

Combining Ability Effects and Heterosis Estimates through Line X Tester Analysis for Yield, Yield Components and Fiber Traits in Egyptian Cotton

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ABSTRACT

The Objectives of this study were to determine the general (GCA) and specific (SCA) combining abilities and heterosis of some cotton genotypes for yield, its components and fiber traits using line × tester mating design. Thirteen parents (ten lines and three testers) along with their thirty F₁ crosses were studied in randomized complete block Design (RCBD) with three replications during 2016 at Sakha Agriculture Research Station, Kafr El- Sheikh Governorate, Egypt. Based on line x tester analysis, the variances due to genotypes, parents, crosses and parent vs cross exhibited significant differences ($P < 0.01$) for most yield, yield component and fiber traits. The variances due to GCA of lines and testers, and SCA of line x tester interactions were highly significant for most studied traits, indicating the importance of both additive and non-additive gene actions in controlling these traits. The proportional contribution of line × tester was higher than individual contribution of lines and testers for most studied traits. The estimates of GCA and SCA effects revealed that the parents and some crosses were having desirable and significantly GCA and SCA effects, respectively. High mean performances and desirable GCA effects values were observed of lines Pima S6, Suvin, G.90, Aust. 12 and tester C.B.58 for most investigated traits, hence these parents can be used for generating superior cotton hybrids. Significant correlation coefficients ($P < 0.05$ or $P < 0.01$) in positive direction were obtained between all possible pairs of F₁ hybrids mean, SCA and heterosis. The best values of mean performances, SCA effects and heterosis were found in the combinations Suvin × G.86 and Aus.12 × C.B.58 for most yield and yield components, and the G.90 × C.B.58 and G.95 × G.86 for fiber traits. These crosses are considered the promising crossed to be used in breeding programs for produce hybrid cotton and improvement for these traits in Egypt.

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Introduction

The main goal in cotton breeding is looking and selection the genotypes with high yield and quality traits, substantial work has been carried out to develop both yield and quality traits of cotton in Egypt.

Selecting parents based on mean performance, adaption and genetic diversity does not lead necessarily to desirable results. This is due to the differential ability of the parents, which depended on the complex interactions among the genes and cannot be judged by the mean performance alone (Allard, 1960). The parents, who perform well in the hybrids, are very important in the breeding program of Egyptian cotton. The information about combining ability and relative magnitude of genetic variance with respect to traits of economic importance is essential for exploitation of the existing gene action in the population. Egyptian cotton breeders seek the most appropriate materials for breeding and the way to present clearly the results of experimental scientific studies.

The general (GCA) and specific (SCA) combining ability have had a significant impact on evaluation of genotypes and population improvement. The GCA is the average performance of a genotype in hybrid combinations with number of genotypes. The SCA is the average performance of a specific cross combination expressed as deviation from the

population mean. Combining abilities estimation can be used to determine the usefulness of the parents in hybrid combinations and to develop best hybrid adaptable to the different environments (Sprague and Tatum, 1942).

The term heterosis was coined by Shull (1914), it is the superiority of F₁ hybrid over the mid-parents or the better parent or over the standard check with regard to agriculturally useful traits. The genetic causes involved in the expression of heterosis are dominance and nonallelic interactions (Hayes and Foster, 1976). The magnitude of heterosis can be maximized if the parents are genetically varied from each other. Exploiting heterosis is one of the methods to improvement yield and fiber quality traits in cotton. Kumar (2008) stated that to maximize heterosis, there is a need for utilizing breeding programs aimed at constantly creating variability and increasing genetic diversity between populations that can further be exploited through selection for combining ability between such diverse populations. Also heterosis can be enhanced by increasing dominant gene action. It is difficult to precisely detect and manipulate the degree of dominant gene action while selecting, based on phenotypic measurements, for high heterosis. However it is possible to create and improve heterotic populations against a tester or reciprocally develop diverse populations which

differ for the alleles at a large number of yield influencing loci (showing dominance).

Different methods have been applied to improve the selection of genes controlling the useful agronomic traits. The most used breeding designs are bi-parental, multiple crosses, test crosses, line $\times$ tester and diallel designs (Nduwumuremyi et al., 2013). The major purpose of these designs is to determine the combining abilities of experimental crosses and parental lines besides understanding the heredity of the evaluated traits (Sharma, 2006).

Line $\times$ Tester mating design is an extension (modified version) of top cross method in which several testers are used. The line $\times$ tester analysis is a common approach for assessing the expression of genetic aspects of traits (Kempthorne, 1957), which provides information about GCA and SCA of parents and at the same time it is helpful in identifying best heterotic crosses. Also, line $\times$ tester analysis provides information about regarding genetic mechanism controlling yield and yield components. The most important merit of this approach is that it enables evaluation with less experimental materials compared to other mating designs. The line $\times$ tester design has been used in studies about yield, its components and fiber quality traits in cotton (Karademir et al., 2016; Usharani et al., 2016; Chinchane et al., 2018; Khokhar et al., 2018; Patel and Patel, 2018; Prakash et al., 2018 and Rajeev and Patil 2018). Therefore, our aim was to investigate the combining abilities of parents and crosses in line $\times$ tester mating fashion (10×3 designs), to known heterotic groups and to study the relationship among mean performances, combining abilities and heterosis for yield, its components and fiber quality traits in Egyptian cotton.

Materials and Methods

Genetic Material and Field Procedure

The evaluation trail carried out in Sakha Agriculture Research Station, Kafr El- Sheikh Governorate, Egypt during the three summer seasons (2014-2016). In the first season (2014), the two cotton varieties i.e. Giza 86 (G.86) and C.B.58 were crossed to obtained their F_1 (G. 86 $\times$ C.B.58). During the second season (2015), three genotypes i.e., G.86, G.86 $\times$ C.B.58 and C.B.58 were used as testers and ten genotypes i.e. G.94, G.85, Pima S6, G.75, G.89, TNB, Suvin, Aust. 12, G.90 and G.95 were used as lines. The thirteen genotypes were crossed to produce thirty F_1 crosses according to the line $\times$ tester mating design developed by Kempthorne (1957) and crossed between G.86 and C.B.58 to again obtained the F_1 (G.86 $\times$ C.B.58) during 2015 growing season. As for the third season (2016), all genotypes (ten lines + three tester + 30 F_1 crosses) were evaluated in Randomized Complete Block Design (RCBD) with three replications. In each replication, parents (lines and testers) and F_1 crosses were sown in single row of 4 m long with a spacing of 70 cm between rows and 30 cm between plants. Recommended cultural practices were carried out and the crop was grown under uniform field conditions to minimize environmental variations to the maximum possible extent. Data were recorded on 10 guarded plants for the studied traits boll weight (B.W.) in gram, seed cotton yield/plant (S.C.Y./P.) in gram, lint cotton yield/plant (L.C.Y./P.) in gram, lint percentage (L.%), number of open bolls/plant (No .B./P.), seed index (S.I.) in gram, fiber fineness (F.F.) micronair reading, fiber strength (F.S.) in Presley, Upper half means (2.5%S.L.) in mm. and Uniformity ratio (U.R.%).

