



Research Article

Genetic Constitution of Multigenic Traits in F₂ Populations of Intrahirsutum Crosses

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ABSTRACT

Genetic analysis for quantitative and qualitative traits of valuable field crops is vital technique to facilitate plant breeders in predicting breeding behavior of the succeeding filial generations. Eight F₂ populations along with their five parental cultivars were studied so as to work-out genetic analysis like, genetic variance (σ^2_g), phenotypic variance (σ^2_p), heritability percentage in broad sense (h^2) and genetic advance (G.A.) at 10% selection pressure. The experiment was laid out in a randomized complete block design with four replications during 2012 at the Botanical Garden, Department of Plant Breeding and Genetics, Sindh Agriculture University Tandojam. The analysis of variance revealed significant differences among F₂ populations for all the multigenic traits studied which suggested that the breeding material is worth for selection of desirable plants from subsequent segregating generations. On an average, F₂ progenies gave higher values for almost all the traits which could be either due heterotic effects or transgressive segregants developed through recombination of genes. On the basis of mean performance, parental cultivars CRIS-134 recorded medium-taller plants, produced higher sympodial branches plant⁻¹ and formed more bolls plant⁻¹, while NIAB-78 weighed bigger bolls and gave maximum seed cotton yield plant⁻¹; yet Sadori ginned higher lint% and measured longer staple length. Results thus revealed that these three cultivars are the potential parents for hybridization and selection programs so as to improve various traits of economic importance in cotton. Genetic analysis suggested that F₂ population from cross CRIS-134 x Sadori exhibited higher heritability estimates associated with greater genetic advances for sympodial branches plant⁻¹ ($h^2=69.06\%$, GA=12.05) and staple length ($h^2=76.91\%$, GA=13.58); while progenies from Chandi x Sadori cross manifested maximum heritability estimates and higher genetic advances for bolls plant⁻¹ ($h^2=75.60\%$, GA=26.98), seed cotton yield plant⁻¹ ($h^2=74.06\%$, GA=81.45), lint% ($h^2=80.41\%$, GA=18.44) and seed index ($h^2=72.97\%$, GA=2.70), respectively. Genetic analysis as a whole indicated that quite a number of F₂ progenies expressed high heritability estimates coupled with greater genetic advances revealed that such progenies possess additive genes, hence are potential breeding material for selection of desirable plants from succeeding segregating generations.

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Introduction

Heritability estimates of important traits and genetic suitability of cotton genotypes for different morpho-yield traits are essentially required for selection of parental lines in breeding programs (Khan *et al.* 2010; Batool *et al.* 2010; Batool, 2011). The yield is highly complex character and is directly influenced by various morpho-yield traits. Thus, a thorough knowledge about the genetic potential of different genotypes, inheritance pattern of different traits and the extent of transmissibility of seed cotton yield and other agronomic characters are crucial to launch any successful cotton breeding program (Ahmad *et al.* 2008; Makhdoom *et al.* 2010). It is generally believed that higher the heritability estimates of given traits, the simpler the selection procedure and better will be the response to selection as suggested by Baloch (2004).

Plant breeders can easily observe and measure phenotypic changes in plant populations, which are caused by the joint action of both genetic and environmental factors. Although, breeders are more interested in determining the proportion of genetic variation from available total phenotypic variation, because environmental effect is considered unimportant hence is neglected (Baloch 2004). The success of any breeding endeavor, therefore, depends mainly on the presence of the abundant genetic variability of a trait which is amenable to selection. Thus, the knowledge about degree of genetic variability that is transferable to the progeny referred to as heritability is also of great importance in improving any quantitative trait. From a total genetic variability, it is again additive variance and additive genes which pass-on from one generation to the next, therefore play an imperative role in selecting and improving quantitative traits. A lot of research work on genetic variability and heritability estimates have already been carried out, yet the differences in results always existed due to either material and

methodology used or environments where the material is tested (Baloch and Bhutto 2003 and Baloch 2004).

