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COMBINING ABILITY STUDIES FOR YIELD AND FIBER TRAITS IN UPLAND COTTON

S. A. Khan[1], N. U. Khan[1], R. Gul[1], Z. Bibi[2], I. U. Khan[2], S. Gul[1], S. Ali[3] and M. Baloch[4]

[1]Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar - Pakistan
[2]Department of Soil and Environmental Sciences, Gomal University, Dera Ismail Khan - Pakistan
[3]Department of Agricultural Sciences, University of Haripur - Pakistan
[4]Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam - Pakistan
Corresponding author's Email: Naqib Ullah Khan <nukmarwat@yahoo.com>

ABSTRACT

Genetic potential and combining ability were studied in 6 × 6 F_1 cross of *Gossypium hirsutum* L. at the University of Agriculture, Peshawar, Pakistan. Six parental genotypes **(**CIM-446, CIM-496, CIM-499, CIM-506, CIM-554 and CIM-707) and their 30 F_1 diallel progenies were grown in a randomized complete block design with three replications. Significant (*$p \leq 0.01$*) differences were observed among the genotypes for bolls per sympodia, bolls per plant, boll weight, seed cotton yield per plant, lint % and lint index. F_1 hybrids showed significant increase over parental means for all the traits. Mean squares due to GCA and SCA were highly significant for all the traits. The GCA mean squares were higher than SCA for majority traits which revealed that additive genes controlled the inheritance. Utilization of best general combiners (CIM-446 and CIM-554) as one of the parents produced promising F_1 population (CIM-446 × CIM-554, CIM-446 × CIM-496 and CIM-506 × CIM-554) with desirable SCA and mean performance for yield and fiber traits. Therefore, high × low, low × high and in some cases high × high GCA parents showed best performance for majority traits. Correlation of seed cotton yield was significantly positive with yield related traits however, the association was negative with lint %. Additive gene action controlled the inheritance, and selection in above promising hybrids could be used in early segregating generations and in hybrid cotton production to enhance the seed cotton yield.

Key words: Combining ability; GCA & SCA effects; additive and non-additive gene action; diallel cross; F_1 hybrids; upland cotton

INTRODUCTION

Generally, the characters of plants and other living creatures are the results of countless gene interactions. Genotypic variance is a part of total variance that remains after eliminating the environmental variance and those variances can be observed in homozygous lines and their progenies. F_1 hybrids have hybrid vigor, which is manifestation of heterozygosity and can be regarded as the converse of the deterioration that escorts inbreeding (Khan, 2011). Past studies revealed that in plants, the heterosis is known to be a multigenic complex trait and can be extrapolated as the sum total of many physiological and phenotypic traits (Baranwal *et al*., 2012), and it enabled the plant and animal breeders to improve the performance for several economic traits (Khan, 2013). Rosas *et al*. (2010) discussed the role of variation in gene expression between parental species and its effect on phenotype, and concluded that F_1 hybrids might be expected to show increased performance with regard to basic physiological traits such as growth.

Combining ability and genetic variation are useful in determining the breeding value of some populations and the appropriate procedures to use in a breeding program (Ilyas *et al*., 2007), however, the most commonly utilized experimental approach is the diallel design. In diallel analysis, Sprague and Tatum (1942) introduced the hypothesis of general combining ability (GCA) and specific combining ability (SCA). The GCA is a measure of the additive gene action, while SCA is assumed a deviation from additivity. Mean performance of a line can be observed by crossing it to several other lines and expressed as a deviation from the mean of all crosses, is called the GCA of the line. Any particular cross has an expected value which is the sum of the GCAs of its parental lines. However, the F_1 hybrid may deviate from this expected value to a greater / lesser extent. This deviation is called the SCA of the two lines in combination (Azhar and Naeem, 2008; Khan *et al*., 2009d). In statistical terms, the GCA is main effect and the SCA is an interaction.

Choice of parental cultivars for development of desirable hybrid population is difficult, and need thorough screening before making a cross. Plant genetic resources, objectives and genetic nature of the variables will affect the final selection of genotypes for breeding program. However, the outcome of various biometrical evaluations can better help the plant breeders in refining the final decision. Griffing's biometrical analysis (Griffing, 1956) has been widely used to aid plant geneticists in selection of genotypes for hybridization program. In a generalized theoretical form, Griffing's combining ability is mostly used for analysis of diallel crosses. Combining ability work as basic tool for improved production of crops in the form of F_1 hybrids. Phenomenon of F_1 hybrids heterosis can also reflect GCA of parental lines and SCA of specific crosses, and provide the basis for exploitation of valuable cross combinations and their future utilization.