Statistical Analysis

Data recorded were subjected to analysis of variance according to Steel and Torrie (1980), to determine significant

differences among genotypes. The combining ability effects of the parents (GCA) and the crosses (SCA) were estimated by the using of the line $\times$ tester analysis methods described by Kempthorn (1957) and adopted by Singh and chaudhary (1985). Heterosis relative to mid parent, better parent and standard check were estimated as per the formula given by Liang et al. (1971). The significance of Heterosis was determined using the least significant difference value (L.S.D) at 0.05 and 0.01 levels of probability according to Steel and Torrie (1960). Pearson correlation coefficients between mean performances, combining abilities and heterosis were performed for better understanding of the relationship among these parameters using computer software program PAST version 2.17c.

Results and Discussions

Analysis of variance

Mean squares in line $\times$ tester analysis for yield, yield components and fiber traits used in the study are shown in Table 1. Preliminary analysis of variance exhibited there were highly significant differences between genotypes for all studied traits. This findings indicating the present of a considerable genetic variability between genotypes, hence subsequent analysis for combining ability was performed (Karademir et al., 2016). The variances due to parents, crosses and parents vs crosses showed highly significance for most investigated traits. While, parents vs crosses displayed no significant difference for fiber fineness and uniformity ratio% traits. The sum of squares due to crosses is partitioned into general combining ability (lines and testers) and specific combining ability (line $\times$ tester). The mean squares of lines (GCA), testers (GCA) and lines $\times$ testers (SCA) showed highly significant differences for most studied traits, indicating the importance of both additive and non-additive gene actions in controlling these traits. Also, indicated that the selection of female and male parents appeared appropriate (Chinchane et al., 2018). The variance due to lines and testers had no significant and significant for fiber fineness trait, respectively. This indicates that the crosses were sufficiently different from each other for these traits and hence, selection is possible to identify the most desirable crosses. These differences could be attributed to large differences between the parental lines of different studies.

The results indicated that pattern of appropriate line combinations may be varying depending on the tester mode. Higher magnitude of the mean square of testers indicating greater diversity among the testers and these testers can be pursued for developing plant heterotic groups with high combining ability (Chandel and Mankotta, 2014). Therefore, the choice of appropriate tester is crucial in developing high yielding hybrid cotton. Karademir et al., (2016) and Chinchane et al., (2018) stated that the GCA was highly significant for testers in terms of most investigated traits, revealing important role of additive type of gene effects in these traits, on the other hand there were non-significant differences of GCA for lines.

The SCA was highly significant for hybrids (line $\times$ testers) for all investigated traits revealing non-additive gene affects as dominance or epistatic. Mean squares of the line $\times$ tester analysis showed significant differences ($P < 0.01$) among the genotypes, parents, crosses, parent vs cross, lines, testers and line $\times$ tester for most yield, yield component and fiber traits, it showed that there is significant variability for the traits under study (Usharani et al., 2016, Chinchane et al., 2018 and Khokhar et al., 2018).

Table 1. Mean squares in line x tester analysis for yield, yield components and fiber traits

S.O.V	df	B.W.	S.C.Y./P.	L.C.Y./P	L.%	N.o.B/P	S.I	F.F.	F.S	2.5%S.L	U.R%
Replications	2	0.004	7.48	0.273	0.057	0.354	0.014	0.09	0.007	0.148	0.178
Genotypes	42	0.181**	3399.7**	548.72**	3.597**	314.9**	0.660**	0.224**	0.662**	2.315**	1.782**
Parents (P)	12	0.119**	1282.5**	226.51**	2.957**	93.6**	0.217**	0.317**	0.895**	1.417**	3.493**
Crosses (C)	29	0.211**	4241.4**	669.37**	3.635**	395.4**	0.851**	0.192**	0.540**	2.748**	1.135**
P. vs. C.	1	0.033**	4396.4**	916.49**	10.167**	636.7**	0.431**	0.032	1.428**	0.534**	0.001
GCA (Lines)	9	0.229**	3071.8**	450.39**	3.695**	484.6**	0.926**	0.114	1.034**	4.53**	0.744**
GCA(Testers)	2	0.635**	3204.4**	675.98**	9.120**	45.89**	0.282**	0.260**	0.388**	2.920**	3.648**
SCA (LinexTester)	18	0.155**	4941.5**	778.13**	2.996**	389.7**	0.877**	0.223**	0.310**	1.838**	1.051**
Error	84	0.003	29.81	7.859	0.381	4.206	0.035	0.076	0.021	0.067	0.318

* and **: significant at 5% and 1% levels of probability, respectively.

Table 2. Mean performances values of lines and testers with respect to yield, yield components and fiber traits

Traits	B.W.	S.C.Y./P.	L.C.Y./P	L.%	N.o.B/P	S.I	F.F.	F.S	2.5%S.L	U.R%
Genotypes										
Lines										
G.94	3.37	199.35	77.96	39.11	59.24	10.04	3.75	9.83	32.59	87.23
G.85	2.88	153.40	54.36	35.44	53.36	9.87	3.60	9.35	33.47	86.60
PimaS6	3.15	147.12	54.55	37.08	46.78	10.10	4.11	10.20	33.22	88.97
G.75	2.88	140.17	51.23	36.55	48.78	9.67	3.47	10.03	32.49	88.58
G.89	2.79	176.65	64.56	36.55	63.43	9.59	3.93	10.08	32.69	86.43
TNB	2.80	138.70	48.42	34.91	49.60	9.59	4.10	8.87	33.67	89.27
Suvin	3.11	145.24	54.53	37.50	46.70	10.03	3.57	8.84	33.63	86.73
Aus.12	3.02	154.53	56.74	36.72	51.25	9.79	3.87	10.74	32.41	87.62
G.90	2.85	140.36	52.02	37.06	49.25	9.36	3.90	9.61	33.67	85.70
G.95	3.15	152.52	56.00	36.64	48.39	9.76	3.65	10.32	32.50	87.60
Testers										
G.86	2.83	164.21	59.75	36.39	58.03	10.00	3.74	9.87	34.17	86.96
G.86 x C.B.58	3.04	176.39	64.63	36.64	58.04	10.06	2.89	9.94	32.51	86.70
C.B.58	3.35	195.69	72.67	37.14	58.50	10.35	4.00	10.11	33.61	86.37
L.S.D. 0.05	0.07	7.41	3.81	0.84	2.78	0.25	0.37	0.20	0.35	0.77
L.S.D. 0.01	0.11	10.51	5.43	1.20	3.97	0.36	0.53	0.28	0.50	1.09