Traditionally, two types of heritability are calculated, which are referred to as heritability in broad sense and heritability in narrow sense. Plant breeders therefore have to decide how effective the selection would be when practicing phenotypic selection. For a trait, with very low heritability, selection on the basis of phenotypes directly may not be promising, however, when heritability for a trait is high, phenotypic selection will be more effective and for obtaining additional information on relatives is of less value than when heritability is low (Pollack 1998). The characters having low heritability appeared to be more influenced by environment (Azhar *et al.* 2004). Moderately high heritability estimates were observed in bolls plant-1, boll weight, lint index and seed cotton yield varying from medium to high. Hence, such characters were mostly studied by genetic factors (Bahadar *et al.* 1993; Banumathy *et al.* 2000; Bertini *et al.* 2001; Joshi *et al.* 2006). High heritability, estimates up to 98% for ginning out turn, fiber fineness and fiber strength indicated higher level of genetic expression for these traits (Banumathy *et al.* 2000). The amount of genetic variation present in plant populations may also differ for quantitative traits, hence improving multigenic traits, it is important that segregating populations should retain more genetic variability in low sample size. Extensive genetic variances and high heritability estimates imply that characters could be improved through selection in segregating filial generations (Baloch 2004; Khan *et al.* 2009; Batool *et al.* 2010; Batool, 2011). Heritability estimates were generally found to be higher in intraspecific crosses of *G. hirsutum* as compared to *G. barbadense* crosses, except for days to flowering and lint % (Esmail 2007). The fate of any cotton breeding program is primarily depends on the choice of promising parental lines for

hybridization followed by selection for the combination of favorable genes. Consequently, in plant breeding, the identification of genotypes with high genetic potential is pre-requisite for synthesis of genetically superior genotypes and predicting increased production on per unit area under a given set of environments. Present research therefore was intended to determine the genetic parameters and potentiality of F₂ populations for multigenic traits.

Materials and Methods

The research trial was conducted in experimental field of the Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam. The soil was sandy loam with 7.8 pH. The seed of 8 intra-hirsutum F₂ populations viz. CRIS-134 x Sadori, Chandi x Sadori, BH-160 x Sadori, Chandi x CRIS-134, NIAB-78 x CRIS-134, BH-160 x CRIS-134, BH-160 x NIAB-78 and Chandi x NIAB-78 along with seven parental lines such as CRIS-134, Sadori, Chandi, NIAB-78, and BH-160 were sown during 2012. Seeds were hand dibbled at the rate of three seeds per hill. The experiment was laid out in a randomized complete block design with four repeats. Before first irrigation, seedlings were thinned to one per hill to maintain uniform plant stand and reduced plant competition for optimum plant growth and development. The distance between plants was maintained at 30 cm, while row to row at 75 cm. All agronomic practices were done at proper time. Fertilizer at the rate of 125-75 kg N & P ha⁻¹ was applied in the form of Urea and DAP. Full dose of phosphorus with 1/3rd of nitrogen was applied at the time of land preparation while remaining nitrogen was applied in three equal split doses with first irrigation, peak flowering and boll setting stages. Other inputs like irrigations were applied at proper times and insecticides as and when required. All the cultural practices including, hoeing, weeding etc. were adopted

uniformly in the entire experiment throughout the experimentation period. Ten plants were randomly tagged from each genotype and replication, harvested individually and ginned on single plant roller gin machine for recording the yield attributing and fiber traits. The analysis of variance was carried out according to Gomez and Gomez (1984) so as to establish the level of significance among the genotypes. Least significant difference statistical method was used to determine the critical differences among the means of genotypes for various traits. The heritability estimates in broad sense and other genetic parameters of F₂ intrahirsutum populations were determined by adopting genetic analysis as suggested by Baloch et al. (2010). The data were collected on plant height (cm), sympodial branches plant-1, bolls plant-1, boll weight (g), Seed cotton yield plant-1 (g), lint (%), seed index (100-seed weight in g) and staple length (mm).

Results and Discussion

In the present research, various multigenic characters of eight intrahirsutum F₂ populations were studied in order to evaluate genetic potential of F₂ hybrids and also to identify the better segregants for selection in subsequent generations so as to improve the important quantitative traits. The experiment was laid-out in a randomized complete block design with four replications at experimental field of the Department of Plant Breeding and Genetics, Sindh Agriculture University Tandojam during 2012. The eight important traits of cotton viz. plant height (cm); sympodial branches plant-1; bolls plant-1; boll weight (g); seed cotton yield plant-1 (g); lint percentage (%); seed index (100- seed weight in g) and staple length (mm) were studied.

Table 1. Mean squares from analysis of variance for various multigenic character in intrahirsutum F₂ population.