Due to GCA and SCA, significant genetic variances were noticed for various yield related traits in *Gossypium hirsutum* L. (Baloch *et al*., 2000; Hassan *et al*., 2000; Islam *et al*., 2001b; Azhar and Naeem, 2008; Khan *et al*., 2009c, d; 2011). Non-additive type of gene action was observed for boll weight, boll number, lint % and seed cotton yield (Muthu *et al*., 2005; Ahuja and Dhayal, 2007; Ilyas *et al*., 2007; Khan *et al*., 2009c). However, additive genetic effects with enough genetic variability were noticed for most of the yield traits, and effective selection was suggested in early segregating generations in upland cotton (Chinchane *et al*., 2002; Yuan *et al*., 2002; Lukonge *et al*., 2008; Khan *et al*., 2007, 2009e). Such contradictions might be due to varied genetic backgrounds of cotton genotypes used under different environmental conditions.

For significant improvement in genetic potential of genotypes for yield and fiber quality traits, the hybrid cotton is a good approach (Khan *et al*., 2010a, 2011). However, for hybrid cotton, the various cotton lines are screened through combining ability to determine their GCA and SCA for new cross combinations. Many commercial cotton cultivars despite their high/low agronomic performance combine in a more good way/poorly when used as a parental cultivars in cross combinations. Therefore, the present study was conducted to analyze the 6 × 6 F_1 diallel cross population regarding their genetic potential and combining ability effects for various yield and fiber related traits in upland cotton.

MATERIALS AND METHODS

The research work was carried out at the University of Agriculture, Peshawar, Pakistan. Six diverse upland cotton genotypes **(**CIM-446, CIM-496, CIM-499, CIM-506, CIM-554 and CIM-707) were hand sown during May 2010 and were crossed in a complete diallel fashion during August and September. During 2011, the 30 F_1s and their parents were planted in a randomized complete block (RCB) design with four replications. Each treatment (Parental or F_1 genotype) in a replication consisted of a single row measuring six meter. The row and plant spacing was 75 and 30 cm, respectively. Thinning was performed after two weeks of germination to ensure single plant per hill. Recommended cultural practices and inputs were applied uniformly. Two hand pickings were made on an individual plant basis during the month of November, and ginning was done with eight saw gins.

Data were recorded for bolls per sympodia, bolls per plant, boll weight, seed cotton yield per plant, lint % and lint index, and were subjected to analysis of variance (Steel *et al*., 1997). Least significant difference (LSD) test was used for means separation and comparison after significance. The data were further subjected to the combining ability analysis according to Griffing (1956) using Method-I based on Eisenhart's Model-II as also stated by Singh and Chaudhary (1985).

RESULTS

The F_1 hybrids and their parental lines showed highly significant ($p \leq 0.01$) differences for all the traits (Table 2), which allowed arbitrating the components of genetic variations due to GCA, SCA and reciprocal effects.

Mean performance of parental cultivars and their F_1 hybrids: Bolls per sympodia varied from 1.54 to 2.55 among the parental genotypes, while 1.52 to 4.48 in F_1 hybrids (Table 3). The F_1 hybrid CIM-506 × CIM-554 manifested maximum bolls per sympodia (4.48), followed by four other F_1 cross combinations i.e. CIM-496 × CIM-446 (3.54), CIM-446 × CIM-496 (3.50), CIM-446 × CIM-554 (3.45), CIM-506 × CIM-496 (3.32). Minimum bolls per sympodia (1.52) were recorded for F_1 hybrid CIM-499 × CIM-707 and the same was found at par with parental genotype (CIM-499, 1.54). All other genotypes showed medium values for boll per sympodia. Boll per sympodia was found positively and significantly correlated with seed cotton yield per plant (Table 4).

Bolls per plant varied from 13 to 36 among the parental genotypes, while 18 to 46 in F_1 cross combinations (Table 3). Maximum number of bolls per plant was observed for F_1 hybrid CIM-506 × CIM-446 (46), and was followed by three other F_1 hybrids i.e. CIM-446 × CIM-496 (45), CIM-446 × CIM-554 (45) and CIM-496 × CIM-446 (41). However, minimum bolls per plant were exhibited by parental genotype CIM-499 (13) and was found at par in performance with five other F_1 hybrids ranging from 18 to 20. The remaining genotypes showed medium values for bolls per plant. Boll per plant were found positively and significantly correlated with seed cotton yield (Table 4).