Mean Performance

The mean performance of the parents (lines and testers) and F1 crosses used in the research can be seen at Tables 2 and 3, respectively. The per se performance was considered as the first important selection index in the choice of parents and the parents with high mean performance will result in superior hybrids. The mean performances values of parents (lines and testers) and F1 crosses displayed highly significant differences for all investigated traits. Significant differences were recorded between means when compared with the L.S.D. values. The superior parents in terms of genotype mean values were G. 94 for boll weight, seed cotton yield/plant, lint yield yield/plant and lint percentage traits; G. 89 for number of bolls/plant; C.B.58 for seed index; Aus.12 for fiber strength; G.86 for 2.5% span length and TNB for uniformity ratio. While, the parent G.86 x C.B.58 had the best fiber fineness.

The results exhibited some F1 crosses were superiority than standard check and grand means for all studied traits. There were relatively large variations in all genotypes for these traits. The cross Suvin x G.86 exhibited best mean values and excelled other crosses for the traits i.e., seed cotton yield/plant (263.87 gm), lint cotton yield/plant (100.31 gm) and number of bolls/plant (91.78). The best boll weight (3.51 gm), lint percentage (38.67 %), seed index (10.78 gm), fiber fineness (3.31), fiber strength (10.90), 2.5% span length (35.01 mm) and uniformity ratio (88.73%) were produced by crosses G.89 x C.B.58, Pima S6 x C.B.58, G.85 x (G.86 x C.B.58), TNB x C.B.58, G.90 x C.B.58, Suvin x C.B.58 and G.95 x G.86, respectively. Generally, these data indicate superiority of some F1 crosses, with respect to their corresponding parents and standard check. These data showed

that heterotic effects emerged highly in point for studied traits in these crosses. These viewpoints were kept in mind while selecting these single crosses as diverse F1 base populations for initiating reciprocal selection for combining ability. The highest combinations indicating that importance of low and average parents in the exploitation of heterosis for studied traits. Consequently, the parents involved in the previous combinations should be used in improving yield, its components and fiber traits, and the best crosses should be used in initiated the breeding program.

Combining Ability Effects

1 – General Combining Ability (GCA) effects

The values of GCA effects for the parents (lines and testers) are presented in Table 4. Positive and negative GCA effects were observed between lines and testers for all studied traits.

Six lines for 2.5% span length; five lines for boll weight, seed cotton yield/plant, lint cotton yield/plant and number of bolls/plant; three lines for lint percentage and two lines for seed index, fiber strength and uniformity ratio were showed positive and highly significant GCA effects, showing predominance of additive genes for these traits (Rajeev and Patil, 2018). The line TNB had the highest negative and significant GCA effect for fiber fineness. While the other lines shown undesirable values for GCA effects and declared as poor general combiner for all investigated traits. Line G.89 for boll weight; Line Pima S6 for seed cotton yield/plant, lint cotton yield/plant and number of bolls/plant; line TNB for lint percentage, fiber fineness and 2.5% span length; line Aus. 12 for seed index; line G.90 for fiber strength and G.95 for uniformity ratio recorded the highest positive GCA effects.

Table 3. Mean performances values of F1 crosses with respect to yield, yield components and fiber traits

Traits Genotypes	B.W.	S.C.Y./P.	L.C.Y./P	L.%	N.o.B/P	S.I	F.F.	F.S	2.5%S.L	U.R%
G.94 x G. 86	3.18	211.60	81.22	38.38	66.54	10.75	3.51	10.07	32.57	87.80
G.94 x (G.86 x C.B.58)	3.13	176.25	67.00	38.01	56.36	9.62	3.60	9.83	33.70	85.93
G.94 x C.B.58	2.86	163.00	61.30	37.61	56.98	8.97	3.97	9.73	33.43	87.60
G.85 x G. 86	2.89	119.50	44.45	37.20	41.39	9.19	3.67	9.96	33.40	87.63
G.94 x (G.86 x C.B.58)	2.92	139.19	51.13	36.73	47.62	10.78	4.24	9.94	32.42	86.23
G.85 x C.B.58	3.19	123.17	46.90	38.08	38.61	9.95	3.59	10.21	32.60	87.07
PimaS6 x G. 86	3.03	182.02	68.72	37.75	60.14	9.96	3.87	10.57	33.30	86.53
G.94 x (G.86 x C.B.58)	2.75	205.08	78.07	38.07	74.85	9.65	3.63	9.90	34.27	87.43
PimaS6 x C.B.58	2.95	191.50	74.11	38.67	64.89	9.21	3.51	10.57	33.68	87.47
G.75 x G. 86	2.93	115.19	41.54	36.06	39.38	9.09	3.70	10.07	34.32	86.63
G.94 x (G.86 x C.B.58)	3.07	181.75	66.90	36.79	59.23	8.93	3.63	10.07	33.72	86.63
G.75 x C.B.58	3.43	219.83	84.18	38.26	64.13	9.81	4.10	10.03	33.67	87.40
G.89 x G. 86	2.81	110.20	37.48	34.01	39.23	10.08	3.33	8.83	34.15	87.60
G.89 x (G.86 x C.B.58)	3.36	199.39	74.72	37.47	59.35	10.77	4.00	9.78	32.47	87.77
G.89 x C.B.58	3.51	215.17	83.08	38.62	61.28	9.85	4.07	9.80	33.40	87.70
TNB x G. 86	2.77	136.75	52.49	38.38	49.49	9.35	3.71	10.01	33.60	86.47
G.94 x (G.86 x C.B.58)	2.71	169.77	64.18	37.80	62.80	10.37	3.58	10.24	34.40	87.63
TNB x C.B.58	3.12	169.28	65.31	38.59	54.36	9.35	3.31	10.14	33.72	87.77
Suvin x G. 86	2.88	263.87	100.31	38.00	91.78	10.06	3.87	9.53	34.41	86.97
G.94 x (G.86 x C.B.58)	2.54	110.67	41.43	37.41	43.67	9.72	4.20	9.94	32.23	87.21
Suvin x C.B.58	2.79	168.28	62.86	37.36	60.31	9.67	3.59	10.42	35.01	87.80
Aus.12 x G. 86	2.88	189.50	68.96	36.38	65.79	10.07	3.84	9.84	31.51	87.71
G.94 x (G.86 x C.B.58)	2.55	139.11	48.97	35.20	54.68	9.91	3.82	9.21	31.30	86.44
Aus.12 x C.B.58	3.47	223.06	84.84	38.03	64.41	10.42	4.07	9.99	32.28	87.77
G.90 x G. 86	2.84	157.61	60.08	38.12	55.55	9.51	3.73	10.41	32.86	87.74
G.94 x (G.86 x C.B.58)	2.74	193.56	71.95	37.16	70.77	9.49	3.61	10.44	33.93	86.59
G.90 x C.B.58	2.79	194.67	71.59	36.78	69.76	9.65	3.97	10.90	34.87	87.57
G.95 x G. 86	3.33	190.11	67.88	35.71	57.08	9.73	3.41	10.67	34.27	88.73
G.94 x (G.86 x C.B.58)	2.76	150.60	54.49	36.18	54.64	8.79	3.94	10.51	32.53	87.10
G.95 x C.B.58	3.28	181.67	68.93	37.94	55.48	9.37	4.07	10.10	34.52	87.60
L.S.D. 0.05	0.07	7.41	3.81	0.84	2.78	0.25	0.37	0.20	0.35	0.77
L.S.D. 0.01	0.11	10.51	5.43	1.20	3.97	0.36	0.53	0.28	0.50	1.09