Source of variation	Degrees of freedom	Mean squares			
		Plant height	Sympodial branches plant ⁻¹	Bolls plant-1	Boll weight
Replications	3	2.84	4.00	1.05	0.02
Genotypes	12	951.72**	37.60**	129.66**	0.13**
Parents (P)	4	1622.47**	70.38**	202.88**	0.30**
F ₂ hybrids (H)	7	465.56**	18.76**	102.25**	0.05**
P vs H	1	1156.91**	51.62**	100.63**	0.25**
Error	36	4.10	1.04	1.55	0.01
Source of variation	Degrees of freedom	Mean squares			
		Seed cotton yield plant ⁻¹	Seed index	Lint%	Staple length
Replications	3	18.70	0.70	0.06	0.65
Genotypes	12	985.53**	15.13**	2.60**	6.22**
Parents (P)	4	1093.81**	13.09**	3.87**	8.01**
F ₂ hybrids (H)	7	1007.29**	5.70**	1.82**	4.62**
P vs H	1	86.52**	7.39**	2.05**	3.39**
Error	36	5.96	0.82	0.11	0.80

**= Significant at 1% level of probability

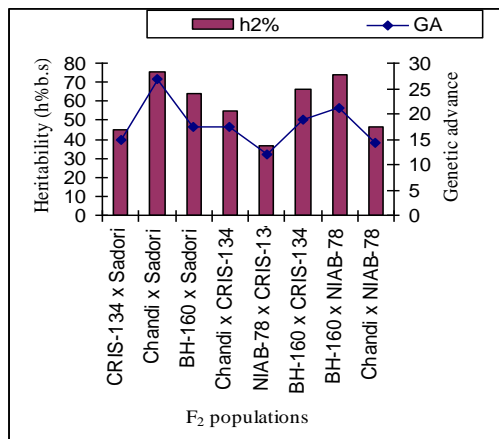


Figure 1. Association of heritability with genetic advance for bolls

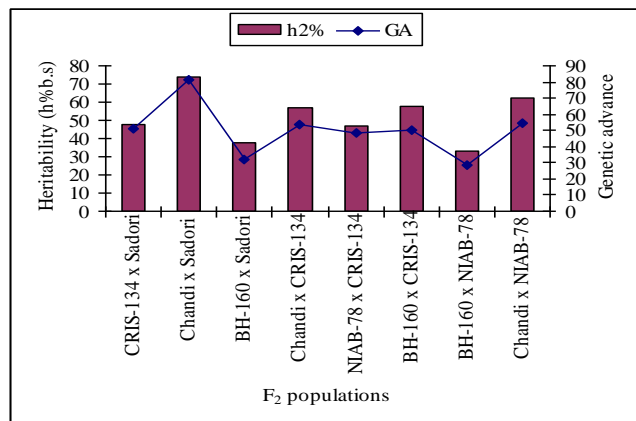


Figure 2. Association of heritability with genetic advance for yield plant⁻¹

Table 2. Mean performance of parents and their F₂ progenies for various multigenic traits in intrahirsutum crosses

Sr. No.	Parents and their F ₂ progenies	Plant height (cm)	Sympodial branches plant ⁻¹	Bolls ⁻¹ plant	Boll weight (g)	Seed cotton yield Plant ⁻¹ (g)	Seed index (g)	Lint %	Staple length (mm)
1	CRIS-134	147.80	31.20	57.20	2.96	169.34	6.60	37.00	27.60
2	Sadori	157.20	24.20	53.20	2.90	154.20	5.60	38.20	29.00
3	Chandi	127.00	21.00	49.20	3.02	148.62	7.60	36.00	27.40
4	NIAB-78	105.80	21.00	56.80	3.12	177.22	6.60	35.60	26.40
5	BH-160	142.80	25.40	39.20	3.42	134.16	7.60	35.40	27.60
	Average	136.12	24.56	51.12	3.09	156.71	6.80	36.44	27.60
6	CRIS-134 x Sadori	166.20	30.20	57.20	3.16	180.82	5.40	39.60	30.60
7	Chandi x Sadori	145.80	27.20	61.20	3.06	187.08	6.80	39.60	28.60
8	BH-160 x Sadori	155.80	25.40	47.40	3.12	147.92	5.80	42.20	28.20
9	Chandi x CRIS-134	135.80	26.80	55.00	2.94	161.60	5.40	39.20	28.40
10	NIAB-78 x CRIS-134	139.00	25.80	55.40	3.18	176.36	6.80	37.40	27.20
11	BH-160 x CRIS-134	148.20	26.60	47.80	3.08	147.46	6.80	38.20	26.40
12	BH-160 x NIAB-78	134.20	25.40	48.60	3.04	147.98	6.80	36.20	27.00
13	Chandi x NIAB-78	153.80	23.40	49.20	3.02	148.64	6.80	38.80	27.20
	Average	147.35	26.35	52.73	3.08	162.23	6.33	38.90	27.95
	LSD (5%)	2.90	1.46	1.78	0.17	3.50	0.47	1.30	1.28

