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### Estimation of Combining Ability, Heterosis and Heritability in some Egyptian Cotton Crosses

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#### ABSTRACT

The present investigation was carried out to study heterosis, general and specific combining ability and heritability in broad and narrow sense for yield and yield component traits using line  $\times$  tester analysis design for eight parents (five lines and three testers) of cotton and their 15 F<sub>1</sub> hybrids. Mean squares due to genotypes (parents and their F<sub>1</sub> hybrids) were highly significant for all studied traits revealing a large amount of variability among them. Results indicated that the cross (No. 1) had displayed the best heterosis (desirable) relative to mid-parent and better parent for (L. %) with values 7.76 and 7.25%. While, the cross (No. 4) had showed the best heterosis (desirable) relative to mid-parent and better parent for (S.I.) and (L.I.) with values 10.31, 9.15, 18.04 and 15.77%, respectively. In addition, the estimates of (G.C.A.) effects for (No.O.B. / P.), (B.W.), (S.C.Y. / P.) and (L.Y. / P.) were positive and highly significant in line (L<sub>s</sub>) in F<sub>1</sub> hybrids. In addition, the cross (No. 12) in F<sub>1</sub> hybrids had showed positive and highly significant for (No.O.B. / P.), (B.W.) and (S.C.Y. / P.). Results clarified that the estimates of broad sense heritability in F<sub>1</sub> hybrids for (No.O.B. / P.), (B.W.), (S.C.Y. / P.), (L.Y. / P.), (L. %), (S.I.) and (L.I.) were moderate to high with values 96.25, 96.04, 97.35, 93.09, 54.70, 97.42 and 41.49%, respectively.

**Keywords:** *Gossypium barbadense* L., line  $\times$  tester analysis, Heterosis, Combining ability and Heritability.



#### INTRODUCTION

Cotton is the world's first fiber crop and an important economic crop in Egypt. Cotton contributes to reducing unemployment through the agricultural operations that take place from the preparation of land for agriculture to harvest and then the operations of the textile industry and its products can be used to improve livestock and some additional industries such as oils, soap and other industries.

hence great effort have been devoted to increase the yield capacity and fiber quality through breeding programs, which depends on the knowledge concerning multiple factors such as heterosis and the nature of the interactions of genes controlling different characters.

El-Said (2016) reported that the best desirable heterotic values over mid parents were detected by eight crosses for yield and its component traits. Ibrahim (2016) studied heterosis in crosses of a half diallel mating of seven Egyptian cotton varieties. The results cleared that the crosses (Ashmouni  $\times$  Giza 95), (Giza 80  $\times$  Giza 95), (Giza 85  $\times$  Giza 95) and (Giza 90  $\times$  Giza 95) had super heterosis for yield and yield components traits, which exhibited the greatest values of heterosis versus mid and better parents. Khalifa *et al.* (2016) evaluated six cotton (*G. barbadense* L.) genotypes in a half diallel mating design. They mentioned that estimates of narrow sense heritability for boll weight, seed cotton yield/plant, linyield /plant and lint percentage were 57.29, 29.70, 30.96 and 38.09%, respectively. Salem (2016) estimated heterosis for yield and its component traits in crosses derived from half diallel crossing of six cotton genotypes. The results indicated that the best heterosis (desirable) relative to mid-parents and

