Identification of Potential F$_2$ Populations from Intraspecific Crosses in Upland Cotton

Muhammad Jurial Baloch*, Muhammad Sharif Kakar, Wajid Ali Jatoi and Nasreen Fatima Veesar

Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam, Pakistan

Abstract. Ten intraspecific F$_2$ progenies alongwith their six parental lines were evaluated for genetic parameters. The mean performance of genotypes differed significantly for various traits. Further, among F$_2$ progenies, NB-111/S × CIM-499 expressed maximum heritability percentage coupled with high genetic variance and more genetic gains for days to open first flower and plant height, whereas CIM-497 × CIM-506 exhibited higher heritability percentage, associated with more genetic variance, consequently higher genetic gains for boll weight and seed cotton yield. Progeny NB-111/S × CIM-506 exhibited moderate heritability percentage paired with fair amount of genetic variance and appreciable genetic gains for number of sympodia per plant. For number of bolls and lint percentage, progeny BH-147 × CIM-499 expressed maximum heritability percentage coupled with high genetic variance and greater genetic gains. Nevertheless, progeny B.T. cotton × CIM-499 displayed higher heritability percentage, paired with more genetic variance and greater genetic gains for fibre length and also expressed maximum values for all the other traits except plant height, boll weight and G.O.T%. As a whole, quite a number of F$_2$ progenies expressed moderate to high heritability estimates, fair amount of genetic variance and sufficient amount of predicted genetic gains, suggesting reliability of such breeding material for use as potential segregating populations for screening desirable segregants from subsequent generations of selfing for improvement of most of the traits studied.

Keywords: heritability estimates, genetic gains, F$_2$ intraspecific populations, *Gossypium hirsutum* L.

Introduction

Plant breeders are more interested in determining the genetic variances from the available total phenotypic variance; because environmental effect is misleading and hence is neglected. The presence of real genetic variability in a segregating population is pre-requisite for the execution of an efficient breeding programme. Thus, the knowledge of degree of genetic variability that is transmittable/heritable to the progeny, referred to as 'heritability', is of great importance in improving any quantitative trait. From a total genetic variability, additive variance and additive genes pass-on from one generation to the next, and therefore play a significant role in selecting the desirable plants from segregating populations and improve multigenic traits. Though, a lot of work on genetic variability and heritability estimates has already been done, yet differences always exist due to either the material and the methodology used or the environment in which the material is evaluated (Baloch, 2004; Baloch and Bhutto, 2004). Kumari and Chamundeswari (2005) estimated higher phenotypic and genotypic variances for seed cotton yield per plant but found lower heritability and lower genetic advance for boll weight and number of sympodial branches per plant. While, Ahmed *et al.* (2006) observed that plant height and seed cotton yield per plant displayed moderate to

higher estimates of heritability and genetic advances which were indicative of additive with partially dominant gene action, yet bolls per plant, boll weight, sympodia per plant and staple length exhibited moderate to high heritability but lower genetic advances.

Breeding for any particular trait must be practiced to affect a change while the success of selection is advocated by the extent to which the desired character is transmitted from parents to the offspring. Thus, heritability is considered a major component of response to selection. Nevertheless, selection capacity of a population mainly depends on the amount of heritable variations available in the breeding material for selection. Therefore, to develop an efficient breeding strategy for a crop species, sufficient knowledge of the mode of inheritance of quantitative traits is very imperative. In this context, heritability of a character helps the plant breeder in predicting the behaviour of the succeeding generations for making desirable selections. It is well established fact that, the higher the heritability, the simpler the selection process and greater will be the response to selection (Baloch, 2004). Moreover, when heritability estimates are available, progress from selection can be predicted for any breeding programme, since expected genetic gain is a function of heritability. Hence, such a guided selection produces substantial genetic advance. This change

*Author for correspondence; E-mail: j.rind58@gmail.com

is of greater interest to plant breeders, because it changes the population mean. Heritability and genetic advance (genetic gain) have been advocated as dependable tools to aid in selection by a number of workers including Tang *et al*. (1996) and Tyagi (1994). In this context, present research was undertaken to study the genetic parameters of eight quantitative traits in six parents and their ten F_2 progenies of upland cotton (*Gossypium hirsutum* L.).