Analysis of variance and mean performance of parents and their F₂ populations

The mean squares from analyses of variance for all the multigenic traits presented in Table 1 indicated that parents and their F₂ progenies differed significantly for plant height, sympodial branches plant⁻¹, bolls plant⁻¹, bolls weight, seed cotton yield plant⁻¹, lint percentage, seed index and staple length. These results indicated the presence of considerable genetic variability among the parents and their F₂ populations; therefore, data is worth for the estimation of genetic parameters like genetic variance (δ^2g), phenotypic variance (δ^2p), heritability estimates in broad sense (h^2) and genetic advance (GA) at 10% selection intensity. The F₂ populations consisted of eight progenies derived from the crosses of five parental cultivars for eight multigenic characters are presented in Table 3.

Mean performance of five parental cultivars and their eight F₂ populations/progenies derived from intrahirsutum crosses for various multigenic characters presented in Table 2 revealed that, on an average, F₂ progenies gave higher mean values against their respective parents for all the traits studied.

The plant height of parents varied from 105.80cm (NIAB-78) to 157.20cm (Sadori) which means NIAB-78 produced the shorter plants whereas Sadori recorded the taller plants. The parental cultivars Chandi (127.00cm) and NIAB-78 (105.80cm), however attained shorter plants. F₂ progenies gave variable plant height ranging from 135.50 to 166.20cm recorded by the progenies Chandi x CRIS-134 and CRIS-134 x Sadori respectively. Two progenies like Chandi x CRIS-134 (135.80cm) and BH-160 x NIAB-78 (134.20cm) produced plants with desirable plant height. The parental lines produced sympodial branches in the range of 21.00 by Chandi to 31.20 by CRIS-134. The F₂ progenies, CRIS-134 x Sadori produced maximum sympodial branches (30.20) followed by Chandi x Sadori (27.20),

nevertheless lower number of sympodial branches plant-1 were produced by rest of the progenies with small difference of 23.40 to 26.80 branches plant-1. In case of a number of bolls/plant, parental cultivars set bolls in the range of 39.20 (BH-160) to 57.20 (CRIS-134), while progenies Chandi x Sadori set maximum number of bolls plant-1 (61.20) followed by CRIS-134 x Sadori (57.20), minimum bolls plant-1 however were produced by F₂ populations BH-160 x Sadori and BH-160 x CRIS-134 with 47.40 and 47.89 bolls plant-1, respectively.

The boll weight of parental cultivars varied from 2.90g (Sadori) to 3.42g (BH-160), while F₂ progenies gave some what higher boll weight varied from 2.94 to 3.16g produced by Chandi x CRIS-134 and CRIS-134 x Sadori, respectively. The smaller bolls, nevertheless were obtained from progenies Chandi x CRIS-134 (2.94 g), Chandi x NIAB-78 (3.02 g) and BH-160 x NIAB-78. The results in Table-2 further revealed that parental lines, on average, gave seed cotton yield of 156.71g whereas the average of F₂ progenies was much higher (162.23 g) than those of parental cultivars. Yet, two F₂ progenies like Chandi x Sadori gave maximum seed cotton yield plant-1 (187.08g) followed by CRIS-134 x Sadori (180.82g). Regarding lint%, the results revealed that parental lines recorded variable lint% was 35.40 to 38.20% whereas this range in F₂ progenies was 36.20 to 42.20%. Maximum lint% nonetheless was ginned by F₂ BH-160 x Sadori (42.20%) followed by CRIS-134 x Sadori (39.60%) and Chandi x Sadori (39.60%). The seed index values of parental lines varied from 5.60g (Sadori) to 7.60g (Chandi), nevertheless F₂ progenies recorded less average seed index against their parental lines and the range of F₂ progenies was 5.40g to 6.80g. The staple length of parental lines varied from 26.40 (NIAB-78) to 29.00mm (Sadori), yet these ranges in F₂ progenies were recorded as 26.40 (BH-160 x CRIS-134) to 30.60mm (CRIS-134 x Sadori).

Table 3. The values of genetic variance (σ^2_g), heritability percentage (h^2) in broad sense and genetic advance (GA) of intrahirsutum F_2 populations.

