Pak. j. sci. ind. res. Ser. B: biol. sci. 2018 **61B**(3) 136-144

Genetic Variability, Heritability and Correlation Studies in F_2 Populations of Upland Cotton

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(received April 7, 2016; revised June 29, 2017; accepted August 7, 2017)

Abstract. A field experiment was conducted at the experimental area of the Department of Plant Breeding & Genetics, Sindh Agriculture University Tandojam, during the year 2014-2015 in order to carry-out genetic analysis in F_2 populations of upland cotton. The trial was laid-out in a Randomized Complete Block Design with four replications. The material was consisted of eight parents and ten F_2 populations. The analysis of variance revealed significant differences among the parents and F_2 populations for all the traits studied except that fibre length was non-significant in parents. The results further suggested that maximum heritability, higher genetic variances coupled with more genetic gains were expressed by the F_2 populations CRIS-134 × CRIS-508 and CRIS-134 × CIM-598 for 1st sympodial node number; CRIS-134 × Neelum-121 and CRIS-134 × CRIS-508 for sympodial branches/plant; CRIS-342 × FH-113 for boll weight; CRIS-342 × Neelum-121 for bolls/plant, seed cotton yield/plant, lint % and micronaire value and progenies CRIS-342 × MNH-886 followed by CRIS-342 × Neelum-121 for staple length. These results also suggested that a number of F_2 populations indicated their potential for various seed cotton yield and fibre traits. The phenotypic correlations revealed that most of the traits were significantly and positively associated with seed cotton yield/plant. However, higher correlations of sympodial branches/plant (r = 0.69**) and bolls/plant (r = 0.82**) with seed cotton yield indicated that both the traits are more reliable as compared to other traits for selection of higher seed cotton yields. Very interestingly, fibre traits like lint%, fibre length and micronaire were also significantly correlated with seed cotton yield, suggesting that fibre quality traits can be improved without compromising on seed cotton yield. Thus, the material under study is very promising and worthy of selection to improve many traits simultaneously.

Keywords: genetic variability, heritability, F_2 populations, correlations, cotton genotypes

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Introduction

Genetic variability is referred as observed phenotypic variation which occurs in plant populations and is mainly attributable to genetic differences among them. Broad sense heritability may be defined as the ratio of genotypic variance over the phenotypic variance. In other words, it determines the magnitude of transmissibility of traits from parents to their offspring (Baloch *et al*., 2004). The additive variance, which is the variance of breeding values, is the important component of heritability. It is the chief source of measurement between the traits of parental and progenies.

The genetic potential of genotypes, genotypic and phenotypic correlations between different plant characters is available in the literature. The studies of Khan (2003) found that the seed cotton yield was positively correlated with bolls per plant and bolls weight. Further studies indicated that seed and lint indices were positively associated with seed cotton yield. Genetic variability and positive correlations were observed for yield traits in *Gossypium hirsutum* L. (Batool *et al*., 2010; Wang *et al*., 2004; Iqbal *et al*., 2003). The principal objectives in cotton breeding are higher production of seed cotton, lint yields with better fibre quality, early maturity and resistance to diseases and insect pests (Khan *et al*., 2009). For achieving these objectives, plant breeders have devoted a lot of efforts to use quantitative genetic analysis because most of the traits in cotton are considered as polygenic in nature. Quantitative traits possess continuous variation thus can be altered significantly by suitable breeding procedures (Baloch *et al*., 2010). Crop development requires breeders' ability to identify and select good performing genotypes from a population. Some difficulties may be encountered when breeders make selections for quantitative traits that are largely affected by the environmental factors (Ragsdale and Smith, 2007; Khan, 2003). Heritability of various traits and