Materials and Methods

The breeding material consisted of six cultivars *viz*., CIM-499, CIM-506, CIM-497, B.T.cotton, BH-147 and NB-111/S and their ten intra-hirsutum F_2 hybrids of upland cotton (*Gossypium hirsutum* L.). All the parental lines were considered as resistant to cotton leaf curl virus (CLCV) disease. The experiment was conducted in sandy loam soil with pH 7.8. The seeds of ten F_2 progenies along with their six parental lines were sown during 2007 in the experimental fields of Plant Breeding and Genetics Department. Seeds were hand dibbled at the rate of three seeds per hill. Before first irrigation, seedlings were thinned to leave one plant per hill to ensure uniform stand and reduced plant competition for optimum plant growth and development. The experiment was randomized complete block design with 3 replicates. The distance between plants was maintained at 30 cm, while row to row, at 75 cm. All the agronomic practices were affected at proper time. Fertilizer at the rate of 125-75 kg N and P/ha was applied in the form of urea and DAP. Full dose of phosphorus with 1/3 of nitrogen was applied at the time of land preparation while remaining $2/3^{rd}$ nitrogen was spilt in three equal doses and applied at the first irrigation, peak flowering and boll setting stages. Irrigation was applied at proper time while insecticides were applied as and when required. All the required cultural practices including weeding etc. were adopted uniformly in all replications throughout the growing period. Each plant selected from F_2 progeny was harvested individually and ginned on single plant roller gin for recording the yield, yield contributing and fibre characters.

Data were collected from fifteen randomly tagged index plants from each plot and per replication relating to days to first flower, plant height (cm), number of sympodial branches per plant, number of bolls per plant, boll weight (g), seed cotton yield per plant (g), lint percentage/ ginning outturn (G.O.T.)% and fiber length/staple length (mm). The analysis of variance (ANOVA) for all the traits was carried out according to Gomez and Gomez (1984) for determining significance among various F_2 hybrids and their parental lines while L.S.D. at 5% was used for mean-comparison. Heritability percentage in broad sense and other genetic parameters of F_2 populations were determined as suggested by Falconer (1989).

Results and Discussion

For improvement of any plant character, plant breeders heavily rely on the availability of genetic variability rather than the environmental variability in a segregating population. It is the additive portion of genetic variability which is heritable from one generation to the next. Quantitative traits which are controlled by polygenes are largely influenced by environmental factors. If environmental variation is small in relation to genetic differences, selection will be more efficient. Therefore, such guided selection produces higher genetic advance and hence changes the population mean.

The mean performance summarized in Table 1 revealed that parental line CIM-506 (43.09) took maximum days to open first white flowers followed by NB-111/S (42.10), whereas CIM-497 (41.02) took the lowest number of days. As for plant height, parent CIM-497 produced the tallest plants (88.13 cm), while parent B.T. cotton, the shortest plants (77.35 cm). Maximum number of sympodial branches (17.73) was produced by the parent BH-147, whereas, minimum number (15.00) of branches, by B.T. cotton. Among all the parental lines, B.T. cotton set maximum number of bolls (30.02), produced bigger bolls (3.66 g) and maximum seed cotton yield per plant (108.62 g); while CIM-499 ginned maximum lint or G.O.T (39.30%) and measured longer fiber length (29.69 mm) followed by B.T. cotton with G.O.T. % of 38.54 and the 2nd longest fibre (29.42 mm).