Boll weight ranged from 2.89 to 3.53 g among the parental genotypes, while 3.26 to 4.14 g in F_1 hybrids (Table 3). Maximum boll weight was recorded for F_1 hybrid CIM-554 × CIM-446 (4.14 g) and was found at par with five other hybrids ranging from 3.84 to 4.12 g. Lowest boll weight (2.89 g) was observed in parental genotype CIM-554 and was found comparable with five parental genotypes and 13 F_1 genotypes ranging from 3.22 to 3.58 g. The remaining genotypes showed average boll weight. Boll weight was found positively and significantly correlated with seed cotton yield per plant (Table 4).

Seed cotton yield per plant ranged from 46.77 to 125.86 g among genotypes, while 53.69 to 190.88 g in F_1 hybrids (Table 3). The F_1 hybrid CIM-506 × CIM-554 showed maximum seed cotton yield per plant (190.88 g), however, it was followed by eight other F_1 hybrids ranging from 140.07 to 178.50 g. Lowest seed cotton yield was noted in parental genotype CIM-499 (46.77 g) and was found at par with four parental cultivars and thirteen F_1 hybrids ranging from 53.69 to 104.38 g. All other genotypes showed medium values for seed cotton yield per plant.

Lint % varied from 32.73 to 37.42% among the parental genotypes, while 30.84 to 38.78% in F_1 hybrids (Table 3). Maximum lint % (38.78) was recorded for F_1 hybrid CIM-554 × CIM-707 and was followed by parental line CIM-496 (37.42%) and its two F_1 hybrids i.e. CIM-496 × CIM-554 (37.79%) and CIM-554 × CIM-499 (37.80%). The lowest lint % (30.84%) was observed for CIM-506 × CIM-707 and was followed by F_1 hybrid CIM-707 × CIM-496 (31.69). The remaining genotypes showed medium values for lint %. Lint % was found negatively and significantly correlated with seed cotton yield (Table 4).

Lint index ranged from 4.04 to 5.07 g among the parental genotypes, while 3.83 to 5.37 g in F_1 hybrids (Table 3). Maximum lint index (5.37 g) was recorded in F_1 hybrid CIM-554 × CIM-499 which was at par with three other parental lines and six F_1 hybrids ranged from 4.93 to 5.22 g. The lowest lint index was observed in F_1 hybrid CIM-506 × CIM-707 (3.83 g) and was found equal with two other parental cultivars and nine F_1 hybrids ranged from 3.84 to 4.27 g. The remaining genotypes showed medium values for lint index. Lint index showed positive correlation with seed cotton yield which was, however, non-significant (Table 4).

According to genetic potential and mean performance (Table 3), the parental genotypes i.e. CIM-554, CIM-446 and CIM-496 were found with medium performance for all the traits. However, their use in F_1 hybrids showed extraordinary performance. The involvement of the genotype CIM-554 as paternal / maternal parent in F_1 hybrids (CIM-554 × CIM-446, CIM-554 × CIM-499, CIM-554 × CIM-496, CIM-554 × CIM-707 and CIM-506 × CIM-554) exhibited excellent mean values and excelled all other genotypes for the traits i.e. boll weight (4.14 g), lint index (5.37 g), bolls per sympodia (4.48), lint % (38.78%) and seed cotton yield per plant (190.88 g), respectively. The second promising genotype was CIM-446, and its involvement in F_1 hybrids (CIM-506 × CIM-446, CIM-554 × CIM-446 and CIM-499 × CIM-446) showed best performance for traits viz; bolls per plant (46) and boll weight (4.14 g). The hybrids involving CIM-496 F_1 i.e. CIM-496 × CIM-446, CIM-446 × CIM-496, CIM-446 × CIM-499 and CIM-506 × CIM-446 and CIM-554 × CIM-496 showed 2nd top scoring mean values for bolls per sympodia (3.54), bolls per plant (45), boll weight (4.12 g) and seed cotton yield per plant (178.50 g).

Combining ability analysis: Significant mean squares due to GCA, SCA and reciprocal effects were observed for all the characters studied except non-significant reciprocal effects in case of seed cotton yield per plant, indicating importance of both additive and dominant effects (Table 2). Overall, GCA mean squares were greater in magnitude than SCA and reciprocals for all the traits, depicting the preponderance of additive genes for the control of all the traits. SCA mean squares were greater than reciprocal mean squares for boll weight and seed cotton yield. However, reciprocal mean squares were greater than SCA for bolls per sympodia, bolls per plant, lint % and lint index signifying the importance of maternal effects for the manifestation of these traits.