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the genetic potential of different populations in the form of their expression for different morpho-yield traits are urgently needed for selection of useful parental lines (Khan *et al*., 2010). Substantial genetic variances and higher heritability estimates of seed cotton yield and its component traits implied that such characters can be improved through hybridization and selection from segregating populations (Baloch *et al*., 2010; Baloch, 2004). A quantitative trait like yield being multigenic is significantly affected by environmental factors. Thus, the overall performance of a genotype may vary due to changes in the environment. It is generally stated that the higher the heritability, the simpler will be the selection process and greater will be the response to selection (Baloch *et al*., 2010). In addition, a thorough knowledge about the mean performance, extent of relationship and correlation of yield with various agronomic characters is indispensable for breeder to tackle the problems of low yield and increase the yield successfully. Ahsan *et al*. (2015); Farooq *et al*. (2015) and Rajamani *et al*. (2015) determined genotypic, phenotypic and environmental coefficient of variation and also estimated broad sense heritability and genetic advance in cotton. They estimated higher genotypic and phenotypic coefficient of variation for plant height, bolls per plant, boll weight, nodes to first fruiting branch and seed cotton yield per plant. The heritability was above 80% and the significant amount of genetic advance for these traits provided a clear picture that selection can be effective to improve these traits. Srinivas *et al*. (2015) conducted correlation analysis and observed that monopodia/plant, sympodia/plant, bolls/plant, boll weight and 2.5% span length were positively associated with seed cotton yield. While Farooq *et al*. (2015) noted that sympodia per plant expressed significant and positive correlation with bolls per plant, boll weight and yield at both genotypic and phenotypic levels. Thus, the objectives of the present research were to determine genetic variability, heritability correlations in intra-hirsutum F_2 populations for yield and fibre quality traits in upland cotton.

Materials and Methods

The present study was conducted at Experimental Field, Department of Plant Breeding and Genetics, Faculty of Crop Production, Sindh Agriculture University Tandojam so as to estimate genetic variability, heritability and correlation studies of ten intraspecific F_2 populations of upland cotton (*Gossypium hirsutum* L). Eight parents including CRIS-134, CRIS-342, Neelum-121, CIM-598, MNH-886, FH-113, IR-3701 and CRIS-508 were randomly crossed to develop ten F_2 intraspecific populations. For evaluation, the experiment was conducted in a randomized completer block design with four replications. The observations were taken on ten randomly tagged plants from each genotype per replication. Thus, forty plants were included in the study. The characters studied were; 1st sympodial node number, sympodial branches/plant, bolls/plant, boll weight, lint percentage, fibre length, micronaire value and seed cotton yield/plant. The data were analyzed according to statistical technique outlined by Gomez and Gomez (1984) through Statistix 8.1 computer software so as to calculate the differences among the genotypes for various traits. Whereas, means were compared by using the least significant difference (L.S.D.) test at 5% probability level. The genetic and phenotypic environmental variances, broad sense heritability (h^2) and expected response to selection were estimated according to Baloch *et al*. (2010). The correlations were determined according to formulae developed by Raghavrao (1983).

Results and Discussion

Analysis of variance and mean performance of parents and F_2 populations. In the present research, genetic variability, heritability and correlations were studied in F_2 populations of upland cotton (*Gossypium hirsutum* L.) so as to identify the better segregates from subsequent filial generations. The eight important traits of cotton such as 1st sympodial node number, sympodial branches/plant, boll weight, bolls/plant, lint%, micronaire, fibre length, and seed cotton yield/plant were studied.

The analysis of variance revealed significant differences among the genotypes (comprising eight parents and their ten F_2 hybrids) for all the characters. The mean squares of parents, F_2 hybrids and parents vs. F_2 hybrids were also significant for all the traits except that fibre length was non-significant for parents only (Table 1). The mean performance of parents and hybrids (Table 2) indicated that most of the F_2 hybrids gave higher average values over their parents for all the traits under test. In parental lines, CRIS-134 formed 1st sympodial node at the lowest node of 7.50 being earlier while FH-113 formed 1st sympodia at the highest node of 10.15, thus it was considered as a late maturing parent. The F_2 population developed from crosses CRIS-134 × NMH-886 and CRIS-134 × CRIS-508 formed the lowest

Table 1. Mean squares from analysis of variance of parents and their intra hirsutum F_2 populations for yield and fibre traits