Characters	F ₂ progenies	Genetic variance (σ^2_g)	Heritability (h^2 %) broad sense	Genetic advance (GA)
Plant height	CRIS-134 x Sadori	1551.06	50.82	49.41
	Chandi x Sadori	1200.23	51.14	43.60
	BH-160 x Sadori	1135.28	42.35	38.59
	Chandi x CRIS-134	915.23	44.97	35.70
	NIAB-78 x CRIS-134	2133.51	18.61	35.07
	BH-160 x CRIS-134	1012.88	41.75	36.19
	BH-160 x NIAB-78	1741.73	87.59	68.74
Sympodial branches plant ⁻¹	Chandi x NIAB-78	1505.88	57.63	51.85
	CRIS-134 x Sadori	67.99	69.06	12.05
	Chandi x Sadori	51.41	64.51	10.13
	BH-160 x Sadori	33.70	48.57	7.12
	Chandi x CRIS-134	48.15	62.19	9.63
	NIAB-78 x CRIS-134	34.38	45.36	6.95
	BH-160 x CRIS-134	50.70	58.36	9.57
Bolls plant ⁻¹	BH-160 x NIAB-78	41.39	59.78	8.75
	Chandi x NIAB-78	38.33	65.39	8.81
	CRIS-134 x Sadori	160.04	44.74	14.89
	Chandi x Sadori	310.94	75.60	26.98
	BH-160 x Sadori	156.09	63.69	17.54
	Chandi x CRIS-134	180.68	54.58	17.47
	NIAB-78 x CRIS-134	129.27	36.42	12.07
Boll weight	BH-160 x CRIS-134	172.92	65.99	18.80
	BH-160 x NIAB-78	192.44	74.14	21.02
	Chandi x NIAB-78	143.40	46.55	14.37
	CRIS-134 x Sadori	0.43	56.58	0.86
	Chandi x Sadori	0.51	71.83	1.06
	BH-160 x Sadori	0.53	71.62	1.08
	Chandi x CRIS-134	0.40	63.49	0.88
Seed cotton yield plant ⁻¹	NIAB-78 x CRIS-134	0.08	10.39	0.16
	BH-160 x CRIS-134	0.27	38.03	0.56
	BH-160 x NIAB-78	0.24	34.78	0.50
	Chandi x NIAB-78	0.19	27.94	0.40
	CRIS-134 x Sadori	1735.47	47.75	50.66
	Chandi x Sadori	2891.84	74.06	81.45
	BH-160 x Sadori	907.14	37.42	32.43
Lint (%)	Chandi x CRIS-134	1664.47	56.95	53.90
	NIAB-78 x CRIS-134	1627.25	47.03	48.69
	BH-160 x CRIS-134	1403.14	57.93	50.17
	BH-160 x NIAB-78	798.96	32.83	28.50
	Chandi x NIAB-78	1536.42	62.59	54.57
	CRIS-134 x Sadori	129.66	76.29	17.50
	Chandi x Sadori	136.66	80.41	18.44
Seed index	BH-160 x Sadori	133.38	68.97	16.88
	Chandi x CRIS-134	67.53	40.55	9.20
	NIAB-78 x CRIS-134	91.30	60.22	13.04
	BH-160 x CRIS-134	47.96	30.36	6.71
	BH-160 x NIAB-78	41.62	29.37	6.15
	Chandi x NIAB-78	24.53	76.29	17.14
	CRIS-134 x Sadori	1.93	71.22	2.06
Staple length	Chandi x Sadori	3.24	72.97	2.70
	BH-160 x Sadori	2.27	71.84	2.24
	Chandi x CRIS-134	2.03	74.91	2.17
	NIAB-78 x CRIS-134	2.40	52.98	1.98
	BH-160 x CRIS-134	2.20	48.57	1.81
	BH-160 x NIAB-78	2.40	52.98	1.98
	Chandi x NIAB-78	2.40	71.22	2.66
Staple length	CRIS-134 x Sadori	77.46	76.91	13.58
	Chandi x Sadori	54.59	62.62	10.32
	BH-160 x Sadori	50.78	59.51	9.67
	Chandi x CRIS-134	45.68	50.76	8.31
	NIAB-78 x CRIS-134	34.94	44.09	6.90
	BH-160 x CRIS-134	41.37	55.44	8.42
	BH-160 x NIAB-78	56.02	71.62	11.14
Chandi x NIAB-78	57.13	72.02	11.28	

Genetic parameters

The goal of plant breeders is to evolve new varieties of economically valuable crops through improved and efficient breeding programs which should be better than the existing ones. Higher yield is still and will always remain the foremost objective of cotton breeders; however, disease and insect-pest resistance, improvement in quality and yield traits are all important. For improvement in any plant trait, plant breeders heavily rely on either available genetic variability or creating new variability rather than the environmental variability in segregating populations. 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 advances in which plant breeders are more interested because it changes the breeding value of population. Eight intra-hirsutum F₂ populations were ascertained for their genetic constitution/inheritance pattern via genetic analysis of eight important multigenic traits. After the mean squares were found significantly different over the genotypes, parents, F₂ progenies and parent vs F₂ progenies, the data were further processed for determining genetic parameters. Several researchers like Baloch (2004), Soomro *et al.* (2008); Ranganatha *et al.* (2013) also noted significant differences among intrahirsutum F₂ progenies for various quantitative traits.