General combining ability: The parental genotype CIM-446 was found promising genotype and excelled all other genotypes for GCA (Table 5) by having highest GCA effects for bolls per sympodia (0.43), bolls per plant (6.46), boll weight (0.17) and seed cotton yield (26.69). Genotype CIM-554 was the 2nd best genotype by obtaining desirable GCA effects for bolls per plant (2.33), boll weight (0.03), seed cotton yield (19.85) and lint index (0.24), while CIM-496 showed 2nd scoring GCA value for bolls per sympodia (0.12). For lint %, the genotype CIM-496 was having maximum GCA effects (0.71). Parental cultivar CIM-499 revealed poor performance and showed maximum negative GCA effects for majority traits i.e. bolls per sympodia (-0.42), bolls per plant (-5.84) and seed cotton yield (-33.23). Results confirmed that parental genotypes CIM-446 and CIM-554 were found as best general combiners.

Specific combining ability: Among F_1 hybrids, the positive SCA effects ranged from 0.09 to 0.68 for bolls per sympodia, 1.41 to 8.11 for bolls per plant, 0.02 to 0.29 for boll weight, 4.32 to 58.58 for seed cotton yield per plant, 0.06 to 0.48 for lint % and 0.05 to 0.26 for lint index (Table 6). The F_1 hybrid CIM-446 × CIM-554 was observed as the prominent specific combination by having maximum positive SCA effects for boll weight (0.29), lint index (0.26) and seed cotton yield (11.84) involving both parental genotypes as good general combiners. Thus, high × high GCA parents were involved in expression of these traits. The best general combiner CIM-446 by crossing with low GCA parent CIM-496 showed best performance for majority traits. The second best general combiner CIM-554 also exhibited highest SCA effects by crossing as paternal parent with low GCA parent (CIM-506) for the traits i.e. bolls per sympodia (0.68) and seed cotton yield (58.58).

Reciprocal combining ability: The F_1 reciprocal cross (CIM-554 × CIM-506) having the maternal parent as good general combiner (Table 7), manifested maximum reciprocal effects for bolls per sympodia (1.27) and seed cotton yield (51.46). The remaining six traits were controlled by such reciprocal crosses which involve the general combiners (CIM-446 and CIM-554) as one of the parents and manifested maximum reciprocal effects for bolls per plant (CIM-707 × CIM-446, 9.17), boll weight (CIM-499 × CIM-446, 0.36), lint % (CIM-554 × CIM-496, 2.11) and lint index (CIM-496 × CIM-446, 0.45).

The good general combiners (CIM-554, CIM-446) showed stability in reciprocal crosses also as in SCA effects (Table 7). The CIM-554 was found as best maternal parent in reciprocal crosses for three traits viz., bolls per sympodia (1.27), seed cotton yield per plant (51.46) and lint % (2.11). CIM-446 also proved as best pollen parent in F_1 hybrids i.e. CIM-707 × CIM-446, CIM-499 × CIM-446 and CIM-496 × CIM-446 and revealed maximum reciprocal effects for bolls per plant (9.17), boll weight (0.36) and lint index (0.45), respectively.

DISCUSSION

Diallel analysis is a mating design whereby the selected parental lines are crossed in a certain order to predict combining ability of the parents and elucidate the nature of gene action involved in the inheritance of traits (Basal and Turgut, 2003; Azhar and Naeem, 2008; Khan *et al*., 2009c, d; Bibi *et al*., 2011a, b). Combining ability can play a better role in identifying the precious genotypes for having specific cross combinations that can be used for heterosis and for further selection in segregating generations.

