmukh *et al.* (1999), Mukhtar *et al.* (2000), Subhan *et al.* (2002) and Murtaza *et al.* (2002) and of Iqbal *et al.* (2003) and Nadeem and Azhar (2004) revealed additive type of gene action with partial dominance, whilst Liu *et al.* (1998), Kumaresan *et al.* (2000), Ahmad *et al.* (2000), Abd-El-Rahim *et al.* (2001), Bertini *et al.* (2001) and Subhan *et al.* (2003) reported the presence of genes showing over-dominance for most of these traits. Abd-El-Rahim *et al.* (2001), Murtaza *et al.* (2002) and Subhan *et al.* (2003) repoted addive gene action for lint percentage. Tariq *et al.* (1995), Iqbal *et al* (2003) and Ali *et al.* (2008) observed additive genes for staple length. Additive genetic effects were found for fibre fineness (Ahmad & Azhar, 2000; Ahmad *et al.*, 2003; Ali *et al.*, 2008) and fibre strength (Akbar *et al.*, 2001; Iqbal *et al.*, 2003; Ahmad *et al.*, 2003; Yuan *et al.*, 2005).

To generate such information a five parent's diallel cross experiment was conducted in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the year 2005-2007 by using diallel technique. The purpose of this experiment was to study gene action and heritability estimates. The diallel technique was developed by Hayman (1954) and Jinks (1954).

MATERIALS AND METHODS

The present experiment was carried out at experimental area of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the years 2005-

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07. The experimental material consisted of five parental genotypes namely CIM-443, NIAB Krishma, Cris-420, RH-112 and Coker-207, representing a range of variation in yield and its attributes (Table I), were sown in earthen pots (12′ × 12′) in greenhouse during November 2005. During germination and growth environmental conditions were possibly controlled and required agronomic practices were followed. At flowering, the parental lines were crossed in a complete diallel fashion (5 × 5) to generate 20 F_1 crosses (direct & indirect) along 5 parents. All necessary precautionary measures were taken to avoid contamination of genetic material at the time of crossing and selfing. At maturity, crossed and selfed bolls were picked and seed cotton of each cross was ginned separately using single roller electric ginner.

The F_0 seed from all crosses along with their selfed parents were sown in the field in a Randomized Complete Block Design with three replications during June-2006. In a replication each of 25 entries was planted in a single row having 10 plants with plant to plant and row to row distances of 30 cm and 75 cm, respectively. All the recommended agronomic practices and crop protection measures were applied from sowing to the harvesting of crop. At maturity, the data were recorded for number of monpodial branches, number of sympodial branches, boll weight, seed cotton yield, lint percentage, staple length, fibre fineness and fibre strength from five guarded plants from each entry, both in field as well as laboratory on individual plant basis. The data was subjected to analysis of variance (Steel *et al*., 1996) to establish the level of genotypic differences for the plant traits under study. The characters showing significant genotypic differences were further analyzed genetically following additive dominance model of genetic analysis developed by Hayman (1954) and Jinks (1954).