Character	Source of variation					
	Replication D.F. = 3	Genotypes D.F. = 17	Parents (P) D.F. = 7	F_2 Hybrids (P) D.F. = 9	P vs. H D.F. = 1	Error D.F. = 51
1st sympodial node number	0.34	2.85**	1.84**	0.54**	30.62**	0.32
Sympodia/plant	3.91	172.01**	61.19**	88.28**	1701.29**	2.046
Bolls/plant	2.68	441.91**	224.67**	74.33**	5270.85**	5.418
Boll weight	0.04	0.22**	0.06**	0.36**	0.15**	0.057
Seed yield/plant	199.64	6101.81**	1330.43**	1304.31**	82679.20**	134.51
Lint %	3.85	63.08**	70.60**	56.00**	74.22**	11.122
Fibre length	0.45	1.450**	0.33^{ns}	2.06**	3.80**	0.671
Micronaire value	0.005	0.033**	0.03**	0.017*	0.22**	0.008

** = significant at 1% probability level; ns = non significant

Table 2. Mean performance of parents and their intra-hirsutum F_2 populations for various yields and fibre traits

Genotypes (Parents and hybrids)	Characters							
	1st sympodial node no.	Sympodial branches/ plant	Bolls/ plant	Boll weight (g)	Yield/ plant (g)	GOT %	Staple length (mm)	Micronaire value (µg/inch)
Parents								
CRIS-134	7.50	19.45	40.90	3.17	129.65	36.13	28.45	3.94
CRIS-342	8.70	20.35	38.10	2.92	111.25	40.56	27.66	3.82
Neelam-121	8.35	20.90	36.99	3.26	120.59	42.34	28.03	3.10
CIM-598	9.95	17.85	28.85	3.05	87.99	45.52	28.47	3.91
MNH-886	9.00	18.10	35.22	3.06	107.77	50.45	28.36	3.73
FH-113	10.15	19.60	35.85	3.09	110.78	42.34	28.19	3.92
IR-3701	9.75	18.15	31.80	3.24	103.03	43.27	28.22	3.87
CRIS-508	9.60	18.30	28.65	2.96	84.80	39.98	27.86	3.85
Average	9.13	19.09	34.55	3.09	106.98	42.57	28.16	3.77
F_2 hybrids								
CRIS-134 × Neelam-121	11.40	24.25	45.35	3.54	160.54	45.10	30.14	3.92
CRIS-134 × CIM-598	10.90	21.15	42.45	3.11	132.02	45.12	28.12	4.15
CRIS-134 × IR-3701	11.25	21.50	44.70	3.18	142.15	44.14	27.95	3.96
CRIS-134 × MNH-886	10.40	22.10	44.65	3.48	155.38	50.39	29.24	4.01
CRIS-134 × FH-113	10.95	22.40	48.70	3.16	153.89	42.76	28.60	3.99
CRIS-342 × Neelum-121	10.45	24.65	52.60	3.38	177.79	44.84	27.83	3.97
CRIS-342 × IR-3701	10.45	23.60	50.35	3.10	156.09	43.32	28.74	3.97
CRIS-342 × MNH-886	11.05	22.85	48.75	2.62	127.73	40.99	29.12	3.98
CRIS-342 × FH-113	10.75	26.10	49.85	2.82	140.58	39.00	28.25	3.94
CRIS-134 × CRIS-508	10.40	25.45	38.15	3.46	132.00	48.50	28.18	4.03
Average	10.80	23.41	46.56	3.19	147.82	44.42	28.62	3.99
LSD (5%)	0.81	2.03	0.34	3.30	16.46	4.73	1.16	0.13

sympodia at node number 10.40, whereas the highest sympodia were formed by CRIS-134 × Neelum-121 at node number 11.40. The sympodial branches/plant varied from 17.85 (CIM-598) to 20.90 (Neelum-121) among the parental lines while the progenies from cross CRIS-342 × FH-113 produced maximum number of sympodial branches/plant (26.10). Similarly, in the case of boll weight, progenies CRIS-134 × Neelum-121 recorded the bigger bolls (3.54g), while the parental lines Neelum-121 showed the highest mean value (3.26g). With respect to bolls/plant, progenies from CRIS-342 × Neelum-121 formed the highest number of bolls per plant (52.60). With respect to lint %, the parental line MNH-886 ginned higher lint (50.45%), while the progenies derived from CRIS-342 × Neelum-121 ginned maximum lint of 50.39%. The F_2 progenies gave higher seed cotton yield/plant against their parents and that ranged from 127.73g (CRIS-342 × MNH-886) to 177.79g (CRIS-342 × Neelum-121). The fibre length of parental lines ranged from 27.66mm to 28.47mm, however progenies from CRIS-342 × Neelum-121 and CRIS-134 × Neelum-121 measured the fibre ranging from 27.83mm to 30.14mm, respectively. The progenies exhibited micronaire ranging from 3.92 to 4.15μg/inches measured by progenies CRIS-134 × Neelum-121 and CRIS-134 × CIM-598, respectively.