The yield is highly complex character and is directly influenced by the different morphological and yield contributing traits. Knowledge about the genetic potential of different genotypes and inheritance of the morphological and yield traits is indispensable for the breeders to tackle with the problems of low yield (Basal *et al*., 2009; Khan *et al*., 2009b, 2010b; Makhdoom *et al*., 2010). According to genetic potential, the parental genotypes (CIM-554 and CIM-446) and their F_1 hybrids showed best performance. The involvement of CIM-554 with other genotypes (CIM-446, CIM-496, CIM-499, CIM-707 and CIM-506) in F_1 hybrids exhibited excellent mean values for bolls per sympodia, boll weight, seed cotton yield, lint % and lint index. Upland cotton genotypes showed best performance for various yield related traits and were used in selection of parental lines for breeding program (Khan *et al*. 2009a, e; Batool *et al*., 2010; Ahmad *et al*., 2011; Panni *et al*., 2012; Baloch *et al*., 2014; Gul *et al*., 2014). The second promising genotype was CIM-446 and by crossing with CIM-496, CIM-506 and CIM-554, its F_1 hybrids showed best performance for bolls per plant and boll weight. The correlation of seed cotton yield was significant positive (*$p \leq 0.01$*) with yield contributing traits (bolls per sympodia, bolls per plant and boll weight), nonsignificant positive with lint index. However, correlation between lint % and seed cotton yield was negative. Therefore, the yield components have direct positive impact on yield with some sacrifice of ginning outturn. Positive association was observed between seed cotton yield and yield components with significant genetic variability among *G. hirsutum* L. genotypes for various traits (Khan *et al*., 2010a, b; Khan and Hassan, 2011; Baloch *et al*., 2014; Gul *et al*., 2014).

Significant mean squares due to GCA and SCA revealed the significant differences between the GCA and SCA of parental cultivars and their F_1 hybrids, respectively. However, GCA mean squares were larger than SCA for majority traits and assumed that additive gene action controlled the inheritance, and therefore, simple selection can be made for improvement in early segregating generations. Significant GCA and SCA mean squares for boll weight, bolls and seed cotton yield have been reported by earlier researchers in upland cotton (Islam *et al*., 2001a, b; Tuteja *et al.*, 2003; Khan *et al*., 2009c, d; 2011; Braden *et al*., 2009; Karademir *et al*., 2009; Basal *et al*., 2011). Significant genetic effects due to GCA and SCA for various yield and fiber traits were noticed in upland cotton (Baloch *et al.*, 2000; Hassan *et al.*, 2000; Hague *et al.*, 2008; Abro *et al*., 2009; Ashokkumar and Ravikesavan, 2008; Ashokkumar *et al*., 2010). Additive gene action for most of the traits was noticed in upland cotton (Chinchane *et al.*, 2002; Yuan *et al.*, 2002; Lukonge *et al.*, 2008; Khan *et al*., 2009e, 2011). However, non-additive type of gene action was observed for boll weight, boll number, seed cotton yield and lint % (Meredith and Brown, 1998; Muthu *et al.*, 2005; Ahuja and Dhayal, 2007; Ilyas *et al*., 2007; Khan *et al*., 2009c, d; Basal *et al*., 2011). Both additive and non-additive gene effects were responsible for yield and fiber related traits (Rauf *et al*., 2006; Karademir *et al*., 2009; Khan and Hassan, 2011). Such inconsistency might be due to genetic makeup of cotton genotypes and the environment where the crop was grown.

Mean squares due to reciprocals were highly significant, and most of the traits followed the GCA, however, had greater values than SCA, and revealed that maternal effects play key role in manifestation of these traits. Most of the reciprocal crosses involving one of the general combiners (CIM-446, CIM-554) and manifested maximum reciprocal effects for majority traits. Majority of the traits exhibited least reciprocal variances and it is pertinent that maternal effects were not so much pronounced (Islam *et al*., 2001a, b; Yuan *et al.*, 2002).

Table 1. Breeding material of upland cotton used in a 6 × 6 F_1 diallel cross with some salient features.

Cultivars	Parentage	Breeding centre	Release (year)	Seed cotton yield (kg ha^{-1})	GOT (%)	Staple length (mm)
CIM-473	CIM-402 × LRA-5166	CCRI, Multan	2002	3000	39.7	29.5
CIM-496	CIM-425 × 755-6/93	CCRI, Multan	2005	3000	41.1	29.7
CIM-499	CIM-433 × 755-6/93	CCRI, Multan	2003	3000	40.0	29.6
CIM-506	CIM-360 × CP-15/2	CCRI, Multan	2004	3000	38.6	28.7
CIM-554	2579-04/97 × W-1103	CCRI, Multan	2009	4241	41.5	28.5
CIM-707	CIM-243 × 738-6/93	CCRI, Multan	2004	3000	39.0	32.2

Table 2. Mean squares for ANOVA and combining ability in a 6 × 6 F_1 diallel cross of upland cotton.