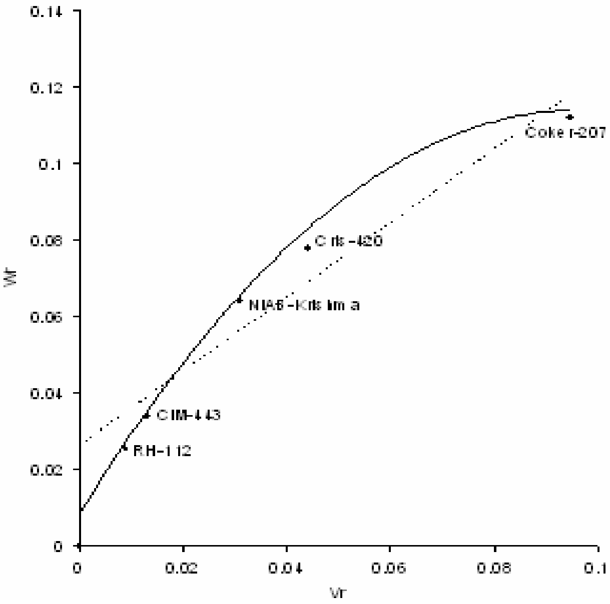
RESULTS AND DISCUSSION

Number of monopodial branches. The results indicated highly significant differences among the parents and their crosses showing that these genotypes differed genetically from each other for this trait (Table II). Variance (Vr) and covariance (Wr) values were calculated. Results of joint regression analysis suggested that data were fit for additive dominance model, because the value of b was significant at zero and non-significant at unity (Table III). Values of t square, Vr+Wr and Vr-Wr also confirmed the validity of the data for further genetic analysis. Positive value of intercept confirmed the predominance of additive type of gene action with partial dominance for monopodial branches (Fig. 1). The regression line did not deviate significantly from unit slope, which suggested the absence of non-allelic interactions. These results are in accordance with those of Malek and Shamsuddin (1998), Deshmukh *et al*. (1999) and Iqbal *et al*. (2003) that advocated the use of selection to improve this trait, while differed from the results of Ahmad *et al*. (2000) who observed over dominance type of gene action for this character. The position of the array points on regression line showed that variety Coker-207 had maximum dominant genes being closest to the point of origin, while variety Cris-420 possessed maximum recessive genes being farthest from origin.

Table I. Means of parents for number of monopodial branches (NM), number of sympodial branches (NS), boll weight (BW), yield of seed cotton (SCY), lint percentage (LP), staple length (SL), fibre fineness (FF) and fibre strength (FS)

Parents	NM	NS	BW	SCY	LP	SL	FF	FS
CIM-443	3.17	20.74	2.74	38.76	36.65	27.63	5.22	2.74
NIAB-Krishma	2.92	21.9	2.9	32.55	37.32	28.09	4.96	2.90
Cris-420	2.9	18.64	2.65	42.12	37.80	27.12	5.05	2.65
RH-112	3.17	18.59	2.6	50.83	36.62	27.85	4.83	2.60
Cocker-207	2.79	20.38	2.73	50.49	37.88	27.18	4.92	2.73

Fig. 1. Number of Monopodial Branches



The presence of additive gene action with incomplete dominance and moderate estimates of narrow sense heritability (0.62) (Table II) for this character recommended the selection breeding as an appropriate procedure for the improvement of this character. However, moderate heritability also showed that selection should be delayed to later generations.

Number of sympodial branches. Mean squares were highly significant among the parents and their crosses showing that these genotypes differed genetically from each other for this trait (Table II). Results of scaling test (Table III) suggested that data were fit for additive-dominance model as proposed by Hayman (1954) and Jinks (1954). Regression line intercepted the Wr-axis above the point of origin indicating partial dominance with additive type of gene action (Fig. 2). The regression line did not deviate significantly from unit slope, which suggested the absence of non-allelic interactions as indicated by the values of

Table II. Mean squares and habitability estimates in narrow sense of seed cotton yield and its attributes

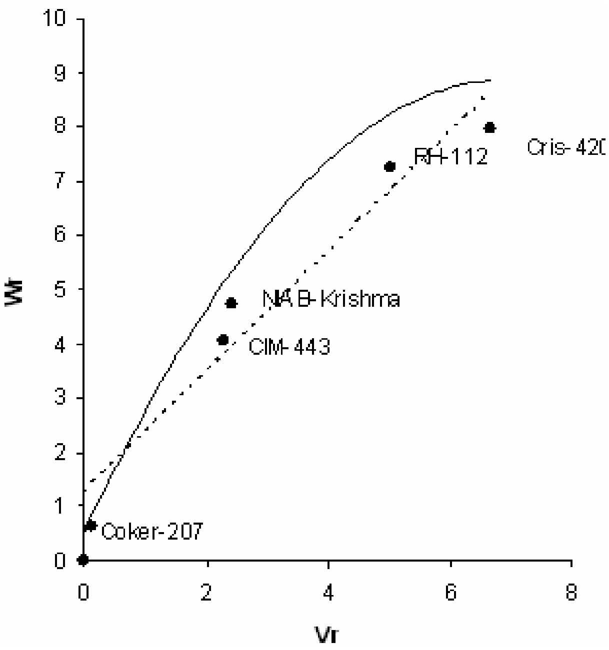
Source of variation	NM	NS	BW	SCY	LP	SL	FF	FS
Replications	0.036^{NS}	3.522 ^{NS}	0.0001 ^{NS}	1.04 ^{NS}	4.7842*	0.3855 ^{NS}	0.0164 ^{NS}	0.0001^{NS}
Genotypes	0.968**	16.935**	0.173**	409.96**	11.16**	1.842**	0.2021**	6.6870**
Error	0.076	2.235	0.00629	5.02	1.5380	0.7545	0.0228	1.0941
h^2_{ns}	0.70	0.69	0.87	0.88	0.44	0.43	0.73	0.87