Plant breeders in the past were of the view that plant height is monogenic while some reported it as digenic, but now, most of the researchers believe that plant height is multigenic based on inheritance pattern of this trait in the segregating populations. In cotton, medium-tall plants with production capacity of setting maximum number of bolls due to higher number of fruiting branches for obtaining higher yields are more desirable.

The genetic analysis for plant height (Table 3) indicated that fair amount of genetic variance (δ^2_g) is available in F₂ population, yet it was about half of the phenotypic variance (δ^2_p) which was attributed by the environmental variance. With only one exception where F₂ population from cross BH-160 x NIAB-78 exhibited high heritability ($h^2=87.59\%$), majority of F₂ progenies expressed medium heritability in the range of $h^2=41.75$ to 57.63% . High heritability estimates coupled with greater genetic advance of 68.74 and 51.85cm were recorded by progenies BH-160 x NIAB-78 and Chandi x NIAB-78 respectively. Generally, higher genetic gains in F₂ populations suggested that plant height was predominantly controlled by additive genes. Thus, populations with high heritability and greater genetic advances are more amenable to selection in earlier segregating generations. Deshmukh *et al.* (1999), Hu-Shou-Lin *et al.* (2001) and Pandey *et al.* (2002) also recorded higher genotypic variations, high heritability values coupled with higher genetic advances for plant height. The present results are also in consonance with the findings of Hafiz *et al.* (2006) who observed highly significant differences among the parents and their crosses for plant height. They also observed moderate to higher heritability estimates and genetic advances which were indicative of additive with partial dominance type of gene actions. Contrary to present findings, Banumathy and Shanti (2000) reported that plant height was governed by over dominant genes.

Higher number of sympodial branches may produce more fruiting points, consequently higher seed cotton yield plant⁻¹. Thus, plant breeders and researchers recommended that sympodial branches do serve as the good criterion for selecting high yielding cotton genotypes. Most of the F₂ progenies presented greater genetic variability and less environmental variance which resulted into moderate to higher heritability estimates ranging from $h^2=45.36\%$ to $h^2=69.06\%$ (Table 3). Higher heritability estimates were

associated with higher genetic advances. F₂ progenies from CRIS-134 x Sadori followed by Chandi x NIAB-78 crosses exhibited higher heritability estimates of $h^2 = 69.06$ and 65.39% which proportionally expressed more genetic gains. The genetic gains were correspondingly higher and were proportionally associated with their heritability estimates. This type of situation indicates that the character is controlled by additive genes. High heritability estimates of progenies CRIS-134 x Sadori followed by Chandi x NIAB-78 and BH-160 x NIAB-78 coupled with more genetic advances advocated that these specific progenies are potential material to select the plants with higher number of fruiting branches from segregating populations, hence rigorous plant selection is required to identify desirable plants from F₂ generation. Our results are in consonance with those of Reddy and Kumari (2004) and Hafiz *et al.* (2013) who evaluated genetic components of variation in American cotton (*Gossypium hirsutum* L.) for number of sympodia per plant. The estimates of genetic coefficient of variation and phenotypic co-efficient of variation were higher, consequently heritability estimates in broad sense were high for number of sympodia per plant. Contrary to present findings, Hafiz *et al.* (2006) observed highly significant differences among the parents and their crosses but, low to moderate heritability and low genetic advances were recorded for number of sympodia. Baloch (2004) observed low to high heritability percentage in F₂ hybrids for number of sympodial branches per plant and suggested that number of sympodial branches in cotton is controlled by additive genes.