Variables	Mean Squares						
	ANOVA			Combining ability			
	Reps.	Genotypes	Error	GCA	SCA	Rec.	Error
Bolls per sympodia	0.70	1.28**	0.12	1.13**	0.28**	0.34**	0.04
Bolls per plant	82.69	219.87**	20.29	249.72**	42.73**	45.05**	6.77
Boll weight	0.01	0.20**	0.04	0.12**	0.09**	0.04**	0.02
Seed cotton yield plant^{-1}	1883.37	4798.73**	1275.21	5566.19**	1390.01**	495.30$^{N.S}$	425.25
Lint %	0.15	9.92**	0.24	5.12**	2.22**	3.79**	0.08
Lint index	0.03	0.55**	0.08	0.36**	0.13**	0.18**	0.03

** *Significant at pá0.01.*

Parental genotypes CIM-446 and CIM-554 were found as best general combiners by having leading position for majority traits in F_1 generation. The promising hybrids CIM-446 × CIM-554 (boll weight, lint index) and CIM-506 × CIM-554 (bolls per sympodia, seed cotton yield) were the leading and best specific combinations by having desirable SCA effects for each of the two traits. In first cross, both genotypes were good general combiners and high × high GCA parents were involved in the expression of the said traits. While in 2nd promising cross, the low × high GCA parental lines were involved. Present studies proved that both parents with high GCA and or their utilization as one of the parents produced superior F_1 hybrids. Genotypes with high GCA produced high yielding F_1 hybrids in upland cotton (Hassan *et al.*, 2000; Lukonge *et al.*, 2008; Khan *et al*., 2009d; 2011).

Crossing of the best general combiner CIM-446 as maternal parent with low GCA parent (CIM-496) showed best performance for majority traits including seed cotton yield. The said high × low GCA F_1 hybrids (CIM-446 × CIM-496, CIM-446 × CIM-499) exhibited maximum SCA effects for bolls per plant and lint %, respectively. The general combiner CIM-554 involved in F_1 hybrid CIM-499 × CIM-554 as paternal parent, revealed desirable SCA for lint %, lint index and boll weight. Therefore, mostly high × low and low × high GCA parents performed well in SCA determination and revealed best mean performance. It can be attributed to dominance control of these traits due to higher SCA effects (Khan *et al.*, 2009c). These hybrids may further confirm their position in F_2 studies even after segregation and inbreeding depression. Parent with best GCA, used as a pollen parent produced better combinations (Khan *et al.*, 2009d). Past studies revealed that higher GCA of parents does not necessarily confer higher SCA, and the GCA and SCA were independent (Islam *et al.*, 2001a, b). However, for some traits, the low × low GCA parents (CIM-496 × CIM-707) were also involved for presentation of maximum SCA effects.

The F_1 hybrids (CIM-446 × CIM-554, CIM-446 × CIM-496 and CIM-506 × CIM-554) with promising SCA for majority traits could also provide transgressive segregates by having low magnitude of inbreeding depression with additivity for inheritance in early segregating generations. However, Yuan *et al.* (2002) was of the view that F_1 hybrids obtained from parent cultivars with similar performance had relatively higher dominant effects. Therefore, F_1 hybrids do not predict the yield of the bulk in the following generations but the combined performance of the F_1 and F_2 hybrids could be a good indicator to identify the promising population (Khan *et al*., 2011). Identification and selection of best F_1 hybrids should not be only based on GCA and SCA, but it must be coupled with mean performance (Basal *et al*., 2011).

The hybrids involving genotypes CIM-446 and CIM-554 (by crossing with each other or using as pollen / maternal parent) showed best mean performance which can be utilized for isolation of base material through selection to enhance the seed cotton yield.

Table 3. Mean performance of 6 × 6 F_1 diallel cross for yield and fiber related traits in upland cotton.