Among the F_2 progenies/populations (hereafter progeny and population will be used interchangeably), the mean performance (Table 1) indicated that B.T. cotton × CIM-506 had taken maximum days (44.88) for the first flower to open followed by CIM-499 × CIM-506 (44.15); however, minimum days were taken by the progeny BH-147 × CIM-506 (41.99). Regarding plant height, progeny BH-147 × CIM-506 produced the tallest plants (100.73 cm) followed by BH-147 × CIM-499 (98.82 cm). The shortest plant height, nonetheless, was recorded by CIM-499 × CIM-506 (84.24 cm). Regarding sympodial branches, progenies NB-111/S × CIM-499 produced maximum branches/plant (20.31) and also remained the 2nd ranker in seed cotton yield/plant (109.11 g) and lint percentage (39.54%). The progeny B.T.cotton x CIM-506 set maximum number of bolls per plant (34.57) and produced the highest seed cotton yield per plant (122.12 g), however, the first ranker in boll weight (3.75 g) was NB-111/S × CIM-506. As regards the lint %, progeny B.T. cotton × CIM-499 ginned maximum lint of 40.44%. Progenies CIM-499 × CIM-506 followed by B.T. cotton × CIM-499 produced the longest fibre, measuring 30.17 and 29.96 mm, respectively.

Table 1. Mean performance of parents and their F₂ progenies for various quantitative traits in upland cotton (*Gossypium hirsutum* L.)

Parents and their F₂ progenies	Days to first flower	Plant height (cm)	No. of sympodia per plant	Bolls per plant	Boll weight (g)	Seed cotton yield/plant (g)	Lint %	Fiber length (mm)
CIM-499	42.07	79.17	17.37	24.51	3.50	85.72	39.30	29.69
CIM-506	43.09	84.55	16.13	29.08	3.26	94.65	35.59	27.53
CIM-497	41.02	88.13	17.11	24.95	3.29	82.06	35.56	27.66
B.T. COTTON	41.95	77.35	15.00	30.02	3.66	108.62	38.54	28.29
BH-147	41.04	87.51	17.73	27.31	3.27	89.19	37.58	28.28
NB-111/S	42.10	82.93	17.16	26.24	3.37	87.89	37.03	29.42
Average	**41.88**	**83.27**	**16.75**	**27.02**	**3.39**	**91.36**	**37.27**	**28.48**
CIM- 499 × CIM- 506	44.15	84.24	17.11	28.31	3.70	104.36	38.42	30.17
CIM- 499 × CIM- 497	43.24	88.44	17.29	27.91	3.49	96.61	37.54	28.09
CIM- 497 × CIM- 506	42.19	97.22	18.31	29.91	3.27	97.28	36.62	28.81
B.T. COTTON × CIM-506	44.88	98.02	16.57	34.57	3.57	122.12	38.00	29.32
B.T. COTTON × CIM-497	42.13	84.44	17.73	31.73	3.44	108.07	38.52	28.68
B.T. COTTON × CIM-499	43.33	86.58	16.67	30.67	3.48	104.56	40.44	29.96
BH-147 × CIM-499	43.84	98.82	19.00	33.17	3.04	100.13	38.84	29.75
BH-147 × CIM- 506	41.99	100.73	18.06	33.27	3.14	104.04	37.95	28.57
NB-111/S × CIM- 506	43.86	94.84	18.44	28.93	3.75	108.02	37.12	28.77
NB-111/S × CIM-499	42.99	90.00	20.31	30.55	3.59	109.11	39.54	29.84
Average	**43.26**	**92.33**	**17.95**	**30.90**	**3.45**	**105.43**	**38.30**	**29.20**
L.S.D. (5%)	0.127	0.488	0.195	0.168	0.027	0.438	0.120	0.081