Table III. Results of adequacy tests for additive-dominance model of seed cotton yield and it's attributes

Characters	Test for b = 1	Test for b = 0	Regression Coefficient (b)	t^2	Vr + Wr	Vr - Wr	Conclusion
Number of sympodial branches	-0.666^{NS}	6.92*	1.106	0.885	2.321	0.572	The data were partially fit for genetic analysis
No of monopodial branches	0.289ns	6.91**	0.960	0.006	1.586	0.600	The data were partially fit for genetic analysis
Boll weight	2.51^{NS}	22.20**	0.898	5.396*	2.247^{NS}	3.507^{NS}	The data were partially fit for genetic analysis
Yield of seed cotton	1.49 ^{NS}	6.18**	0.805	1.326	21.93**	6.175**	The data were partially fit for genetic analysis
Lint percentage	-0.9520^{NS}	7.085*	1.155	1.6143	2.5093 ^{NS}	0.4126 ^{NS}	The data were partially fit for genetic analysis
Staple length	0.0874^{NS}	3.508**	0.975	0.1094	2.706 ^{NS}	0.2063 ^{NS}	The data were partially fit for genetic analysis
Fibre fineness	0.2747^{NS}	5.086**	0.9487	0.0001	37.56**	3.208 ^{NS}	The data were partially fit for genetic analysis
Fibre strength	2.51 ^{NS}	22.20**	0.95	5.3916*	2.247 ^{NS}	0.035 ^{NS}	The data were partially fit for genetic analysis

regression coefficient b, t-square, Vr+Wr and Vr-Wr. These results are in accordance with those of Malek and Shamsuddin (1998), Deshmukh *et al*. (1999) and Iqbal *et al*. (2003), who pointed out that progress in this parameter might be made through a selection breeding program, while varied from the results of Ahmad *et al.* (2000) who observed over dominance of gene action for this character and suggested the use of hybrid vigor to improve this trait. The position of the array points on regression line showed that variety Coker-207 had maximum dominant genes being closest to the point of origin while variety Cris-420 possessed maximum recessive genes being farthest from origin. Preponderance of additive genetic effects and moderately high heritability estimates (0.69) advocated that selection should be carried out for the betterment of this character (Table II).

Fig. 2. Number of Sympodial Branches



Boll weight. Analysis of variance for boll weight for (Table II) showed highly significant differences existing among the genotypes evaluated. The results of adequacy tests (Table III) indicated that b value deviated significantly from zero but not from unity so the data were fit for further genetic analysis as suggested by Hayman (1954) and Jinks (1954). Mean values of parents are given in Table I. The values of variances (Vr) and covariances (Wr) were calculated and the graphical representation (Fig. 3) showed that regression line (b) intercepted the Wr-axis above the origin indicating additive type of gene action. The estimates of narrow sense heritability for this character were high due to additive type of gene action. The regression line did not deviate from unit slope, therefore interactions of genes was not involved. These results are in accordance with the findings of Iqbal *et al.* (2003) and Nadeem and Azhar (2004), which confirmed additive gene action for this character, while Bertini *et al.* (2001) and Subhan *et al.* (2003) reported non-additive type of gene action, suggesting the involvement of over dominant genes in the phenotypic expression of this character. From the position of array points on the regression line it is clear that the variety CIM-443 closest to the origin had maximum dominant genes where as Coker-207 that occupied the farthest position from point of origin possessed maximum recessive genes (Fig. 3). Dominance of additive gene action involved in the inheritance of the trait and high narrow sense heritability estimates (Table II) concluded that selection should be carried out for the improvement of boll weight.