better parent were detected by four crosses for yield and its component traits. Shaker *et al.* (2016) evaluated ten cotton genotypes of (*G. barbadense* L.) in a half diallel design. The results indicated that the crosses (Karshanky  $\times$  C.B58) and (Giza 94  $\times$  C.B 58) exhibited the highest positive heterosis values for seed cotton yield / plant and lint yield / plant of (33.49, 28.85 %) and (37.47, 24.31 %), respectively. Monicashree *et al.* (2017) detected that the dominance variance is higher than the additive variance for all the biometric traits indicating the preponderance of dominance gene action. The ratio between additive and dominance variance is less than one for days to first flowering and number of fruiting nodes per plant. Based on the estimates of gca effects, the line TCH 1705-152 recorded high significant gca effects for most of the traits viz., number of fruiting nodes per plant (14.15). Among the testers, TCH 1705-250 obtained high gca effect for number of fruiting nodes per plant (2.67). Based on the sca effects, the hybrid TCH 1705-152  $\times$  BS-1 had significant sca effects for number of fruiting branches per plant (11.25), while the hybrid ARBC 1301  $\times$  KC3 recorded significant sca effects for the traits viz., number of fruiting nodes per plant (1.98). The sca effect obtained by the above hybrids is a clear indication of the presence of dominance gene action and such hybrids are highly suitable for heterosis breeding to fully exploit the dominance gene action and to improve the yield. Sivia *et al.* (2017) noticed that line-tester analysis revealed significant GCA and SCA effects for all the traits. Among the parents: H1156 for days to first flowering. Makhdoom *et al.* (2019) noticed that genotypes revealed significant ( $P \leq 0.01$ ) variations for earliness (days to flowering). Mean squares due to general (GCA) and specific combining

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ability (SCA) were highly significant, which suggested that additive and non-additive gene actions were involved in controlling earliness (days to flowering). However, the preponderance of non-additive type of gene action observed for majority of the traits. Lines (SLH-284, CIM-473) and pollinators (CIM-707, CIM-496) were leading general combiners for majority of the trait. The significance of additive and non-additive components suggested integrated breeding strategies with delayed selection for development of cotton hybrids with improvement in earliness and seed cotton yield.

The objectives of the present work were to study heterosis, general and specific combining ability, gene action, broad and narrow sense heritability of yield and yield component traits.

## MATERIALS AND METHODS

The present investigation used eight divergent cotton genotypes as parents. These genotypes are (Giza 90, [(G.83 × G.80) × G.89] × Australy, (G.91 × G.90) × G.80, [(G.83 × G.80) × G.89] × (G.83 × Daltabain 703), Giza 95, TNB I, BBB and 10229. The first five genotypes were used as lines while the late three genotypes were used as testers and all genotypes belong to (*G. barbadense*, L.).

The present investigation was conducted during two seasons 2018 and 2019 at Sids Agricultural Research Experiment Station, Beni-Suef Governorate, Agricultural Research Center, Egypt. The eight cotton genotypes (*G. barbadense*, L.) were involved in a series of hybridization according to line × tester mating design Kempthorne (1957) and detailed by Singh and Chaudhary (1985), Allard (1960) and Dudley *et al.* (1969).

**- First season (2018):** Eight parental genotypes were sown on the 5<sup>th</sup> of April, each plot consist of six rows for each line and nine rows for each tester. Each row was four meter long, 0.65 m apart. Seeds were sown at 80 cm, the five parental lines were top crossed to each of the three testers to produce 15 F<sub>1</sub> hybrid seeds. Moreover, all parental lines and testers were self-pollinated to obtain additional seeds for each one.

**- Second season (2019):** The eight parental genotypes with 15 F<sub>1</sub> hybrids were grown at Sids Experimental Station. The experiment was set as a Randomized Complete Blocks Design (R.C.B.D.) with three replications. The plot size was two rows for parents and three rows for F<sub>1</sub> hybrids. Rows were 4.0 m long with row wide of 0.65 m and hills were spaced of 0.40 m apart to give 10 hills /row, and thinned at one plant per hill. The experiment was planted on the 29<sup>th</sup> of March. All cultural practices were followed throughout the growing season as usually done with ordinary cotton culture.

The measurements were recorded for yield and yield component traits on five individual guarded plants from the middle of each plot. Yield and yield component traits i.e. number of open bolls per plant (No.O.B. / P.), boll weight (B.W.) (g), seed cotton yield (S.C.Y. / P.) (g), lint cotton yield (L.Y. / P.) (g), lint percentage (L. %), seed index (S.I.) (g) and lint index (L.I.) (g).