The genetic parameters *viz.*, genetic variance, heritability estimates in broad sense and genetic gain at 10% selection intensity for eight important quantitative traits revealed that most of F₂ progenies expressed moderate to high heritability estimates for majority of the traits which was generally associated with more genetic advance or genetic gains (Table 2). For the days taken for opening of the first flower, progeny NB-111/S × CIM-499 recorded maximum genetic variance (1.23) and high heritability (69.60%) associated with the highest value of genetic advance (1.63). The next maximum heritability (68.79%) coupled with high genetic advance (1.61), however, was recorded by CIM-499 × CIM-506. Mahmoud *et al*. (2004) conducted inheritance studies on days to the first flower in interspecific crosses of cotton (*Gossypium hirsutum* L. × *Gossypium barbadense* L.). He, thus, found high heritability estimates in a broad sense. For plant height, maximum genetic variance (62.52) and the highest heritability in broad sense (83.42%) associated with greater genetic advance (12.71) were revealed by the progeny NB-111/S × CIM-499. The next scorer in respect of the above-mentioned genetic parameters was NB-111/S × CIM-506. In consonance with our findings, Ahmed *et al*. (2006) observed highly significant differences among the parents and crosses for plant height yet observed moderate to higher estimates of heritability and genetic advance which were indicative of additive with partial dominance type of gene actions. On the contrary, Banumathy and Patil (2000) estimated lower heritability for plant height from incomplete diallel crosses in

Gossypium hirsutum L. The maximum genetic variance (σ²g=4.69) and the highest heritability but moderate in range (h²= 52.81%) associated with appreciable amount of genetic advance (GA=2.77) were recorded by the progeny NB-111/S × CIM-506 for sympodial branches. Similar to these findings, Ahmed *et al*. (2006) observed highly significant differences among the parents and the crosses but low to moderate heritability and low genetic advances for number of sympodia. Baloch (2004) also observed low to moderate heritability percentage in F₂ hybrids and suggested that number of sympodial branches in cotton is controlled by additive genes.

Regarding the number of bolls per plant, progeny BH-147 × CIM-499 expressed maximum heritability of 69.96% but stood second ranker in genetic variance (10.38) and genetic advance (GA=5.07). The next scorer in respect to heritability (67.30%) was B.T. cotton × CIM-499 which yet remained on top for genetic variance (18.13) and genetic gains (8.03). Jatoi (2007), Murthy *et al*. (2005) and Baloch (2004) also observed moderate to high heritability estimates for bolls per plant. Among the F₂ progenies, CIM-497 × CIM-506 manifested fair amount of genetic variance (0.102) and the highest heritability of 83.35% coupled with high genetic advance (0.52) followed by BH-147 × CIM-506 which displayed the heritability estimates of h²=73.74% paired with fair amount of genetic advance (0.34) for boll weight. Coinciding with the present results, Khan *et al*. (2007), Mahmoud *et al*. (2004) and Basbag

Muhammad Jurial Baloch *et al.*

Table 2. The values of genetic variance (d^{2}g), heritability percentage (h^2) in broad sense and genetic advance (GA) of intra-hirsutum F$_2$ progenies