Number of bolls plant⁻¹ is the major yield component with strong influence on seed cotton yield. Through breeding for improvement in this trait, it was generally observed that yield has ultimately increased in cotton crop. It was noted from the results that the progenies expressed substantial amount of genetic variability. As compared to environmental variance (δ^2e), the

genetic variance (δ^2g) was about double with only few exceptions which resulted in moderate and high heritability estimates (Table 3). Heritability estimates in broad sense of F₂ populations varied from $h^2 = 36.42\%$ being the lowest and $h^2 = 75.60\%$ as the highest estimates. The genetic advance was higher in progenies derived from CRIS-134 x Sadori. Similar to present results, Baloch (2004), Murthy *et al.* (2005) and also observed significant genetic variances and moderate to high heritability estimates in upland cotton for bolls plant⁻¹. Rangnatha *et al.* (2013) evaluated F₂ segregating generations of upland cotton and observed high broad sense heritability and genetic gains for bolls plant per plant i.e. 0.81, 8.04 respectively, along with higher genetic coefficient of variation for number of bolls per plant. Our results suggested that substantial genetic advance of 18.95 bolls plant⁻¹ which was expressed by the progenies NIAB-78 x CRIS-134, hence proved as a choice segregating material for selection to improve number of bolls per plant in cotton.

Boll weight causes direct influence on seed cotton yield because more number of bigger bolls is expected to produce more seed cotton yield. Bolls are classified as large, medium and small, depending on each boll weight. For higher yields, larger bolls may be more important, however, in cotton, genotypes with medium bolls and more in numbers may produce higher yields. The results with respect to genetic parameters summarized in Table 3 indicated that half of the progenies expressed greater genetic variability (δ^2g) against their corresponding environmental variances (δ^2e). The F₂ populations expressed low, medium and high heritability percentages. Because of lower genetic variability in half of the populations, the genetic gains were correspondingly low, yet progenies which exhibited relatively higher heritability also expressed higher amount of genetic advances. Nonetheless, progenies Chandi x Sadori and BH-160 x Sadori were among the two top rankers in

exhibiting more genetic variability, higher heritability and greater genetic advances as compared to other F₂ progenies. These results indicate that F₂ populations from these two crosses suffered less by the environment effects and had predominantly additive genes. Such populations are expected to have more scope of selection in improving boll size, consequently seed cotton yield. Several other researchers like Basbag and Gancer (2004), Mahmoud *et al.* (2004) and Khan *et al.* (2007) also observed high heritability estimates for boll weight in F₂ populations of cotton. Ranganatha *et al.* (2013) observed phenotypic variance and genotypic variance being 0.32 and 0.41, respectively and h² was 78.0%, while the genetic advance under 5% selection intensity was 1.02g. Conversely, Kumari and Chamundeswari (2005) reported lower heritability and lower genetic advance for boll weight, which also confirm our results for some of the F₂ progenies.

Among all the traits in any crop plants, yield is considered as the most important character. In cotton, special attention is required to boost-up the seed cotton yield to its maximum level, because it plays a vital role in strengthening the socio-economic conditions of the growers and ultimately the country. Genetic analysis revealed that genetic variability (δ^2g) in four out of eight F₂ populations was greater than environmental variance (δ^2e). The heritability estimates varied from h²=32.83 to h²=74.06%, which means low, medium and high heritability estimates were observed the progenies (Table 3). The maximum heritability (h²=74.06%) however, was exhibited by F₂ population developed from Chandi x Sadori. There was positive association between genetic variability, heritability and genetic advance for seed cotton yield, which indicated that additive genes were present in the said populations. In all eight F₂ populations, fairly high percentage of heritability was recorded suggesting that seed cotton yield is fairly amenable to selection and

population developed from Chandi x Sadori is an important breeding material to be exploited for higher yields in subsequent filial generations and may provide more opportunities to breed new high yielding cotton varieties. Hafiz *et al.* (2006) also observed high genotypic variance and heritability in broad sense for seed cotton yield coupled with high genetic advance. Similar results were also obtained by Mushtaq *et al.*, (2005); Khan *et al.* (2010a); Batool *et al.*, (2010); Soomro *et al.*, (2010) and Tabasum *et al.*, (2012) who estimated high heritability for seed cotton yield.

Lint percentage is a multigenic trait which primarily depends on the proportion of lint weight against the weight of seed cotton sample, which has direct influence on seed cotton yield. It is quite surprising that with three exceptions, genetic variances were quite greater than the environmental variances which led to express higher heritability estimates in other five progenies. Four out of eight populations exhibited higher heritability estimates of above 60.0%, yet other four progenies exhibited low to medium heritability percentage. Progenies from Chandi x Sadori (h²= 80.41%), CRIS-134 x Sadori (h²=76.29%) and BH-160 x Sadori (h²=68.97%) ranked among the top three in exhibiting higher heritability which also expressed maximum genetic variability and more genetic advances. These progenies which are less affected by the environmental factors and having more genetic variability suggested that additive genes are present in such populations. Thus, it is expected that these populations can be choice breeding material to select desirable plants with higher lint% from subsequent filial generations. The present results are in line with those obtained by Baloch (2004) who observed moderate heritability ranging from 33.6 to 63.00% for lint% while Patel *et al.* (2005) noted highest genotypic variability estimates. Naveed *et al.* (2002) observed that additive and dominance genetic

variances pre-dominantly controlled the lint percentage.