Table 4. Predicted general combining abilities (GCA) effects for lines and testers with respect to yield, yield components and fiber traits

Traits Genotypes	B.W.	S.C.Y./P.	L.C.Y./P	L.%	N.o.B/P	S.I	F.F.	F.S	2.5%S.L	U.R%
Lines										
G.94	0.06**	10.57**	5.01**	0.64**	1.94**	0.04	-0.08	-0.18**	-0.19**	-0.17
G.85	0.02	-45.76**	-17.34**	-0.02	-15.47**	0.24**	0.06	-0.02	-0.61**	-0.31
PimaS6	0.01**	19.82**	8.80**	0.80**	8.61**	-0.13*	-0.10	0.29**	0.33**	-0.14
G.75	0.16**	-0.79	-0.63	-0.32	-3.77**	-0.46**	0.04	0.00	0.48**	-0.40*
G.89	0.25**	1.88	0.26	-0.66**	-4.73**	0.50**	0.03	-0.59**	-0.078	0.40*
TNB	-0.12**	-14.45**	-4.17**	0.90**	-2.47**	-0.04	-0.24**	0.08	0.49**	0.00
Suvin	-0.25**	7.90**	3.36**	0.23	7.24**	0.080	0.12	-0.09*	0.47**	0.04
Aust.12	-0.02	10.85**	2.75**	-0.82**	3.61**	0.40**	0.14	-0.38**	-1.72**	0.02
G.90	-0.19**	8.90**	3.04**	-0.01	7.34**	-0.19**	0.00	0.53**	0.47**	0.02
G.95	0.14**	1.08	-1.07	-0.75**	-2.29**	-0.44**	0.03	0.37**	0.36**	0.53**
SE	0.02	1.82	0.94	0.21	0.68	0.06	0.09	0.05	0.09	0.19
Testers										
G.86	-0.03**	-5.41*	-2.53**	-0.36**	-1.38**	0.05	-0.11**	-0.06*	0.020	0.01
G.86 x C.B.58	-0.13**	-6.51**	-2.95**	-0.28**	0.38	0.07*	0.06	-0.01**	-0.32**	-0.39**
C.B.58	0.16**	11.92**	5.46**	0.63**	1.00**	-0.11**	0.05	0.13**	0.30**	0.29**
SE	0.01	0.99	0.51	0.11	0.37	0.03	0.05	0.03	0.05	0.10

* and **: significant at 5% and 1% levels of probability, respectively.

Genotype C.B.58 showed highly significant GCA effects in positive direction and revealed as good among testers for all studied traits except, seed index and fiber fineness traits. While the genotypes G.86 x C.B.58 and G.86 had significant positive and highly significant negative GCA effects for seed index and fiber fineness traits, respectively. Similar results were reported by Yehia *et al* (2009a), El-Hashash (2012), Usharani *et al.*, 2016, Chinchane *et al.*, (2018), Prakash *et al.*, (2018) and Rajeev and Patil (2018) for these investigated traits.

The general Combining Ability Effects (GCA) provide information which is useful to classify the parental lines and testers. Since presence of desirable GCA effect is related to additive and additive x additive interaction which represents preponderance of friable genetic variance (Chinchane *et al.*, 2018). Parental lines, with higher GCA effects in cross combination with different testers, were expected to yield better hybrids for that particular trait. The plant researchers had been reported, new cross combination under line x tester

analysis with at least one parental line, which displayed higher GCA effects (Khokhar, et al., 2018). Based on estimates of GCA effects for various characters, it was observed that none of the parents was found to be good general combiner for all the traits (Bilwal et al., 2018). However, an overall appraisal of GCA effects revealed that lines Pima S6, Suvin, G.90, Aust. 12 and tester C.B.58 proved to be a good general combiners for most investigated traits. Thus, for recurrent selection based on GCA effects, these parents appear more appropriate in crossing programme directed towards cotton improvement in Egypt.

2 – Specific Combining Ability (SCA) effects

The estimates of SCA effects for F1 crosses are given in Table 5. Out of 30 F1 crosses studied, the 14 crosses for boll weight; 13 crosses for seed cotton yield/plant, lint cotton yield/plant and number of bolls/plant; 12 crosses for 2.5% span length; 10 crosses for seed index and fiber strength; 7 crosses for lint percentage, 5 crosses for uniformity ratio% and 4 crosses for fiber fineness showed significant or highly significant SCA effects in desired direction. The estimates of SCA effect revealed that none of the hybrids was consistently proved to be superior for all studied traits. On the other hand, the significant or insignificant SCA effects in undesired direction revealed the presence of undesirable types in these combinations (El-Hashash, 2012).