Characters	F$_2$ population/progenies	Genotypic variance (d^{2}g)	Heritability percentage (h^2 b.s.)	Genetic advance (GA)
Days to first flower	CIM- 499 × CIM-506	1.21	68.79	1.61
	CIM- 499 × CIM-497	0.89	61.16	1.30
	CIM- 497 × CIM-506	0.79	57.00	1.18
	B.T. cotton × CIM-506	1.10	65.37	1.49
	B.T. cotton × CIM-497	1.10	64.83	1.49
	B.T. cotton × CIM-499	1.12	66.96	1.52
	BH-147 × CIM-499	0.35	35.22	0.61
	BH-147 × CIM-506	0.32	32.18	0.56
	NB-111/S × CIM-506	0.63	52.92	1.02
	NB-111/S × CIM-499	1.23	69.60	1.63
Plant height	CIM- 499 × CIM-506	14.41	59.38	5.15
	CIM- 499 × CIM-497	10.75	50.82	4.11
	CIM- 497 × CIM-506	3.74	32.93	1.95
	B.T. cotton × CIM-506	11.23	61.55	4.62
	B.T. cotton × CIM-497	3.18	29.66	1.71
	B.T. cotton x CIM-499	2.12	17.81	1.08
	BH-147 × CIM-499	2.76	19.60	1.29
	BH-147 × CIM-506	7.01	45.06	3.12
	NB-111/S × CIM-506	29.36	75.29	8.27
	NB-111/S × CIM-499	62.52	83.42	12.71
Sympodia branch	CIM- 499 × CIM-506	4.46	51.39	2.66
	CIM- 499 × CIM-497	3.28	45.05	2.14
	CIM- 497 × CIM-506	1.35	26.99	1.06
	B.T. cotton × CIM-506	0.73	23.63	0.73
	B.T. cotton × CIM-497	1.99	47.90	1.71
	B.T. cotton × CIM-499	2.74	50.29	2.06
	BH-147 × CIM-499	1.05	23.15	0.86
	BH-147 × CIM-506	0.63	16.66	0.57
	NB-111/S × CIM-506	4.69	52.81	2.77
	NB-111/S × CIM-499	0.41	8.45	0.33
Bolls per plant	CIM- 499 × CIM-506	5.53	30.59	1.52
	CIM- 499 × CIM-497	6.72	36.26	1.98
	CIM- 497 × CIM-506	7.45	51.17	2.80
	B.T. cotton × CIM-506	6.12	24.86	1.86
	B.T. cotton × CIM-497	9.87	40.91	3.52
	B.T. cotton × CIM-499	18.13	67.30	8.03
	BH-147 × CIM-499	10.38	69.96	5.07
	BH-147 × CIM-506	6.15	53.57	2.64
	NB-111/S × CIM-506	7.25	48.84	2.58
	NB-111/S × CIM-499	5.80	34.14	1.82
Boll weight	CIM- 499 × CIM-506	0.016	30.02	0.12
	CIM- 499 × CIM-497	0.053	57.89	0.30
	CIM- 497 × CIM-506	0.102	83.35	0.52
	B.T. cotton × CIM-506	0.043	46.25	0.25
	B.T. cotton × CIM-497	0.053	51.17	0.29
	B.T. cotton × CIM-499	0.055	43.61	0.27
	BH-147 × CIM-499	0.010	20.70	0.08
	BH-147 × CIM-506	0.051	73.74	0.34
	NB-111/S × CIM-506	0.045	61.05	0.29
	NB-111/S × CIM-499	0.033	40.29	0.20

Contd........

Contd.......... (Table 2)

Characters	F$_2$ population/progenies	Genotypic variance (d^{2}g)	Heritability percentage (h^2 b.s.)	Genetic advance (GA)
Seed cotton yield	CIM- 499 × CIM-506	2.56	8.89	0.84
	CIM- 499 × CIM-497	8.10	19.57	2.21
	CIM- 497 × CIM-506	63.04	76.81	12.24
	B.T. cotton × CIM-506	141.13	70.60	17.56
	B.T. cotton × CIM-497	40.86	38.32	6.96
	B.T. cotton × CIM-499	150.00	67.37	17.74
	BH-147 × CIM-499	57.50	68.04	11.00
	BH-147 × CIM-506	32.47	71.82	8.50
	NB-111/S × CIM-506	38.43	76.61	9.55
	NB-111/S × CIM-499	11.08	29.88	3.20
Lint %				
	CIM- 499 × CIM-506	0.012	18.89	0.08
	CIM- 499 × CIM-497	0.043	45.62	0.24
	CIM- 497 × CIM-506	0.088	51.95	0.37
	B.T. COTTON × CIM-506	0.034	30.84	0.18
	B.T. COTTON × CIM-497	0.015	17.15	0.09
	B.T. COTTON × CIM-499	0.009	16.77	0.07
	BH-147 × CIM-499	0.103	68.04	0.46
	BH-147 × CIM-506	0.161	67.02	0.57
	NB-111/S × CIM-506	0.010	12.16	0.06
	NB-111/S × CIM-499	0.023	34.25	0.15
Fibre length	CIM- 499 × CIM-506	0.157	51.52	0.50
	CIM- 499 × CIM-497	0.070	27.57	0.24
	CIM- 497 × CIM-506	0.468	78.58	1.06
	B.T. cotton × CIM-506	0.210	78.81	0.73
	B.T. cotton × CIM-497	0.230	71.14	0.72
	B.T. cotton × CIM-499	0.630	84.46	1.28
	BH-147 × CIM-499	0.490	77.27	1.09
	BH-147 × CIM-506	0.120	59.32	0.48
	NB-111/S × CIM-506	0.360	62.69	0.83
	NB-111/S × CIM-499	0.070	20.99	0.21