## RESULTS AND DISCUSSION

Analysis of variance for yield and yield component traits are presented in Table (1). Mean squares due to genotypes (parents and their F<sub>1</sub> hybrids) were highly significant for number of open bolls per plant (No.O.B. / P.), boll weight (B.W.), seed cotton yield per plant (S.C.Y. / P.), lint cotton yield per plant (L.Y. / P.), lint percentage (L. %), seed index (S.I.) and lint index (L.I.), revealing a large amount of variability among them. In addition, mean squares due to parents were highly significant for (No.O.B. / P.), (B.W.), (S.C.Y. / P.), (L.Y. / P.), (L. %), (S.I.) and (L.I.) in F<sub>1</sub> hybrids. Moreover, mean squares of crosses were highly significant for (No.O.B. / P.), (B.W.), (S.C.Y. / P.), (L.Y. / P.), (L. %), (S.I.) and (L.I.) in F<sub>1</sub> hybrids. Mean squares of parents versus crosses as an indication of average heterosis over crosses. Mean squares due to parents versus crosses for (No.O.B. / P.), (B.W.), (S.C.Y. / P.), (L.Y. / P.), (L. %), (S.I.) and (L.I.) were highly significant in F<sub>1</sub> hybrids.

**Table 1. Line × tester analysis of variance for yield and yield component traits.**

S.O.V.	D.F.	No.O.B./P.	B.W.(g)	S.C.Y./P.(g)	L.Y./P.(g)	L. %	S.I.(g)	L.I.(g)
Replication	2	0.57	0.00	3.13	1.25	0.46	0.00	0.03
Genotypes	22	260.49**	0.11**	3901.19**	699.50**	5.94**	0.82**	0.49**
Parents	7	476.78**	0.09**	5108.87**	697.32**	5.44**	1.17**	0.29**
Crosses	14	59.01**	0.04**	761.45**	207.83**	5.19**	0.43**	0.20**
Parents Vs. Crosses	1	1567.18**	1.14**	39403.85**	7598.03**	19.81**	3.95**	5.97**
Lines (L)	4	56.32**	0.04**	1293.22**	400.54**	9.02**	0.55**	0.27
Testers (T)	2	136.39**	0.22**	1021.79**	266.13**	7.85**	1.18**	0.23
Lines × Testers	8	41.01**	0.01**	430.48**	96.90**	2.61**	0.18**	0.15**
Error	44	0.57	0.00	4.50	2.91	0.69	0.00	0.0522

\*, \*\* Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.

Sum squares of crosses using line × tester analysis was further partitioned to lines (females), testers (males) and lines × testers interaction. The results indicated that, the mean squares among lines were highly significant for (No.O.B. / P.), (B.W.), (S.C.Y. / P.), (L.Y. / P.), (S.I.) and (L. %) in F<sub>1</sub> hybrids while for (L.I.) were nonsignificant. Concerning mean squares among testers for (No.O.B. / P.), (B.W.), (S.C.Y. / P.), (L.Y. / P.), (S.I.) and (L. %) in F<sub>1</sub> hybrids were highly significant while for (L.I.) was nonsignificant. Regarding to lines × testers, mean squares of these interactions were highly significant for (No.O.B. / P.), (B.W.), (S.C.Y. / P.), (L.Y. / P.), (L. %), (S.I.) and (L.I.) in F<sub>1</sub> hybrids were highly significant.

Mean performance due to parental lines, testers and F<sub>1</sub> hybrids for yield and yield component traits are presented in Tables (2) and (3), respectively. Results showed that the highest mean performance was found for the line (L<sub>1</sub>) for (B.W.) and (S.I.) with values 3.31g and 10.43g, respectively. The highest mean performance was found for the line (L<sub>2</sub>) for (No.O.B. / P.), (S.C.Y. / P.) and (L.Y. / P.) with values 85.96, 274.38g and 103.57g, respectively. The highest mean performance was found for the line (L<sub>3</sub>) for (L. %) with value 40.38%. The highest mean performance was found for the line (L<sub>5</sub>) for (L.I.) with value 6.33g. Results showed that the highest mean performance was found for the tester (T<sub>1</sub>) for (No.O.B. /