Seed index is also an important yield factor and plays imperative role in increasing seed cotton production. Genetic analysis revealed that four populations viz. CRIS-134 x Sadori, Chandi x Sadori, BH-160 x Sadori and Chandi x CRIS-134 exhibited heritability estimates above 70%, however maximum heritability was manifested by Chandi x CRIS-134 ($h^2=74.91\%$) followed by Chandi x Sadori ($h^2=72.97\%$). The trend of genetic advance was similar to that of heritability estimates in that, the F_2 progenies which exhibited higher heritability, gave proportionally greater genetic advances (Table 3). The F_2 populations like CRIS-134 x Sadori, Chandi x Sadori, BH-160 x Sadori and Chandi x CRIS-134 which ranked among top four progenies in expressing maximum genetic variability and higher heritability also recorded greater genetic advances. It may be predicted that these populations are more amenable to selection of desirable plants with higher seed index from subsequent segregating generations. Mahmoud *et al.* (2004) also reported higher heritability estimates in broad sense for seed index from interspecific crosses of *G.hirsutum* x *G.barbadense*.

The most important among the fiber properties in cotton is the staple length. This trait is valuable for local textile mills and simultaneously for international trade for the preparation of good quality fabrics. The results regarding genetic parameters summarized in Table-3 revealed fair amount of genetic variability (δ^2g) that varied from 34.94 to 77.46 and environmental variance varying from 22.20 to 40.90. Majority of F_2 progenies, expressed medium to high heritability estimates in broad sense that varied from $h^2=44.09$ to $h^2=76.91\%$) and was associated with appreciable amount of genetic gains ranging from 6.90 to 13.58. However, progenies like CRIS-134 x Sadori, Chandi x NIAB-78, BH-160 x NIAB-78

and Chandi x Sadori exhibited highest values for genetic variability, less environmental variance, maximum heritability percentage in broad sense, consequently recorded greater genetic advances, hence these populations have proved as potential breeding material for further selection in subsequent generations to improve fiber length in cotton. Baloch (2002) while working with F_2 hybrids obtained moderate heritability estimates associated with high genetic coefficient of variability, genetic variability and genetic advance. Baloch (2004) also recorded high heritability percentage ($h^2=81.8\%$), yet Yuan *et al.* (2002), Zhang and Yong (2004), and Saeed *et al.* (2007) while working on fiber trait also found significantly higher heritability in broad sense.

Conclusions

The analysis of variance revealed significant differences among genotypes, parents and F_2 populations for all the multigenic traits studied which suggested that the breeding material is worth of genetic analysis. On an average, F_2 progenies gave higher mean values for almost all the traits which could be due to heterotic effects or transgressive segregants. On the basis of mean performance, parental cultivars CRIS-134 recorded medium-taller plants, produced higher sympodial branches plant⁻¹ and formed more number of bolls plant⁻¹; NIAB-78 weighed bigger bolls, gave maximum seed cotton yield plant⁻¹; while Sadori ginned higher lint% and measured longer staple length. Results revealed that these three are the potential parents for hybridization and selection programs to improve various traits of economic importance. Genetic analysis revealed that F_2 population derived from CRIS-134 x Sadori exhibited higher heritability estimates associated with greater genetic advances for sympodial branches plant⁻¹ ($h^2=69.06\%$, $GA=7.32$) and staple length ($h^2=76.91\%$, $GA=8.27$); while Chandi x Sadori manifested maximum heritability estimates

coupled with higher genetic advances for bolls plant⁻¹ ($h^2=75.60\%$, $GA=16.49$), seed cotton yield plant⁻¹ ($h^2=74.06\%$, $GA=49.48$), lint% ($h^2=80.41\%$, $GA=11.16$) and seed index ($h^2=72.97\%$, $GA=1.65$), respectively. Results by and large suggested that quite a number of F₂ progenies expressed higher heritability estimates

coupled with greater genetic advances possessed additive genes, hence can be potential population for selection of desirable plants from subsequent segregating generations.

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