The Specific Combining Ability effects (SCA) provide information which is useful to classify new cross combination. The highest positive SCA values and the best

(G.86 x C.B.58) for 2.5% span length and the cross G.95 x G. 86 for uniformity ratio, indicating the non-additive and additive x non-additive type of interactions were significantly higher among hybrids, thus non-additive gene action could be exploited by heterosis breeding. Comparable findings were given by El-Hashash (2012), Usharani et al., (2016), Khokhar, (2018) and Rajeev and Patil (2018). High yielding hybrids also possessed high SCA effects, high heterosis as well as high per se performance for most of its yield contributing characters. This appeared appropriate as yield being a complex character depends on a number of its component traits (Bilwal et al., 2018).

Bilwal et al., (2018) mentioned that the good general combining parents may not necessarily always produce good specific combinations for different traits. In many cases, it was observed that at least one good general combining parents was involved in heterotic hybrid having desirable SCA effects. Most of the crosses with high SCA have at least the highest one GCA parent. Therefore, high × low, low × high and in some cases high × high GCA parents performed well in SCA determination and revealed also the best mean performance (El-Hashash, 2012). The best general combiners have given best specific combination for seed cotton yield (Rajeev and Patil, 2018). In this study, only one cross Aus.12 x C.B.58 had both the parents showing high GCA effects, while the other crosses either involved poor x good, poor x poor or good x poor GCA combination.

Table 5. Predicted specific combining abilities (SCA) effects for yield, yield components and fiber traits

Genotypes	Traits	B.W.	S.C.Y./P.	L.C.Y./P	L.%	N.o.B/P	S.I	F.F.	F.S	2.5%S.L	U.R%
G.94 x G. 86		0.15**	33.39**	13.90**	0.74*	7.96**	0.93**	-0.08	0.25**	-0.69**	0.59*
G.94 x (G.86 x C.B.58)		0.20**	-0.859	0.11	0.29	-3.98**	-0.23*	-0.15	0.03	0.79**	-0.79**
G.94 x C.B.58		-0.35**	-32.534**	-14.01**	-1.03**	-3.99**	-0.70**	0.22	-0.28**	-0.10	0.20
G.85 x G. 86		-0.09**	-2.375	-0.52	0.22	0.23	-0.83**	-0.06	-0.01	0.57**	0.56*
G.85 x (G.86 x C.B.58)		0.05*	18.409**	6.58**	-0.33	4.70**	0.74**	0.35*	-0.03	-0.07	-0.36
G.85 x C.B.58		0.03	-16.035**	-6.07**	0.11	-4.93**	0.09	-0.29	0.04	-0.51**	-0.20
PimaS6 x G. 86		0.15**	-5.438*	-2.39	-0.06	-5.11**	0.31**	0.31*	0.29**	-0.47**	-0.71*
G.94 x (G.86 x C.B.58)		-0.03	18.711**	7.39**	0.18	7.85**	-0.02	-0.08	-0.38**	0.84**	0.68*
PimaS6 x C.B.58		-0.11**	-13.282**	-5.00**	-0.13	-2.74*	-0.29**	-0.21	0.09	-0.37**	0.03
G.75 x G. 86		-0.18**	-51.658**	-20.14**	-0.62*	-13.49**	-0.23*	0.00	0.08	0.39**	-0.35
G.75 x (G.86 x C.B.58)		0.06*	16.003**	5.64**	0.03	4.61**	-0.41**	-0.23	0.08	0.14	0.13
G.75 x C.B.58		0.13**	35.655**	14.50**	0.59	8.88**	0.64**	0.24	-0.16*	-0.54**	0.22
G.89 x G. 86		-0.39**	-59.309**	-25.09**	-2.33**	-12.68**	-0.19*	-0.36*	-0.58**	0.79**	-0.19
G.89 x (G.86 x C.B.58)		0.26**	30.98**	12.58**	1.05**	5.68**	0.47**	0.14	0.39**	-0.55**	0.46
G.89 x C.B.58		0.13**	28.33**	12.51**	1.2818**	6.99**	-0.27**	0.22	0.19*	-0.24	-0.28
TNB x G. 86		-0.07*	-16.44**	-5.65**	0.484	-4.68**	-0.39**	0.28*	-0.06	-0.33*	-0.92**
TNB x (G.86 x C.B.58)		-0.03	17.68**	6.48**	-0.178	6.87**	0.61**	0.00	0.18*	0.81**	0.73*
TNB x C.B.58		0.09**	-1.24	-0.82	-0.306	-2.20*	-0.23*	-0.28*	-0.12	-0.49**	0.19
Suvin x G. 86		0.17**	88.34**	34.63**	0.7718*	27.91**	0.20*	0.09	-0.38**	0.50**	-0.45
Suvin x (G.86 x C.B.58)		-0.07*	-63.76**	-23.82**	0.0931	-21.96**	-0.17	0.26	0.05	-1.33**	0.27
Suvin x C.B.58		-0.10**	-24.58**	-10.81**	-0.8649**	-5.95**	-0.04	-0.35*	0.32**	0.83**	0.18
Aus.12 x G. 86		-0.06*	11.02**	3.89**	0.2051	5.55**	-0.11	0.04	0.22**	-0.21	0.30
G.94 x (G.86 x C.B.58)		-0.29**	-38.27**	-15.67**	-1.06**	-7.33**	-0.29**	-0.14	-0.40**	-0.08	-0.48
Aus.12 x C.B.58		0.34**	27.25**	11.77**	0.86**	1.78	0.40**	0.10	0.18*	0.29**	0.18
G.90 x G. 86		0.08**	-18.93**	-5.27**	1.13**	-8.43**	-0.08	0.07	-0.11	-1.05**	0.34
G.90 x (G.86 x C.B.58)		0.078**	18.12**	7.03**	0.08	5.03**	-0.13	-0.21	-0.07	0.36**	-0.32
G.90 x C.B.58		-0.16**	0.80	-1.75	-1.21**	3.10**	0.21*	0.14	0.18*	0.68**	-0.02
G.95 x G. 86		0.24**	21.39**	6.64**	-0.54	2.73*	0.39**	-0.29*	0.31**	0.48**	0.82**
G.95 x (G.86 x C.B.58)		-0.23**	-17.02**	-6.32**	-0.15	-1.47	-0.57**	0.08	0.16**	-0.92**	-0.32
G.95 x C.B.58		0.00	-4.37	-0.31	0.70*	-1.26	0.18*	0.21	-0.46**	0.45**	-0.50
SE		0.03	3.15	1.62	0.35	1.18	0.11	0.16	0.08	0.15	0.33

* and **: significant at 5% and 1% levels of probability, respectively.