Yield of seed cotton. The result of analysis of variance revealed that means genotypic differences among all the genotypes were highly significant for yield of seed cotton (Table II). The adequacy tests showed partial fitness of the data for additive-dominance model (Table III). Fig. 4 showed that regression line intercepted the Wr-axis above the origin signifying additive type of gene action involved in the phenotypic expression of yield of seed cotton. The relative position of array points on the regression line revealed that variety CIM-443 being near to the origin

Fig. 3. Boll Weight

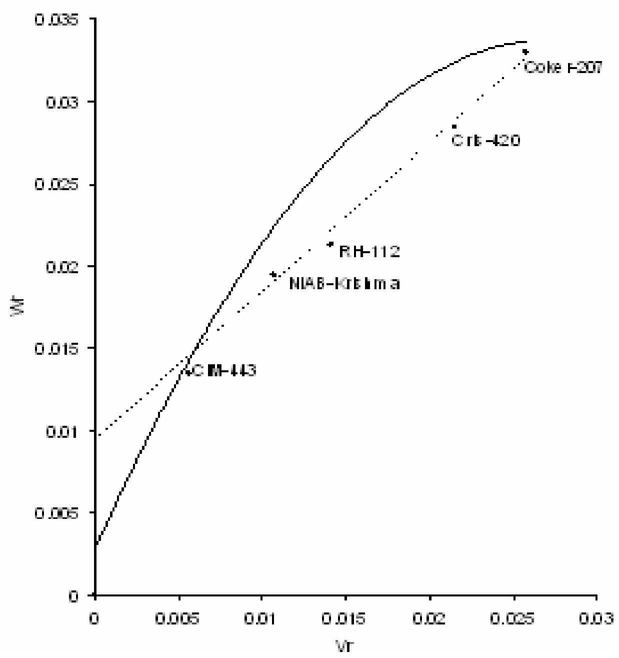


Fig. 5. Lint percentage

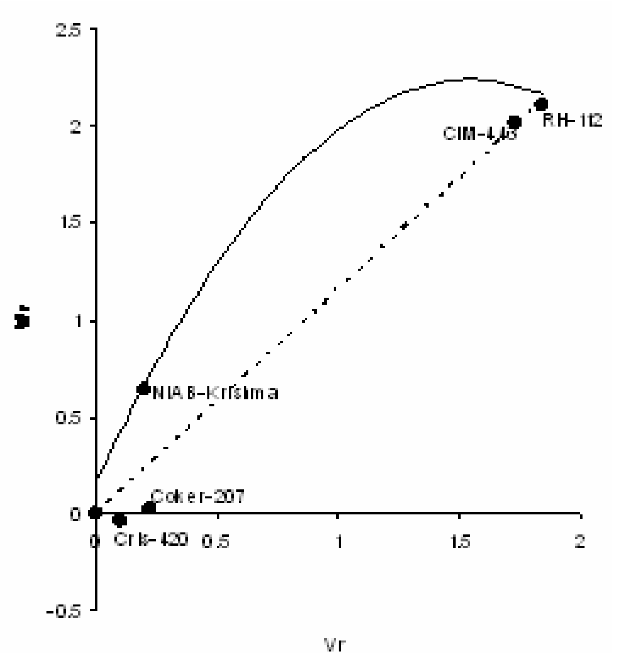


Fig. 4. Yield of Seed Cotton

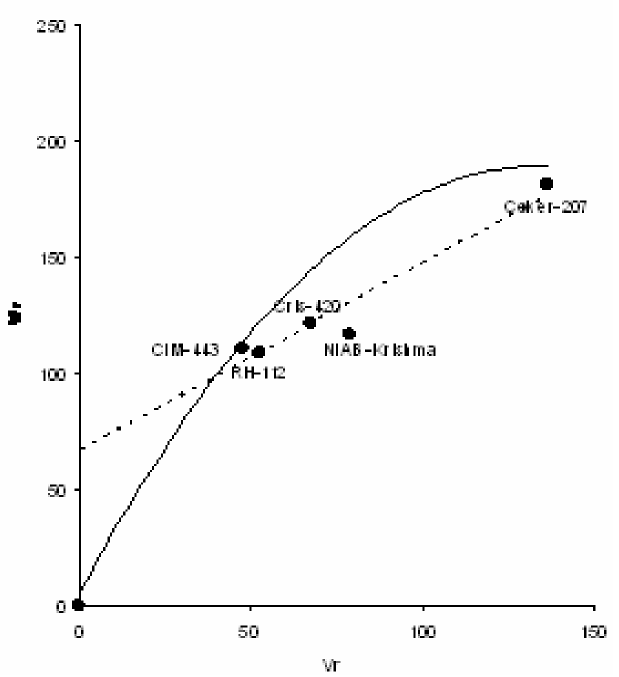
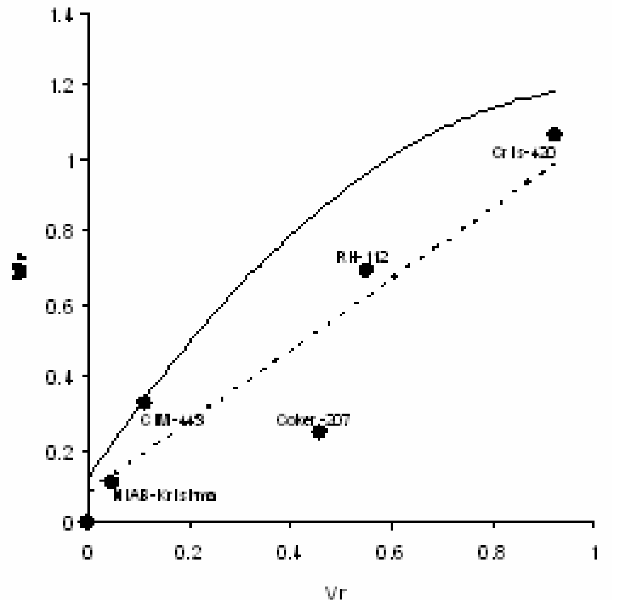


Fig. 6. Staple length



possessed maximum dominant genes, while variety Coker-207 being away had maximum recessive genes. These results were supported by the findings of Hussain *et al.* (1999), Deshmukh *et al.* (1999), Mukhtar *et al.* (2000), Subhan *et al.* (2002) and Murtaza *et al.* (2002), who also reported additive genes for the character and suggested that progress in this parameter might be made through a selection breeding program, whereas it differs from the non-additive type of gene action reported by Liu *et al.* (1998), Kumaresan *et al.* (2000) and Abd-El-Rahim *et al.* (2001).

Lint percentage. The results of analysis of variance given in Table II indicated highly significant differences among the parents and their crosses showing that these genotypes differed genetically from each other for this trait. Variance (Vr) and covariance (Wr) values were calculated. Results of joint regression analysis (Table III) suggested that data were fit for additive-dominance model, as the value of b was significant at zero and non-significant at unity. Values of t