and Gancer (2004), also observed high heritability estimates for boll weight. However, on the contrary, Kumari and Chamundeswari (2005) obtained lower heritability and lower genetic advance. Based on genetic parameters, the results indicated that progenies CIM-497 × CIM-506, BH-147 × CIM-506, NB-111/S × CIM-506, CIM-499 × CIM-497 and B.T. cotton × CIM-497 may produce better segregants in subsequent generations of selfing which could be selected to evolve new varieties with higher yields. In respect of seed cotton yield, though progeny B.T. cotton × CIM-499 exhibited superiority in genetic variance (σ^{2}g=150.00) and genetic advances (GA=17.74) yet ranked sixth in heritability estimates (67.37%). The next scorer in respect of genetic variance (141.13) and genetic gains (17.56) was B.T. cotton × CIM-506. The first ranker in heritability estimates (76.81%) however was CIM-497 × CIM-506 but it ranked the third in the remaining three genetic parameters. Murthy *et al*. (2005),

Abbasi (2003) and Esmail *et al*. (1999) also observed high genotypic variance and heritability in a broad sense ranging from 89.75% to 99.74% for seed cotton yield. Similar results were also obtained by Jatoi (2007), Baloch (2004), Kumaresan *et al*. (2000) and Pandy *et al*. (1995), who estimated high heritability estimates up to 94.2% for seed cotton yield.

In respect of lint or ginning outturn percentage, progeny BH-147 × CIM-499 revealed the highest heritability estimates (68.04%) which was associated with greater genetic gain (0.46) while the next scorer was BH-147 × CIM-506 which gave 67.02% heritability but ranked the first in genetic variance (0.161) and genetic gains (0.57). Baloch (2004) observed moderate heritability ranging from 33.6 to 63.00% but with little contradiction; Hu *et al*. (2001) recorded high heritability estimates in a broad sense. As regards to fiber length, the highest heritability of 84.46% coupled with high genetic gain (1.28) was manifested by the progeny B.T. cotton ×

CIM-499. The next ranker for heritability (h^2=78.81%) paired with more genetic advance (0.73) was expressed by progeny B.T. cotton × CIM-506. Present results are in conformity with those of Baloch (2002) who worked with F_2 hybrids and obtained moderate heritability estimates associated with high genetic variability and genetic advance. Baloch (2004) also recorded high heritability of 81.8% for staple length and concluded that fibre length was controlled by additive genetic factors. Several other researchers like Jatoi (2007), Saeed *et al.* (2007), Zhang and Yong (2004), Yuan *et al.* (2002), estimated moderate to high heritability in broad sense for fibre length in F_2 populations of intra-hirsutum crosses. Based on genetic parameters, it is apparent that progenies, B.T. cotton × CIM-499, B.T. cotton × CIM-506, BH-147 × CIM-499 and B.T. cotton × CIM-497 may best be utilized as potential breeding material for selection from segregating

Table 3. Mean squares from analysis of variance for quantitative characters in F_2 populations of *Gossypium hirsutum* L.