The good $\times$ good GCA combination could be due to additive and additive $\times$ additive types of gene action which is fixable in nature which had significant SCA effects for studied traits (Yehia 2015 and Chinchane *et al.*, 2018). This suggested that information of GCA effects of parents should be considered along with SCA effects and per se performance of hybrid for predicting the value of any hybrid. It is desirable to search out parental lines with high GCA effects and low sensitivity to environmental variation in a crop improvement programme (Bilwal *et al.*, 2018).

Contribution

Line $\times$ tester interaction contributed to total variances was found much more than lines and testers for all investigated traits (depicting the importance of non-additive type of gene action) except fiber strength and 2.5% span length traits (Figure 1). On the other hand, the contributions of testers had lowest contributions for all studied traits except uniformity ratio. Hence, line $\times$ tester interactions provide much more variation for the appearing of the traits. It is remarkable that hybrid combinations had higher values than their parents for these investigated traits. Khokhar *et al.* (2018) findings are in accordance with present study for studied traits. Karademir *et al.*, (2016) mentioned that the maximum contributions to total variance of all studied traits were made by line $\times$ tester interactions and testers (male parents), on the other hand lines (female parents) had small contributions to all traits.

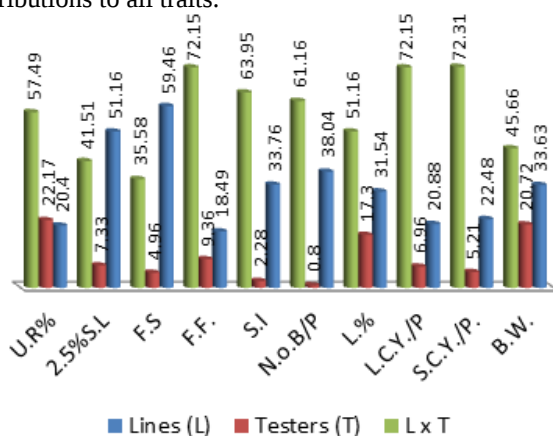


Figure 1. The contribution rates of lines, testers and lines $\times$ testers mean squares for yield, yield components and fiber traits.

Heterosis

The other result obtained from conventional line $\times$ tester analysis was heterosis with respect to mid-parents and better parent for studied traits are given in Tables 6 and 7, respectively. Outside F_1 s crosses (30), 7 and 0 crosses for boll weight; 16 and 11 crosses for seed cotton yield/plant; 18 and 0 crosses for lint cotton yield/plant; 15 and 0 crosses for lint percentage; 15 and 10 crosses for number of bolls/plant; 6 and 4 crosses for seed index; 16 and 8 crosses for fiber strength; 12 and 6 crosses for 2.5% span length; and 10 and 5 crosses for uniformity ratio showed positive and significant or highly significant heterosis relative to mid-parents and better parent, respectively. As for fiber fineness trait, 3 and 2 crosses had negative and significant or highly significant heterosis relative to mid-parents and better parent, respectively. On the other hand, the other crosses had undesirable heterosis relative to mid-parents and better parent for all investigated traits. The estimates of heterosis revealed that none of the hybrids was consistently proved to be superior for all investigated traits. Present study confirm the findings of Bankar *et al.* (2018), Khokhar *et al.* (2018), and

Patel and Patel (2018) who had reported significant heterosis in desired direction for all studied traits.

From the results can conclude that, the two crosses Suvin $\times$ G.86 and Aus.12 $\times$ C.B.58 for yield and its components traits, and the two crosses G.90 $\times$ C.B.58 and G.95 $\times$ G.86 for fiber traits exhibited the best heterosis versus mid-parents and better parent. These crosses can be introduced into the cross breeding program with multipurpose objectives to improve both yield and fiber quality traits for cotton in Egypt.

These results indicates the importance of low $\times$ average, average $\times$ average, low $\times$ high and high $\times$ high parent combinations in the development of crosses exhibiting high level of hybrid vigour for yield and yield related traits. Thus it can be concluded that the parents possessing only high values need not necessarily produce high yielding hybrids as indicated by the present study (Kumar, 2008). Yehia *et al.*, (2009b) and El-Hashash (2013) reported that some crosses exhibited significant or highly significant positive heterosis over mid-parents for yield, yield components and fiber traits, while, the heterosis over better parent exhibited insignificant positive and desirable for all studied traits. The significant negative heterosis suggested the importance of additive genetic components (Muhammed *et al.*, 2003 and El-Hashash, 2013). Useful and significant heterosis over mid-parents and better parent were observed for yield and yield components traits by Babu *et al.*, (2018) and Bilwal *et al.* (2018), and for fiber quality traits by Babu *et al.*, (2018).

Pearson Correlation

Correlations were estimated between the mean performances, combining abilities (GCA and SCA) and heterosis versus mid-parents (HMP) and better parent (HBP) for yield, yield components and fiber quality traits (Table 8). Non-significant correlations in positive or negative direction were found between parents per se performance and GCA for all investigated traits, which indicated predominance of dominance over additive effects. The previous studies by Anandan (2010) and El-Hashash (2012) did show that the correlation between GCA and LP were significant for some yield, its components and fiber traits. Crosses per se performance showed significant positive correlation ($P < 0.01$) with SCA, HMP and HBP for all studied traits. SCA, HMP and HBP were significantly correlated ($P < 0.05$ or $P < 0.01$) in positive direction with each other for all evaluated traits. El-Hashash (2012 and 2013) reported similar results, when he studied crosses per se performance with combining abilities and heterosis. High and significant correlation was observed for yield and heterosis in corn by Balestre *et al.*, (2008). High correlation between all possible pairs of F_1 per se performance, SCA, HMP and HBP were observed for all investigated traits, indicating predominance of dominance over additive effects, which suggests the possibility of predicting these traits in F_1 crosses from parent values. Therefore, the SCA and heterosis parameters would be useful in the selection of parents or population (Falconer and Mackay, 1997). The heterosis can be explained by divergence and also by the effect of dominance of the alleles that control the trait in question (Falconer, 1981). Also, the SCA can be explained by genes that exhibit dominance and epistasis effects (Hallauer and Miranda Filho, 1988). Therefore, the heterosis and SCA were highly correlated according the theory of quantitative genetics. These correlations among the traits should provide cotton breeders with insights on possible impacts of selection for one trait on the others (Lu and Myers, 2011).