Fig. 7. Fibre Fineness

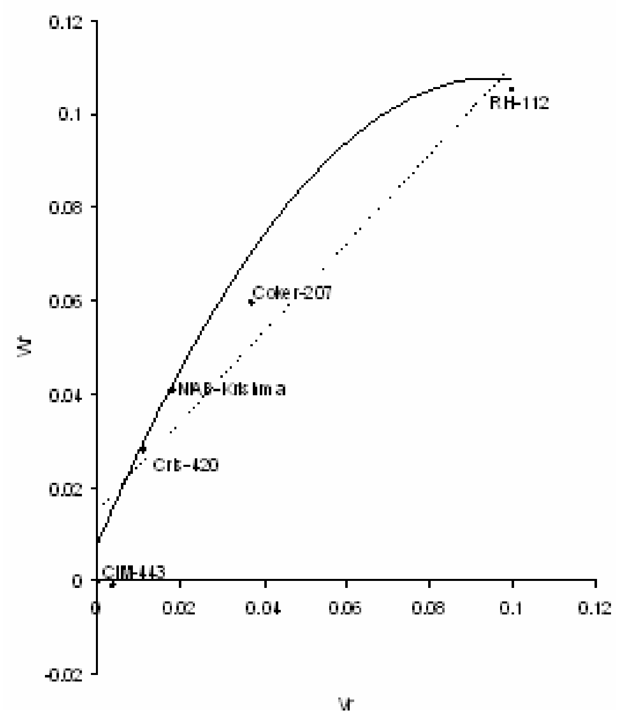
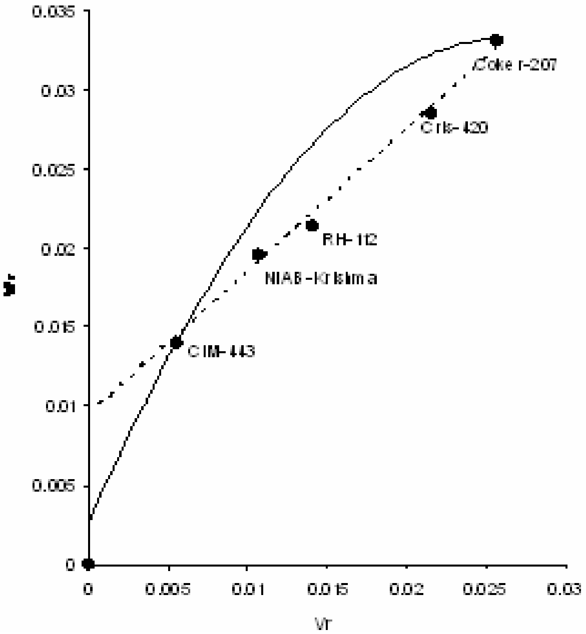


Fig. 8. Fibre strength



square, Vr+Wr and Vr-Wr also confirmed the validity of the data for further genetic analysis.

Positive value of intercept (Fig. 5) confirmed complete dominance. The regression line did not deviate significantly from unit slope that suggested the absence of non-allelic interactions. Broad sense heritability estimates for this character are low, which depicts dominance type of gene action for the phenotypic manifestation of this character. The relative position of array points on the regression line revealed that Cris-420 being near to the origin possessed maximum dominant genes, while RH-112 being away had maximum recessive genes. These results were supported by the findings Tariq *et al.* (1995), McCarty *et al.* (1996), Hussain *et al.* (1999), Abd-El-Rahim *et al.* (2001), Murtaza *et al.* (2002) and Subhan *et al.* (2003), while Yingxin and Xian (1998), Mukhtar *et al.* (2000) and Akbar *et al.* (2001) reported non-additive type of gene action. Prevalence of additive gene action involved in the inheritance of the trait and high narrow sense heritability estimates (Table II) concluded that selection should be carried out for the improvement of this character.

Staple length. The result of analysis of variance revealed that mean genotypic differences among all the entries were highly significant for staple length (Table II). For genetic analysis mean values are given in Table I and Vr/Wr graph is shown in Fig. 6. The regression line did not deviate from a unit slope (Table III), hence there were appeared no non-allelic interaction. The examination of Fig. 6 showed that regression line intercepted the Wr-axis above the origin signifying additive type of gene action with partial dominance in the phenotypic expression of staple length. Heritability estimates for this character are medium. The relative position of array points on the regression line revealed that NIAB-Krishma being near to the origin possessed maximum dominant genes, while Cris-420 being away had maximum recessive genes. Additive type of gene action with partial dominance had been reported by Tariq *et al.* (1995) and Iqbal *et al.* (2003). May and Green (1994) and Chen *et al.* (1999) reported additive gene action, while Mukhtar *et al.* (2000), Akbar *et al.* (2001) and Ahmad *et al.* (2003) non-additive type of gene action for the phenotypic manifestation of this character. Hold of additive genetic effects and moderate heritability estimates (0.43) advocated that selection should be carried out for the betterment of this character (Table II).