Genetic variability analysis of F_2 progenies. The results of genetic variance (d2p), phenotypic variance (d2g), heritability percentages in broad sense (h2b.s.) and genetic gain (GA) at 10% selection intensity for eight important quantitative traits showed that most of the F_2 populations demonstrated moderate to high heritability estimates. Besides, majority of the characters were generally associated with more genetic advances indicating the presence of an appreciable amount of genetic variability mainly due to additive genes in F_2 populations. Results of 1st sympodial node number suggested that sufficient genetic variability was present in F_2 populations. Low, moderate and high heritability estimates were recorded that varied from 23.82 to 75.84% (Fig. 1). Two higher ranking progenies CRIS-134 × CRIS-508, CRIS-134 × CIM-598 however exhibited higher heritability estimates of h^2= 75.84% and h^2=75.61% with greater amount of genetic advances (4.40 and 3.98, respectively). Ahmed and Malik (1996) estimated that a one node decrease in sympodial branch matures the cotton crop by approximately 4 to 7 days earlier. Jatoi *et al.* (2012) reported that 1st sympodial branch node was significantly and positively correlated with node number to set 1st boll and sympodial branch length. For sympodial branches, about half of the progenies displayed higher genetic variability than their corresponding environmental variances resulting in low to high heritability estimates ranging from 40.35 to 76.79% (Fig. 2). The progenies, CRIS-134 × Neelum-121 and CRIS-134 × CRIS-508 nevertheless manifested higher heritability estimates of h^2= 76.79% and h^2= 76.34% and these heritability estimates were related with fair amount of genetic advances (9.94 and 3.48, respectively). Pertaining to bolls/plant (Fig. 3), it was noted that the majority of the progenies expressed higher genetic variability than environmental variances, thus moderate to high heritability percentages in broad sense and higher genetic gains were recorded. Higher heritability estimates and more genetic variances for bolls/plant were generally allied with higher genetic advances. From F_2 population, CRIS-342 × Neelum-121 exhibited higher heritability (h^2 = 91.24%) and recorded maximum genetic gains (31.15). Hussain *et al.* (2010) reported high genotypic variability, genetic

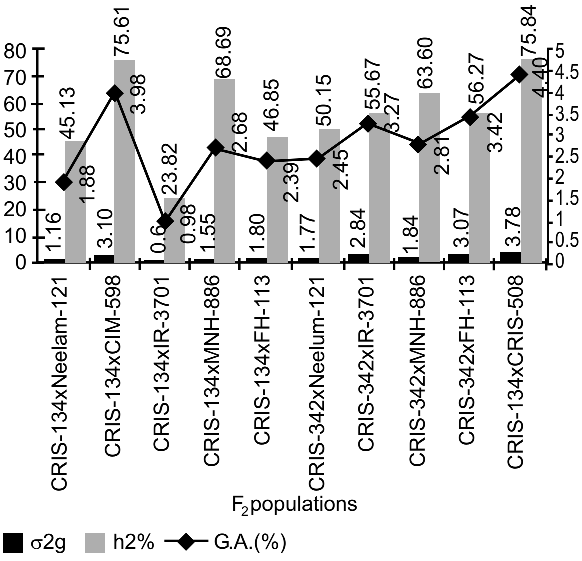

Fig. 1. Genetic components for 1st sympodial node number in F_2 populations of upland cotton.