P.), (S.C.Y. / P.) and (L.Y. / P.) with values 77.83, 220.17g and 82.16g, respectively. The highest mean performance was found for the tester (T<sub>3</sub>) for (B.W.), (S.I.), (L. %) and (L.I.) with values 3.03g, 37.87%, 10.49g and 6.40g, respectively. On the other hand, the line (L<sub>1</sub>) was the lowest mean performance for (L. %) with value 37.67%. The line (L<sub>3</sub>) was lowest mean performance for (No.O.B. / P.), (S.C.Y. / P.), (L.Y. / P.), (S.I.) and (L.I.) with values 53.05, 154.71g, 62.47g, 8.55g and 5.80g, respectively. The line (L<sub>4</sub>) was the lowest mean performance for (B.W.) with value 2.88g. While, the tester (T<sub>1</sub>) was the lowest mean performance for (S.I.) and (L.I.) with values 9.48 and 5.65g, respectively. The tester (T<sub>2</sub>) was lowest mean performance for (B.W.) and (L. %) with values 2.80g and 35.82 %, respectively. The tester (T<sub>3</sub>) was lowest mean performance for (No.O.B. / P.), (S.C.Y. / P.) and (L.Y. / P.) with values 46.32, 140.48g and 53.20g, respectively.

As for crosses, the cross (No. 1) in F<sub>1</sub> hybrids was the highest mean performance for (No.O.B. / P.) with value

83.34. The cross (No. 3) was the highest mean performance in F<sub>1</sub> hybrids for (B.W.) and (S.I.) with values 3.51g and 10.85g, respectively. The highest mean performance was found for the cross (No. 13) in F<sub>1</sub> hybrids for (L.Y. / P.) and (L. %) with values 110.10g and 40.97%, respectively. As for F<sub>1</sub> hybrids, the highest mean performance was found for the cross (No. 15) for (S.C.Y. / P.) and (L.I.) with values 269.19g and 6.99g, respectively. On the other hand, the cross (No. 2) was the lowest mean performance for (L.Y. / P.) with value 84.73g. While, the cross (No. 4) was the lowest mean performance for (B.W.) with value 3.08g. The cross (No. 5) was the lowest mean performance for (L. %) and (L.I.) with values 36.80% and 6.22g, respectively. The cross (No. 8) was the lowest mean performance for (S.I.) with value 9.73g. The cross (No. 11) was the lowest mean performance for (No.O.B. / P.) and (S.C.Y. / P.) with values 68.91 and 214.97g, respectively.

**Table 2. Mean performance of the studied five parental lines and three testers for yield and yield component traits.**

Genotypes	No.O.B. / P.	B.W. (g)	S.C.Y. / P. (g)	L.Y. / P. (g)	L. %	S.I. (g)	L.I. (g)
L <sub>1</sub>	62.75	3.31	207.92	78.32	37.67	10.43	6.31
L <sub>2</sub>	85.96	3.19	274.38	103.57	37.74	9.69	5.87
L <sub>3</sub>	53.05	2.92	154.71	62.47	40.38	8.55	5.80
L <sub>4</sub>	64.37	2.88	185.59	70.03	37.73	9.57	5.80
L <sub>5</sub>	68.71	2.94	202.21	79.37	39.25	9.79	6.33
T <sub>1</sub>	77.83	2.83	220.17	82.16	37.32	9.48	5.65
T <sub>2</sub>	66.02	2.80	185.14	66.31	35.82	10.19	5.69
T <sub>3</sub>	46.32	3.03	140.48	53.20	37.87	10.49	6.40
L.S.D. 0.05	1.47	0.02	3.66	3.26	1.63	0.12	0.45
L.S.D. 0.01	2.04	0.03	5.08	4.52	2.26	0.17	0.63

L<sub>1</sub>, L<sub>2</sub>, L<sub>3</sub>, L<sub>4</sub>, L<sub>5</sub>, T<sub>1</sub>, T<sub>2</sub> and T<sub>3</sub> are (Giza 90, [(G.83 × G.80) × G.89] × Australy, (G.91 × G.90) × G.80, [(G.83 × G.80) × G.89] × (G.83 × Daltabain 703), Giza 95, TNB I, BBB and 10229, respectively.