Fibre fineness. The result of analysis of variance revealed that means genotypic differences among all the entries were highly significant for yield of seed cotton (Table II). For genetic analysis mean values are given in Table I and Vr/Wr graph is shown in Fig. 7. The regression line did not deviate from a unit slope (Table III), hence there appeared no non-allelic interaction. The examination of Fig. 7 showed that regression line intercepted the Wr-axis above the origin signifying additive type of gene action involved in the phenotypic expression of fibre fineness. Narrow sense heritability estimates for this character are high, which depicts additive type of gene action for the phenotypic manifestation of this character. The relative position of array points on the regression line revealed that CIM-443 being near to the origin possessed maximum dominant genes, while RH-112 being away had maximum recessive genes. The results were in agreement with the findings of Ahmad and Azhar (2000) and Ahmad *et al.* (2003), while differs from Larik *et al.* (1997) and Khan *et al.* (2001).

Preponderance of additive genetic effects and moderately high heritability estimates (0.73) advocated that selection should be carried out for the betterment of this character (Table II).

Fibre strength. The result of analysis of variance revealed that means genotypic differences among all the entries were highly significant for fibre strength (Table II). For genetic analysis mean values are given in Table I and Vr/Wr graph is shown in Fig. 8. The regression line did not deviate from a unit slope (Table III), hence there appeared no non-allelic interaction. The examination of Fig. 8 showed that regression line intercepted the Wr-axis above the origin signifying additive type of gene action involved in the phenotypic expression fibre strength. Broad sense heritability estimates for this character are high, which depicts additive type of gene action for the phenotypic manifestation of this character. The relative position of array points on the regression line revealed that CIM-443 being near to the origin possessed maximum dominant genes, while Coker-207 being away had maximum recessive genes. The results were in agreement with the findings of Larik *et al.* (1997), Hussain *et al.* (1999), Akbar *et al.* (2001), Iqbal *et al.* (2003), Ahmad *et al.* (2003) and Yuan *et al.* (2005), while differ from Khan *et al.* (2001), Ali *et al.* (2008).

In conclusion, higher estimates of narrow sense heritability confirmed the presence of additive gene action involved in the manifestation for most of the characters that further proposed that selection could be a helpful procedure for the stepping up yield and its attributes.

REFERENCES

Abd-El-Rahim, A.A., M.A.M. Gomaa and I.S. Damrdash, 2001. Diallel analysis of some important traits in inter and intra specific cotton crosses. *J. Agric. Sci*., 39: 37–52

Ahmad, S., M.Z. Iqbal, A. Hussain, M.A. Sadiq and A. Jabbar, 2003. Gene action and heritability studies in cotton (*Gossypium hirsutum L.*). *J. Biol. Sci*., 3: 443–50

Ahmad, S., T.M. Khan and A.M. Khan, 2000. Genetic studies of some important quantitative characters in *Gossypium hirsutum* L. *Int. J. Agric. Biol*., 2: 121–4

Ali, M.A. and I.A. Khan, 2007. Assessment of genetic variation and inheritance mode of some metric traits in cotton (*Gossypium hirsutum* L.). *J. Agric. Soc. Sci.,* 4: 112–6

Ali, M.A., I.A. Khan, S.I. Awan, S. Ali and S. Niaz, 2008. Genetics of fibre quality traits in Cotton (*Gossypium hirsutum* L.). *Australian J. Crop Sci*., 1: 10–7

Akbar, M., N.I. Khan and J. Ahmad, 2001. Prospects of developing high lint percentage cultivars of upland cotton. *Gomal University J. Res*., 18: 1–6

Anonymous, 2006. *Pakistan Statistical Year Book-2006*. Federal Bureau of Statistics, Statistics Division, Government of Pakistan

Bertini, C.H.C. De. M., F.P. Da Silva, R. De. P. Nunes and J.H.R. Dos Santos, 2001. Gene action, heterosis and inbreeding depression of yield characters in mutant lines of upland cotton. *Pesq.-Agrop. – Brasileria*, 36: 941–8

Chen, A.M., B. Hu, P.Z. Wang, Abulaiti and W.J. Shi, 1999. An analysis of heritability of quantitative characters of upland cotton. *China cottons,* 2: 9–10