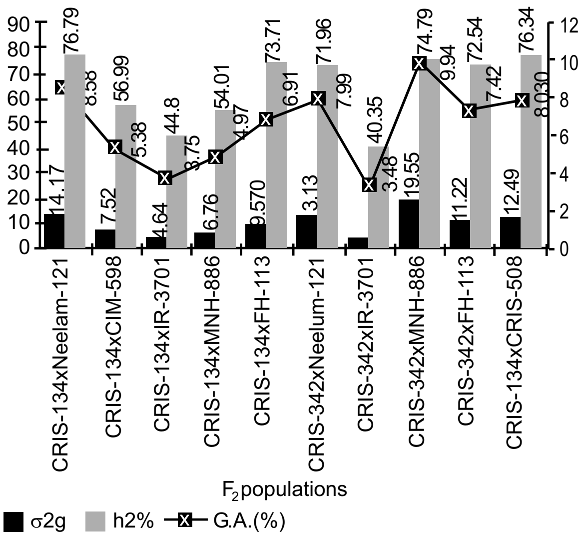

Fig. 2. Genetic components for sympodial branches/ plant in F_2 populations of upland cotton.

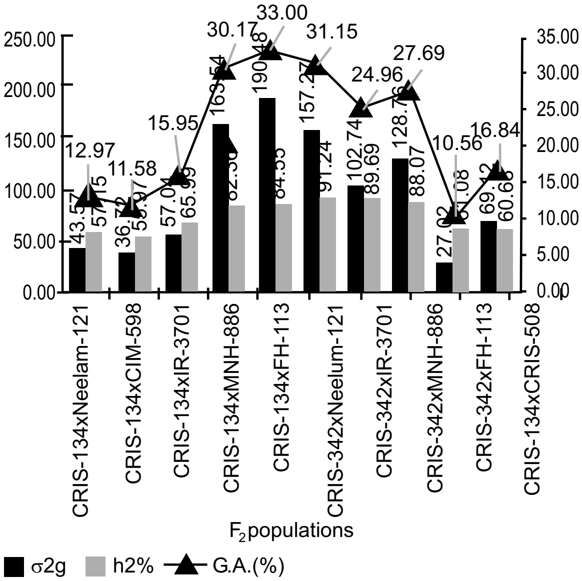

Fig. 3. Genetic components for bolls/plant in F_2 populations of upland cotton.

advance and heritability estimated for number of bolls per plant.

With respect to boll weight, greater genetic variances were displayed by less than half of the progenies as compared to their corresponding environmental variances. By and large, F_2 progenies expressed low to moderate heritability estimates ranging from 31.08 to 68.87%, while genetic gains varied from 0.38 to 1.01 (Fig. 4). The top scoring in relation to heritability percentage and genetic advance were the progenies derived from CRIS-342 × FH-113 (h^2 = 68.87%) and (GA = 1.01) followed by CRIS-342 × Neelum-121 (h^2 = 66.13%) and (GA = 0.98). Batool *et al.* (2010) and Soomro *et al.* (2010) found higher genetic variances and higher heritability estimates for boll weight in upland cotton as well and concluded that this trait is highly heritable in F_2 and F_3 generations. On the contrary, Naveed *et al.* (2004) reported low to moderate heritability estimates for boll weight which also confirm our results for some of the progenies. Regarding seed cotton yield/plant (Fig. 5), F_2 progenies exhibited fair to high genetic variability, recorded moderate to higher heritability estimates that ranged from 63.34% to 95.96% and higher genetic gains varying from 52.45 to 148.75. From the progenies evaluated, CRIS-342 × IR-3701 exhibited highest heritability (h^2 = 95.69%) and consequently demonstrated with higher genetic advance (GA = 148.75). Similar to our findings, Tabasum *et al.* (2012); Mushtaq *et al.* (2011); Batool *et al.* (2010) and Soomro *et al.* (2010) also estimated high heritability for seed cotton yield. Selection for high ginning outturn % often results in an increase in the production/plant and per unit area. The results indicated that progenies CRIS-134 × MNH-886 displayed highest heritability percentage (h^2=97.12%) coupled with greater genetic