Table 6. Mid-parents heterosis values for yield, yield components and fiber traits

Traits	B.W.	S.C.Y./P.	L.C.Y./P	L.%	N.o.B/P	S.I	F.F.	F.S	2.5%S.L	U.R%
Genotypes										
G.94 x G. 86	2.66*	16.40**	17.95**	1.68	13.49**	7.32**	-6.45	2.20*	-2.44**	0.81
G.94 x (G.86 x C.B.58)	-2.36*	-6.18*	-6.03*	0.36	-3.88	-4.28**	8.38	-0.52	3.53**	-1.19*
G.94 x C.B.58	-14.72**	-17.48**	-18.60**	-1.34	-3.22	-12.03**	2.32	-2.36*	1.01	0.92*
G.85 x G. 86	1.21	-24.75**	-22.09**	3.59**	-25.68**	-7.45**	-0.14	3.70**	-1.24*	0.98*
G.85 x (G.86 x C.B.58)	-1.17	-15.59**	-14.07**	1.92	-14.50**	8.16**	30.56**	3.08**	-1.74**	-0.48
G.85 x C.B.58	2.57*	-29.44**	-26.16**	4.94**	-30.96**	-1.55	-5.44	4.97**	-2.80**	0.67
PimaS6 x G. 86	1.31	16.93**	20.24**	2.76**	14.76**	-0.86	-1.57	5.38**	-1.17*	-1.63*
G.94 x (G.86 x C.B.58)	-11.24**	26.78**	31.03**	3.29**	42.82**	-4.23**	3.76	-1.71	4.27**	-0.46
PimaS6 x C.B.58	-9.06**	11.73**	16.51**	4.21**	23.27**	-9.94**	-13.56*	4.09**	0.80	-0.23
G.75 x G. 86	2.54	-24.32**	-25.14**	-1.12	-26.27**	-7.59**	2.64	1.24	2.97**	-1.30**
G.75 x (G.86 x C.B.58)	3.73	14.83**	15.49**	0.55	10.91**	-9.46**	14.32**	0.82	3.76**	-1.15**
G.75 x C.B.58	10.19**	30.91**	35.88**	3.86**	19.56**	-2.03	9.82	-0.38	1.87**	-0.09
G.89 x G. 86	0.09	-35.34**	-39.69**	-6.72**	-35.41**	2.98*	-13.16*	-11.46**	2.17**	1.04*
G.89 x (G.86 x C.B.58)	15.37**	12.96**	15.69**	2.40**	-2.29	9.62**	17.25**	-2.28*	-0.41	1.39**
G.89 x C.B.58	14.55**	15.58**	21.09**	4.82**	0.52	-1.22	2.69	-2.92**	0.76	1.50**
TNB x G. 86	-1.78	-9.71**	-2.96	7.68**	-8.05**	-4.51**	-5.44	6.87**	-0.94	-1.87**
TNB x (G.86 x C.B.58)	-7.36**	7.76**	13.56**	5.67**	16.68**	5.58**	2.58	8.91**	3.96**	-0.40
TNB x C.B.58	1.38	1.25	7.88*	7.12**	0.56	-6.17**	-18.32**	6.90**	0.25	-0.06
Suvin x G. 86	-28.71	70.54**	75.55**	2.87*	75.28**	0.52	5.97	1.84	1.49**	0.14
Suvin x (G.86 x C.B.58)	0.00	-31.18**	-30.46**	0.91	-16.61**	-3.24*	30.20**	5.89**	-2.54**	0.57
Suvin x C.B.58	-13.56**	-1.28	-1.15	0.11	14.66**	-5.12**	-5.19	9.99**	4.14**	1.44**
Aus.12 x G. 86	-1.45	18.91**	18.39**	-0.47	20.41**	1.74	0.92	-4.51**	-5.35**	0.48
G.94 x (G.86 x C.B.58)	-15.77**	-15.92**	-19.30**	-4.05**	0.06	-0.19	13.17*	-10.93**	-3.57**	-0.82
Aus.12 x C.B.58	8.96**	27.38**	31.12**	2.99*	17.37**	3.46*	3.39	-4.13**	-2.19**	0.90*
G.90 x G. 86	-0.11	3.50	7.50*	3.82**	3.56	-1.71	-2.31	6.93**	-3.11**	1.63**
G.90 x (G.86 x C.B.58)	-7.13**	22.22**	23.37**	0.85	31.93**	-2.25	6.43	6.86**	2.54**	0.46
G.90 x C.B.58	-9.93**	15.86**	14.84**	-0.87	29.49**	-2.11	0.42	10.59**	3.67**	1.78**
G.95 x G. 86	11.41**	20.05**	17.28**	-2.21	7.27**	-1.49	-7.76	5.73**	-0.18	1.66**
G.95 x (G.86 x C.B.58)	-10.82**	-8.42**	-9.66**	-1.25	2.68	-11.27**	20.49**	3.78**	-2.92**	-0.06
G.95 x C.B.58	0.85	4.35*	7.14*	2.87*	3.80	-6.80**	6.32	-1.14	1.37*	0.71
L.S.D. 0.05	0.07	7.41	3.81	0.82	2.78	0.25	0.37	0.19	0.35	0.76
L.S.D. 0.01	0.11	10.51	5.43	1.20	3.97	0.36	0.53	0.28	0.50	1.09

* and **: significant at 5% and 1% levels of probability, respectively.

Table 7. Better parent heterosis values for yield, yield components and fiber traits