Parental cultivars	Bolls sympodia^{-1}	Bolls plant^{-1}	Boll weight (g)	Seed cotton yield plant^{-1} (g)	Lint %	Lint index (g)
CIM-446	2.55	36	3.53	125.86	34.71	4.04
CIM-496	2.36	25	3.26	85.69	33.44	5.07
CIM-499	1.54	13	3.33	46.77	30.74	4.26
CIM-506	2.38	32	3.27	109.56	34.69	4.97
CIM-554	2.19	31	2.89	101.36	32.58	4.73
CIM-707	2.28	25	3.22	81.51	32.30	4.96
F_1 Hybrids						
CIM-446 × CIM-496	3.50	45	3.72	165.19	34.69	4.88
CIM-446 × CIM-499	2.17	23	4.12	84.54	33.04	4.27
CIM-446 × CIM-506	2.62	37	3.74	140.07	37.79	3.84
CIM-446 × CIM-554	3.45	45	3.96	176.87	35.51	5.00
CIM-446 × CIM-707	2.91	38	3.47	146.42	34.94	4.18
CIM-496 × CIM-446	3.54	41	3.96	172.00	37.32	3.98
CIM-496 × CIM-499	2.01	18	3.58	66.24	36.28	4.14
CIM-496 × CIM-506	2.12	24	3.55	85.42	33.53	4.17
CIM-496 × CIM-554	2.35	29	3.61	112.83	35.21	5.10
CIM-496 × CIM-707	1.92	19	3.84	77.75	31.95	4.65
CIM-499 × CIM-446	2.21	24	3.41	75.16	36.15	4.00
CIM-499 × CIM-496	2.50	31	3.50	118.20	35.00	5.22
CIM-499 × CIM-506	1.64	26	3.51	91.96	33.28	5.22
CIM-499 × CIM-554	2.07	28	3.84	101.68	30.84	4.63
CIM-499 × CIM-707	1.52	18	3.26	53.69	33.48	4.59
CIM-506 × CIM-446	2.85	46	3.69	178.50	33.57	4.04
CIM-506 × CIM-496	3.32	30	3.48	104.38	37.80	4.93
CIM-506 × CIM-499	2.44	36	3.37	121.88	34.45	4.80
CIM-506 × CIM-554	4.48	38	3.62	190.88	38.78	4.82
CIM-506 × CIM-707	1.69	19	3.30	75.61	34.26	3.83
CIM-554 × CIM-446	2.74	38	4.14	172.84	31.69	4.60
CIM-554 × CIM-496	1.69	23	3.74	89.97	34.16	4.71
CIM-554 × CIM-499	2.20	28	3.65	113.15	35.05	5.37
CIM-554 × CIM-506	1.94	33	3.70	151.29	33.25	4.71
CIM-554 × CIM-707	2.37	36	3.47	130.05	33.28	5.09
CIM-707 × CIM-446	2.66	20	3.49	121.35	37.42	4.70
CIM-707 × CIM-496	2.33	33	3.41	149.13	32.73	4.17
CIM-707 × CIM-499	1.71	26	3.69	78.90	35.68	4.50
CIM-707 × CIM-506	1.62	23	3.35	69.44	34.49	4.74
CIM-707 × CIM-554	1.86	22	3.67	130.26	35.66	4.46
$LSD_{(0.05)}$	0.54	7.33	0.36	64.05	0.79	0.46

Table 4. Correlation of seed cotton yield with yield and fiber related traits in a 6 × 6 F_1 diallel cross of upland cotton.

Variables	Correlation with seed cotton yield
Bolls per sympodia	0.63^{**}
Bolls per plant	0.73^{**}
Boll weight	0.32^{**}
Lint %	-0.19^{*}
Lint index	$0.11^{N.S.}$

**, * = Significant at pá0.01 and pá0.05, N.S. = Non-significant

Table 5. GCA effects for yield and fiber related traits in a 6 × 6 F_1 diallel cross of upland cotton.

Parents	Bolls sympodia^{-1}	Bolls plant^{-1}	Boll weight	Seed cotton yield plant^{-1}	Lint %	Lint index
CIM-446	0.43	6.46	0.17	26.69	-1.06	-0.03
CIM-496	0.12	-0.74	0.01	-4.32	0.71	0.08
CIM-499	-0.42	-5.84	-0.02	-33.23	0.41	0.01
CIM-506	0.07	2.04	-0.08	7.85	-0.35	-0.01
CIM-554	0.08	2.33	0.03	19.85	0.43	0.24
CIM-707	-0.29	-4.25	-0.12	-16.84	-0.15	-0.02

Table 6. SCA effects for yield and fiber related traits in a 6 × 6 F_1 diallel cross of upland cotton.