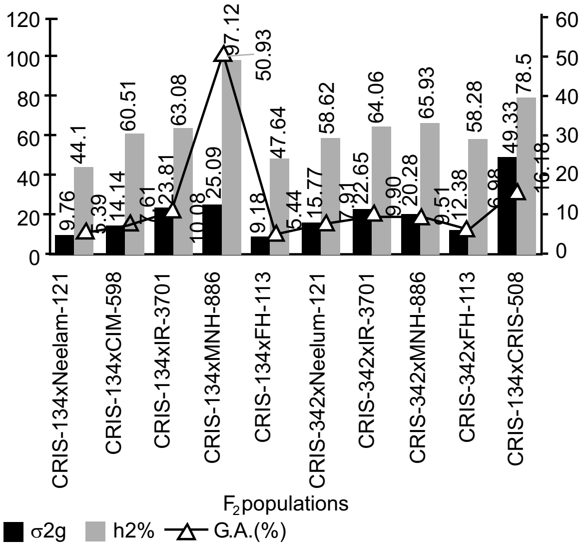

Fig. 4. Genetic components for bolls/plant in F_2 populations of upland cotton.

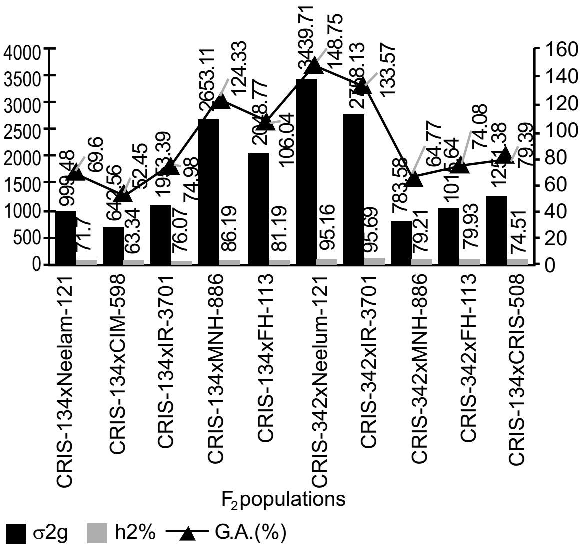

Fig. 5. Genetic components for seed cotton yield/ plant in F_2 populations of upland cotton.

advance (GA=50.93) (Fig. 6).Our results are in agreement with those obtained by Farooq *et al.* (2014). Khan *et al.* (2010) also found greater genetic variance and higher heritability percentage for lint%. Ali *et al.* (2010) noted that heritability estimates were high for lint% indicating that additive genes were controlling these traits. Regarding fibre length, majority of the F_2 populations showed higher genetic variances against their corresponding environmental variances. High heritability estimates were coupled with ample amount of genetic advances varying from 1.04 to 4.20 (Fig. 7). The progenies derived from crosses CRIS-342 × MNH-886, CRIS-342 × Neelum-121 expressed higher heritability, greater genetic variability and more genetic advances. Khan *et al.* (2009) and Memon *et al.* (2008) also recorded greater genetic variability, higher heritability associated with greater genetic advance for staple length in F_2 progenies of upland cotton. Concerning micronaire (µg/inch), flaxen amount of genetic variability from F_2 progenies were observed (Fig. 8). Higher ranking F_2 populations such as CRIS-134 × IR-3701 and CRIS-134 × CIM-598 manifested higher heritability (h^2=84.15, h^2=83.61), and maximum genetic advance (GA = 0.76 and GA = 0.92) suggesting that additive genes were involved in the expression of micronaire.

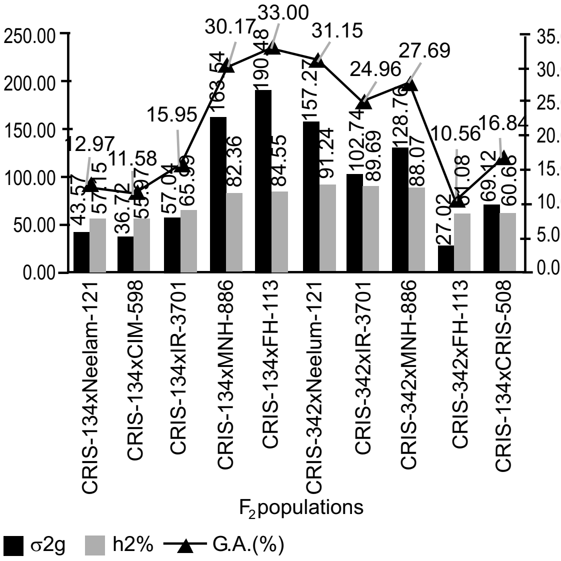

Fig. 6. Genetic components for GOT% in F_2 populations of upland cotton.