Traits	B.W.	S.C.Y./P.	L.C.Y./P	L.%	N.o.B/P	S.I	F.F.	F.S	2.5%S.L	U.R%
Genotypes										
G.94 x G. 86	-5.50**	6.15*	4.17	-1.86	12.32**	7.11**	-6.32	1.99	-4.69**	0.65
G.94 x (G.86 x C.B.58)	-7.07**	0.00	-14.07**	-2.81*	-4.86	-4.38*	24.57**	-1.07	3.41**	-1.49*
G.94 x C.B.58	-14.98**	-18.23**	-21.37**	-3.83**	-3.820	-13.37**	5.68	-3.69*	-0.53	0.42
G.85 x G. 86	0.42	-27.23**	-18.23**	0.00	-28.67**	-8.04**	1.85	0.95	-2.25	0.77
G.85 x (G.86 x C.B.58)	-3.85*	-21.09**	-5.95	0.00	-17.94**	7.16**	46.60**	0.00	-3.14**	-0.54
G.85 x C.B.58	-4.63**	-37.06**	-13.73**	0.00	-33.99**	-3.83*	-0.19	1.02	-3.01**	0.54
PimaS6 x G. 86	-3.76*	10.84**	0.00	0.00	3.64	-1.39	3.30	3.69**	-2.55**	-2.74**
G.94 x (G.86 x C.B.58)	-12.72**	16.27**	0.00	0.00	28.97**	-4.45**	25.72**	-2.94**	3.16**	-1.72**
PimaS6 x C.B.58	-11.78**	-2.14	0.00	0.00	10.92**	-11.01**	-12.33*	3.63**	0.22	-1.69**
G.75 x G. 86	1.74	-29.86**	-18.91**	-1.34	-32.14**	-9.10**	6.73	0.43	0.43	-2.20**
G.75 x (G.86 x C.B.58)	0.00	3.04	0.00	0.00	2.06	-11.20**	25.72**	0.37	3.72**	-2.20**
G.75 x C.B.58	0.00	12.34**	0.00	0.00	9.62**	-5.25**	18.27**	-0.76	0.17	-1.34**
G.89 x G. 86	0.00	-37.62**	-41.94**	-6.93**	-38.16**	0.87	-10.95	-12.37**	-0.05	0.73
G.89 x (G.86 x C.B.58)	0.00	12.87**	0.00	0.00	-6.44**	7.06**	38.41**	-2.94*	-0.67	1.23*
G.89 x C.B.58	0.00	9.96**	0.00	0.00	-3.39	-4.86**	3.56	-3.07*	-0.63	1.47*
TNB x G. 86	-1.25	-16.73**	0.00	0.00	-14.72**	-6.47**	-0.98	1.45	-1.67	-3.14**
TNB x (G.86 x C.B.58)	-3.39*	-3.75	0.00	0.00	8.21*	3.12*	23.99**	3.05*	2.18*	-1.84**
TNB x C.B.58	0.00	-13.50**	0.00	0.00	-7.09*	-9.63**	-17.33**	0.36	0.19	-1.69**
Suvin x G. 86	-7.56**	60.69**	0.00	0.00	58.17**	0.37	8.60**	-3.48**	0.69	0.01
Suvin x (G.86 x C.B.58)	-18.49**	-37.26**	-24.02**	-0.24	-24.75**	-3.38*	45.44**	0.03	-4.16**	0.55
Suvin x C.B.58	-10.29**	-14.01**	0.00	-0.37	3.10	-6.60**	0.56	3.10*	4.10**	1.23*
Aus.12 x G. 86	-4.48*	15.40**	0.00	-0.92	13.38**	0.70	2.58	-8.38**	-7.79**	0.10
G.94 x (G.86 x C.B.58)	-15.42**	-21.13**	-13.69**	-4.15**	-5.79	-1.49	32.30**	-14.25**	-3.73**	-1.34*
Aus.12 x C.B.58	0.00	13.99**	0.00	0.00	10.10**	0.68	5.17	-6.95**	-3.95**	0.18
G.90 x G. 86	-0.46	-4.02	0.00	0.00	-4.27	-4.84**	-0.27	5.51**	-3.82**	0.89
G.90 x (G.86 x C.B.58)	-4.04*	9.74**	0.00	0.00	21.94**	-5.64**	25.03**	5.06**	0.78	-0.12
G.90 x C.B.58	-2.11	-0.52	0.00	-0.77	19.25**	-6.80**	1.71	7.85**	3.58**	1.39**
G.95 x G. 86	0.00	15.77**	0.00	-2.54	-1.64	-2.67	-6.58	3.42**	-0.67	1.29**
G.95 x (G.86 x C.B.58)	-12.38**	-14.62**	-2.71	-1.24	-5.85	-12.60**	36.33**	1.87	-5.72**	-0.57

G.95 x C.B.58	0.00	-7.16**	0.00	0.00	-5.17	-9.47**	11.42	-2.16	0.00	0.00
L.S.D. 0.05	0.09	9.08	4.66	1.03	3.41	0.31	0.46	0.24	0.43	0.94
L.S.D. 0.01	0.13	12.95	6.65	1.46	4.86	0.44	0.65	0.34	0.61	1.34

* and **: significant at 5% and 1% levels of probability, respectively.

Table 8. Pearson correlation between the mean performances, combining abilities and heterosis for studied traits.

Traits	r (P,GCA)	r (F1, SCA)	r (F1, HMP)	r (F1, HBP)	r (SCA, HMP)	r (SCA, HBP)	r (HMP,HBP)
B.W.	-0.50	0.68**	0.72**	0.58**	0.49**	0.41*	0.63**
S.C.Y./P.	-0.18	0.85**	0.95**	0.94**	0.86**	0.86**	0.97**
L.C.Y./P	-0.30	0.85**	0.95**	0.71**	0.87**	0.69**	0.76**
L.%	-0.14	0.71**	0.87**	0.69**	0.68**	0.69**	0.79**
N.o.B/P	0.33	0.78**	0.98**	0.99**	0.73**	0.76**	0.99**
S.I	-0.04	0.80**	0.97**	0.97**	0.77**	0.77**	0.98**
F.F.	0.31	0.85**	0.74**	0.57**	0.52**	0.37*	0.94**
F.S	0.14	0.60**	0.82**	0.88**	0.46**	0.49**	0.93**
2.5%S.L	-0.37	0.64**	0.87**	0.84**	0.69**	0.66**	0.96**
U.R%	0.21	0.76**	0.77**	0.61**	0.51**	0.38*	0.95**

P: parent per se performance; F1: crosses per se performance; GCA: general combining ability; SCA: specific combining ability; HMP: heterosis versus mid-parents; HBP: heterosis versus better parents; *: $P < 0.05$; **: $P < 0.01$.

Conclusions

The variance due to the genotypes, parents, crosses, parent vs cross, lines, testers and line $\times$ tester exhibited highly significance for most studied traits. Line $\times$ tester interaction contributed to combinations' variances was higher than those of lines and testers for most studied traits. The best parents in terms of genotype means and GCA effects values were the lines Pima S6, Suvin, G.90, Aust. 12 and tester C.B.58 for most investigated traits, which could be reliably be used in hybridization programmes so as to select the desirable plants from segregating populations. Positive and significant correlation coefficients were found between all possible pairs of F1 hybrids mean, SCA and heterosis. Based on mean performances, SCA effects and heterosis values, the superior crosses were the two crosses Suvin $\times$ G.86 and Aus.12 $\times$ C.B.58 for most yield and yield components, and the two crosses G.90 $\times$ C.B.58 and G.95 $\times$ G.86 for fiber traits. These hybrids are considered the promising crossed to be used in breeding programs for produce hybrid cotton and improvement for yield, its components and fiber quality traits.

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