Character	Source of variation	Degree of freedom	Mean squares
Days to first flower	Replication	2	0.0155
	Genotypes	15	3.682*
	Error	30	0.0058
Plant height	Replication	2	0.073
	Genotypes	15	151.881*
	Error	30	0.086
No. of sympodial branches/plant	Replication	2	0.0134
	Genotypes	15	4.456*
	Error	30	0.0137
No. of bolls/plant	Replication	2	0.0085
	Genotypes	15	25.349*
	Error	30	0.0102
Boll weight	Replication	2	0.00027
	Genotypes	15	0.125*
	Error	30	0.00026
Seed cotton yield/plant	Replication	2	0.339
	Genotypes	15	333.71*
	Error	30	0.069
Lint %	Replication	2	0.027
	Genotypes	15	5.422*
	Error	30	0.0052
Fiber length	Replication	2	0.009
	Genotypes	15	2.082 *
	Error	30	0.002

* = significant at 1% probability level.

populations in subsequent generations of selfing to improve fibre length in cotton.

The analysis of variance showed significant differences among the genotypes (consisting of ten F_2 progenies and their six parental lines) for all the traits studied (Table 3). Lukogne *et al.* (2008) also found significant genetic variability for yield, lint and fibre traits and thus suggested that improvement through selection is possible for these characters.

Conclusion

It can be concluded from the present research work that among the parental lines, CIM-497, by setting the first white flower earlier and B.T. cotton, by producing desirable plant height, setting highest number of bolls per plant, producing bigger bolls and giving higher seed cotton yield proved to be potential parents for hybridization and selection programme. While parent BH-147 by producing maximum number of sympodial branches per plant and CIM-499 by ginning more lint percent and measuring longer fibre may prove best parents to be utilized in crossing programme for improving respective characters. The analysis of genetic parameters indicated that among the F_2 progenies, NB-111/S × CIM-499 expressed maximum heritability estimates thus more genetic advances for days to open the first flower and plant height, CIM-497 × CIM-506 for boll weight and seed cotton yield and BH-147 × CIM-499 for number of bolls and lint percentage may be best exploited in subsequent generations of selfing to improve these quantitative traits. However, for sympodial branches, progeny NB-111/S × CIM-506 could prove to be the best breeding material. Nevertheless, progeny B.T. cotton × CIM-499 by expressing higher values of genetic parameters for fibre length and substantial values for all other traits except plant height, boll weight and lint% hence could serve as potential segregating populations for producing desirable plants in further selfing generations.

References

Abbasi, S.J. 2003. Genetic Architecture of Important Yield Components in American Cotton. *M.Sc. Thesis*, Sindh Agriculture University, Tandojam, Pakistan.

Ahmed, H.M., Kandhro, M.M., Laghari, S., Abro, S. 2006. Heritability and genetic advance as selection indicators for improvement in cotton (*Gossypium hirsutum* L.). *Pakistan Journal of Biological Sciences*, **1:** 96-99.

Baloch, M.J., Bhutto, H.U. 2004. Design-II analysis for estimating general and specific combining ability effects of cotton leaf curl virus resistant inbred parents. *Zagazig Journal of Agricultural Research*, **30:** 635-649.

Baloch, M.J. 2004. Genetic variability and heritability estimates of some polygenic traits in upland cotton. *Pakistan Journal of Scientific and Industrial Research*, **47:** 451-454.

Baloch, M.J. 2002. Relative performance of F$_1$ and F$_2$ intra-hirsutum hybrids for some quantitative traits in upland cotton. *Pakistan Journal of Scientific and Industrial Research*, **45:** 407-411.

Banumathy, S., Patil, S. 2000. Genetic analysis of fuzzlessness and other attributes in *Gossypium hirsutum* L. *Crop Research*, **20:** 102-104.

Basbag, S., Gancer, O. 2004. Investigations on the heritability of seed cotton yield, yield components and technological characters in cotton (*Gossypium hirsutum* L.). *Pakistan Journal of Biological Sciences*, **7:** 1390-1393.