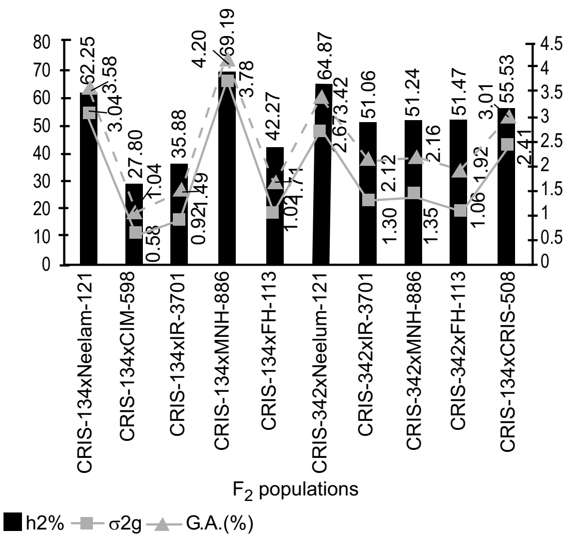

Fig. 7. Genetic components for staple length in F_2 populations of upland cotton.

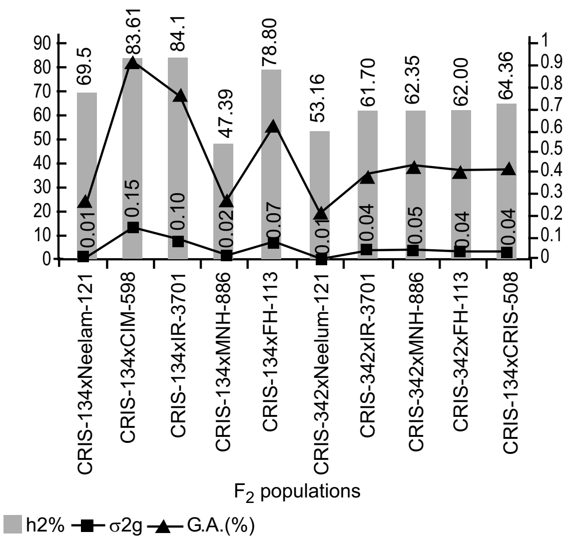

Fig. 8. Genetic components for micronaire in F_2 populations of upland cotton.

Phenotypic correlations. Correlation studies indicated that 1st sympodial node number was significantly and positively correlated with sympodial branches/plant, lint%, micronaire, seed cotton yield/plant, fibre length, and bolls/plant which suggested that increase in appearance of 1st sympodial node number caused a comparable increase in all the above traits. Sympodial branches/plant was significantly and positively correlated with 1st sympodial node number, micronaire, bolls per plant and seed cotton yield (Table 3). The positive relationship of sympodial branches per plant with other traits suggested that increase in sympodial branches will cause an associated increase in 1st sympodial node number, micronaire value, bolls per plant and seed cotton yield and negative correlation with lint% revealed that increase in sympodial branches will decrease lint %. Tamilselven *et al*. (2013) and Rao and Gopinath (2013) studied correlations in upland cotton and found that sympodial branches/plant was significantly and positively correlated with bolls per plant and seed cotton yield. Significant and positive association of boll weight with lint%, micronaire, fibre length and seed cotton yield indicated that while improving boll weight, the increase in other traits like seed cotton yield, fibre length and micronaire can occur. Correlation between bolls/plant and seed cotton yield/plant demonstrated highly significant and positive relationship. Such association revealed that increase in bolls/plant will simultaneously increase seed cotton yield/plant. Results from correlation studies further revealed that lint % was positively and significantly correlated with only seed cotton yield, hence it could be inferred that significant improvement could be made in seed cotton yield along with lint% without causing adverse impact on other important traits. Significant and positive association of fibre length with bolls/plant and seed cotton yield indicated that increase in fibre length will cause a corresponding increase in both bolls/ plant and seed cotton yield. Farooq *et al*. (2014); Islam *et al*. (2013); and Rao and Gopinath (2013) assessed different hirsutum varieties for yield and other economic characters and observed significant variations for boll weight and showed its positive effect on seed cotton yield. The significantly positive correlation of micronaire with sympodial branches, bolls/plant and seed cotton yield further indicated that seed cotton yield can be improved without sacrificing fibre quality traits. Srinivas *et al*. (2015) and Baloch *et al*. (2014) conducted correlation analysis and observed that monopodia/plant, sympodia/plant, bolls/plant, boll weight and 2.5% span length were positively associated with seed cotton yield, while Farooq *et al*. (2015) noted that sympodia per plant expressed significant and positive correlation with bolls per plant, boll weight and yield at both genotypic and phenotypic levels.