F_1 Hybrids	Bolls sympodia^{-1}	Bolls plant^{-1}	Boll weight	Seed cotton yield plant^{-1}	Lint %	Lint index
CIM-446 × CIM-496	0.59	8.11	0.10	46.42	-0.51	0.05
CIM-446 × CIM-499	-0.20	-6.35	0.05	-30.09	0.48	-0.17
CIM-446 × CIM-506	-0.15	3.75	0.06	8.27	-1.61	-0.35
CIM-446 × CIM-554	0.20	3.28	0.29	11.84	0.35	0.26
CIM-446 × CIM-707	0.26	-2.77	-0.13	7.56	0.26	0.17
CIM-496 × CIM-499	0.17	1.73	-0.02	13.30	0.19	-0.01
CIM-496 × CIM-506	0.15	-3.85	0.02	-25.10	-0.14	-0.12
CIM-496 × CIM-554	-0.56	-4.86	0.06	-30.60	0.17	0.00
CIM-496 × CIM-707	-0.09	1.50	0.16	18.13	-1.33	-0.24
CIM-499 × CIM-506	0.15	-3.85	0.02	-25.10	-0.14	-0.12
CIM-499 × CIM-554	0.09	1.81	0.16	4.32	0.46	0.16
CIM-499 × CIM-707	-0.06	2.39	0.04	-0.11	0.06	-0.04
CIM-506 × CIM-554	0.68	1.84	0.14	58.58	-0.58	-0.05
CIM-506 × CIM-707	-0.52	-6.33	-0.05	-34.96	-0.92	-0.28
CIM-554 × CIM-707	-0.06	1.41	0.09	10.67	0.34	-0.03

Table 7. Reciprocal effects for yield and fiber related traits in a 6 × 6 F_1 diallel cross of upland cotton.

F_1 population	Bolls sympodia^{-1}	Bolls plant^{-1}	Boll weight	Seed cotton yield plant^{-1}	Lint %	Lint index
CIM-496 × CIM-446	-0.02	2.13	-0.12	13.26	1.21	0.45
CIM-499 × CIM-446	-0.02	-0.36	0.36	4.69	-0.75	0.13
CIM-506 × CIM-446	-0.11	-4.69	0.02	-19.22	-0.61	-0.10
CIM-554 × CIM-446	0.35	3.19	-0.09	2.01	0.61	0.20
CIM-707 × CIM-446	0.13	9.17	-0.01	12.54	-0.84	-0.26
CIM-499 × CIM-496	-0.25	-6.96	0.04	-25.98	-1.65	-0.54
CIM-506 × CIM-496	-0.60	-2.71	0.03	-9.48	-1.55	-0.38
CIM-554 × CIM-496	0.33	2.89	-0.06	11.43	2.11	0.20
CIM-707 × CIM-496	-0.21	-7.32	0.22	-35.69	1.91	0.24
CIM-506 × CIM-499	-0.40	-5.09	0.07	-14.96	0.38	0.21
CIM-554 × CIM-499	-0.07	0.09	0.10	-5.74	-2.13	-0.37
CIM-707 × CIM-499	-0.10	-3.91	-0.21	-12.61	0.53	0.05
CIM-554 × CIM-506	1.27	2.61	-0.04	51.46	-0.59	0.05
CIM-707 × CIM-506	0.04	-2.15	-0.02	3.09	-2.11	-0.46
CIM-707 × CIM-554	0.26	6.83	-0.10	-0.11	1.43	0.32

The F_1 hybrids having extraordinary performance could also be used for hybrid cotton production to boost up the seed cotton yield. Genotypes with high SCA effects were associated with standard heterosis and could be utilized in hybrid cotton production (Meredith and Brown, 1998; Khan *et al.*, 2009d; Muthu *et al.*, 2005; Panni *et al*., 2012). However, F_1 hybrids with high heterosis were also linked with increased inbreeding depression (Basal and Turgut, 2003; Khan *et al*., 2010a; Khan, 2011). Therefore, present studies revealed that after analyzing the F_1 hybrids through combining ability with reasonable SCA variance, the medium type of heterosis in promising crosses viz., CIM-446 × CIM-554, CIM-446 × CIM-496 and CIM-506 × CIM-554 might have some stability to be used for hybrid cotton production.

Conclusion: Utilization of best general combiners (CIM-446 and CIM-554) as one of the parents produced promising F_1 population (CIM-446 × CIM-554, CIM-446 × CIM-496 and CIM-506 × CIM-554) with desirable SCA determination and mean performance for majority traits. Therefore, high × low, low × high and in some cases high × high GCA parents showed best performance. Additive gene action controlled the inheritance, and selection in such promising hybrids could be practiced in early segregating generations and some specific F_1 hybrids could be identified for hybrid cotton production to enhance the seed cotton yield.

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