Esmail, R.M., Hendawy, F.A., Rady, M.S., Abd-El-Hamid, A.M. 1999. Genetic studies on yield and yield components in one inter- and two intraspectific crosses of cotton. *Egyptian Journal of Agronomy*, **21:** 37-51.

Falconer, D.S. 1989. *Introduction to Quantitative Genetics*, pp. 187-192, 3rd edition, Longman Scientific and Technical, London (UK) and New York (USA).

Gomez, K.A., Gomez, A.A. 1984. *Statistical Procedures for Agricultural Research*, 2nd edition, John Wiley and Sons Inc., New York, USA.

Hu, S.L., Mei, Y.J., Gong, P.P., Cao, X.C., Zeng, C., He, L.R. 2001. Genetic analysis of the yield and morphological characters of F$_2$ in upland cotton. *China Cottons*, **28:** 9-10.

Jatoi, W.A. 2007. Genetic Variability and Heritability Estimates in F$_2$ Population of Intra-hirsutum Crosses. *M.Sc. Thesis*, Sindh Agriculture University, TandoJam, Pakistan.

Khan, N.U., Hassan, G., Kumbhar, M.B., Parveen, A., Aiman, U., Ahamad, W., Shah, S.A., Ahamad, S. 2007. Gene action of seed traits and oil content in upland cotton (*Gossypium hirsutum* L.). SABRAO. *Journal of Plant Breeding*, **39:** 17-30.

Kumaresan, D., Ganesan, J., Ashok, S. 2000. Genetic analysis of some quantitative characters in cotton (*Gossypium hirsutum* L.). *Crop Research*, **19:** 481-484.

Kumari, S.R., Chamundeswari, N. 2005. Studies on genetic variability, heritability and genetic advance in upland cotton. *Research on Crops*, **6:** 98-99.

Lukonge, E.P., Labuschagne, M.T., Herselman, L. 2008. Combining ability for yield and fibre characteristics in Tanzanian cotton germplasm. *Euphytica*, **161:** 383-389.

Mahmoud, A.M., El-Ameen, T.M., Mohamed, A.A., Ali, M.A. 2004. Inheritance of some agro-economic traits in interspecific cotton crosses. *Asian Journal of Agricultural Sciences*, **35:** 95-106.

Murthy, J.S.V.S., Kumari, S.R., Chamundeswari, N. 2005. Genetic variability, correlation and path analysis in *Gossypium herbaceum* L. cotton under saline soil, *Journal of Cotton Research and Development*, **2:** 148-152.

Pandy, S.C., Saxena, M.K., Julka, R. 1995. Studies on genetic variability in upland cotton (*Gossypium hirsutum* L.). *Crop Research Hisar*, **10:** 272-278.

Saeed, R., Khan, T.M., Naveed, A., Munir, H. 2007. Modified path to high lint yield in upland cotton (*Gossypium hirsutum* L.) under two temperature regimes. *The Turkish Journal of Biology*, **31:** 119-126.

Tang, B., Jenkins, J.N., Watson, C.E., McCarty, J.C., Creech, R.G. 1996. Evaluation of genetic variance, heritability and correlations for yield and fibre traits among F$_2$ hybrid cotton populations. *Euphytica*, **91:** 315-322.

Tyagi, A.P. 1994. Association of yield components, fibre traits and their functions in upland cotton (*Gossypium hirsutum* L.). *Indian Journal of Agricultural Research*, **28:** 159-165.

Yuan, Y.L., Zhang, T.Z., Guo, W.Z. 2002. Genetic stability of fibre qualities in upland cotton. *Acta Gossypii Sinica*, **14:** 67-70.

Zhang, W.Y., Mei, Y.J. 2004. Analysis of genetic correlation between boll shape traits and fibre quality traits in upland cotton. *Acta Agronomica Sinica*, **30:** 816-820.