Table 3. Correlation coefficients (r) between seed cotton yield and fibre traits in upland cotton

Character association	Correlation coefficient (r)
Boll weight vs. 1st sympodial node number	0.04^{ns}
Boll weight vs. sympodial branches/plant	0.05^{ns}
Boll weight vs. bolls/plant	0.08^{ns}
Boll weight vs. G.O.T.%	0.27**
Boll weight vs. staple length	0.199**
Boll weight vs. seed cotton yield/plant	0.34**
Boll weight vs. fibre fineness	0.21**
1st sympodial node number vs. sympodial branches/plant	0.37**
1st sympodial node number vs. bolls/plant	0.37**
1st sympodial node number vs. G.O.T.%	0.21**
1st sympodial node number vs. staple length	0.28**
1st sympodial node number vs seed cotton yield/plant	0.44**
1st sympodial node number vs fibre fineness	0.16*
G.O.T. % vs sympodial branches/plant	-0.002^{ns}
G.O.T. % vs bolls/plant	-0.08^{ns}
G.O.T. % vs staple length	0.05^{ns}
G.O.T. % vs seed cotton yield/plant	0.15*
G.O.T. % vs fibre fineness	0.02^{ns}
Fibre fineness vs sympodial branches/plant	0.33**
Fibre fineness vs bolls/plant	0.46**
Fibre fineness vs staple length	0.05^{ns}
Fibre fineness vs seed cotton yield/plant	0.46**
Sympodial branches/plant vs bolls/plant	0.72**
Sympodial branches/plant vs staple length	0.23^{ns}
Sympodial branches/plant vs seed cotton yield/plant	0.69**
Staple length vs bolls/plant	0.21**
Staple length vs seed cotton yield/plant	0.24**
Bolls/plant vs seed cotton yield/plant	0.82**

*,**= Significant at 0.01, 0.05 probability levels, respectively; ^{ns} = non-significant.

Conclusion

Significant differences among parents and the F_2 hybrids were recorded for all the studied traits except that fibre length was non-significant in parents. It may be concluded from the present research that based on average performance, the parents, Neelum-121, CIM-598 and FH-113 performed very well in terms of 1st sympodial node number, boll weight, fibre length, lint%, while parent CRIS-134 produced bigger bolls and higher seed cotton yield with desirable micronaire value. The estimation of genetic parameters indicated that F_2 progenies derived from the cross CRIS-134 × CRIS-508 displayed higher heritability estimates coupled with more genetic gains for 1st sympodial node number and sympodial branches; CRIS-342 × FH-113 for boll weight; CRIS-342 × Neelum-121 for bolls/plant and seed cotton yield; CRIS-134 × MNH-886 produced upper most heritability with more genetic gains for lint% and fibre length and CRIS-134 × IR-3701 for micronaire value. Thus these populations are worth to be explored in further segregating generations so as to improve yield and fibre quality traits. The phenotypic correlations revealed that 1st sympodial node number, sympodial branches per plant, bolls/plant, boll weight, lint %, fibre length and micronaire were highly and positively associated with seed cotton yield hence these yield components can be used as reliable selection criteria to improve seed cotton yield. It further indicated that fibre traits can be improved without compromising seed cotton yield.

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