Deshmukh, V.V., V.K. Mohod, M.K. Pande and S.R. Gulhar, 1999. Variability, heritability in upland cotton (*Gossypium hirsutum* L.). *P.K.V. Res. J*., 2: 21–3

Hayman, B.I., 1954. The analysis of variance of diallel crosses. *Biometrics,* 10: 235–45

Hussain, B., A.G. Ghaffari, M.A. Amin and M.A. Khan, 1999. Genetic analysis of some agronomic traits in cotton. *J. Agric. Res*., 37: 1–8

Hussain, B., M.A. Amin and M.A. Khan, 1999. Quantitative inheritance in cotton. *J. Agric. Res*., 37: 110–6

Iqbal, M., M.A. Chang, M.Z. Iqbal, M.U. Hassan, A. Karim and S. Ahmad, 2003. Breeding behavior effects for yield, its components and fibre Quality Traits in Intraspecific crosses of cotton (*Gossypoum hirsutum L.*). *J. Biol. Sci.,* 3: 451–9

Jinks, J.L., 1954. The analysis of continuous variation in diallel crosses of *Nicotinarustica L.* varieties. *Genetics,* 39: 767–88

Khan, I.A., A. Shakeel and F.M. Azhar, 2001. Genetic analysis of fibre quality traits in upland cotton. *Sci. Int. (Lahore)*, 13: 167–75

Kumaresan, D., J. Ganesan and S. Ashok, 2000. Genetic analysis of quantitative character in cotton (*Gossypium hirsutum* L.). *Crop Res. Hisar*., 18: 430–2

Larik, A.S., S.R. Ansari and M.B. Kumbhar, 1997. Heritability analysis of yield and quality components in *Gossypium hirsutum L. Pakistan J. Bot*., 29: 97–110

Liu, Y.Z., X.M. Han, Y.X. Liu and X.M. Han, 1998. Research on the combining ability and inheritance of 12 economic characters in upland cotton. *China Cottons*, 25: 9–11

Malek, M.A. and A.K.M. Shamsuddin, 1998. Combining ability and heterosis for yield and yield contributing characters in upland cotton (*Gossypium hirsutum L.*). *Annl. Bangladesh Agric*., 8: 49–56

May, O.L. and C.C. Green, 1994. Genetic variation for fibre properties in elite Pee Dee cotton populations. *Crop Sci*., 34: 684–90

McCarty, J.C., J.N. Jenkins, B. Tang and C.E. Watson, 1996. Genetic analysis of primitive cotton germplasm accessions. *Crop Sci*., 36: 581–5

Mukhtar, M.S., T.M. Khan, A.S. Khan, M.A. Khan and M.K. Riaz Khan, 2000. Diallel analysis of some important fibre characteristics of cotton (*Gossypium hirsutum L.*) *Int. J. Agric. Biol*., 02: 261–3

Mukhtar, M.S., T.M. Khan and A.S. Khan, 2000. Genetic analysis of yield and yield components in various crosses of cotton (*Gossypium hirsutum* L.). *Int. J. Agric. Biol*., 2: 258–60

Murtaza, N., A.A. Khan and A. Qayyum, 2002. Estimation of genetic parameters and gene action for yield of seed cotton and lint percent in *Gossypium hirsutum L. J. Res. Sci*., 13: 151–5

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

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., M. Qasim, R.U.D. Ahmad, M.U. Khan, M.A. Khan and M.A. Khan, 2003. Diallel analysis for estimating combining ability of quantitatively inherited traits in upland cotton. *Asian J. Plant Sci.,* 2: 853–7

Subhan, M., M. Qasim, R.U.D. Ahmad, M.U. Khan, M.A. Khan and M.A. Khan, 2002. Combining ability for yield and its components in upland cotton. *Asian J. Plant Sci.,* 2: 519–22

Tariq, M., M.A. Khan and G. Idres, 1995. Inheritance of lint percent, seed and lint indices and fiber length in upland cotton (*Gossypium hirsutum L.*). II. *Sarhad J. Agric*., 11: 607–17

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