**Table 3. Mean performance of the respective F<sub>1</sub> for yield and yield component traits.**

No.	Genotypes	No.O.B. / P.	B.W. (g)	S.C.Y. / P. (g)	L.Y. / P. (g)	L. %	S.I. (g)	L.I. (g)
1	L <sub>1</sub> × T <sub>1</sub>	83.34	3.15	262.62	106.12	40.41	10.09	6.84
2	L <sub>1</sub> × T <sub>2</sub>	72.10	3.17	228.34	84.73	37.12	10.57	6.25
3	L <sub>1</sub> × T <sub>3</sub>	71.95	3.51	252.28	96.84	38.38	10.85	6.76
4	L <sub>2</sub> × T <sub>1</sub>	76.36	3.08	235.47	92.15	39.14	10.57	6.80
5	L <sub>2</sub> × T <sub>2</sub>	75.40	3.14	236.98	87.20	36.80	10.67	6.22
6	L <sub>2</sub> × T <sub>3</sub>	73.47	3.26	239.50	89.42	37.33	10.53	6.27
7	L <sub>3</sub> × T <sub>1</sub>	78.79	3.20	252.27	100.15	39.70	9.86	6.49
8	L <sub>3</sub> × T <sub>2</sub>	81.36	3.28	266.76	106.53	39.94	9.73	6.47
9	L <sub>3</sub> × T <sub>3</sub>	73.52	3.44	253.01	98.54	38.95	10.74	6.85
10	L <sub>4</sub> × T <sub>1</sub>	74.85	3.17	237.41	93.51	39.39	9.87	6.42
11	L <sub>4</sub> × T <sub>2</sub>	68.91	3.12	214.97	86.28	40.15	9.83	6.60
12	L <sub>4</sub> × T <sub>3</sub>	71.37	3.39	242.10	91.60	37.83	10.49	6.39
13	L <sub>5</sub> × T <sub>1</sub>	82.22	3.27	268.78	110.10	40.97	9.93	6.89
14	L <sub>5</sub> × T <sub>2</sub>	71.55	3.32	237.79	95.37	40.10	10.06	6.74
15	L <sub>5</sub> × T <sub>3</sub>	79.29	3.39	269.19	108.40	40.27	10.37	6.99
L.S.D. 0.05		1.17	0.03	3.56	2.81	1.33	0.05	0.37
L.S.D. 0.01		1.58	0.04	4.80	3.79	1.80	0.06	0.49

L<sub>1</sub>, L<sub>2</sub>, L<sub>3</sub>, L<sub>4</sub>, L<sub>5</sub>, T<sub>1</sub>, T<sub>2</sub> and T<sub>3</sub> are (Giza 90, [(G.83 × G.80) × G.89] × Australy, (G.91 × G.90) × G.80, [(G.83 × G.80) × G.89] × (G.83 × Daltabain 703), Giza 95, TNB I, BBB and 10229, respectively.

Estimates of heterosis relative to the mid-parents and better parent for yield and yield component traits are presented in Table (4). Results indicated that the cross (No. 1) had displayed the best heterosis (desirable) relative to mid-parent and better parent for (L. %) with values (7.76 and 7.25%). While, the cross (No. 4) showed the best heterosis (desirable) relative to mid-parent and better parent for (S.I.) and (L.I.) with values (10.31 and 9.15) and (18.04 and 15.77%), respectively. In addition, the cross (No. 9) had recorded the best heterosis (desirable) relative to mid-parent and better parent for (No.O.B. / P.), (B.W.), (S.C.Y. / P.) and (L.Y. / P.) with values (47.95 and 38.56), (15.70 and 13.47), (71.42 and 63.54) and (70.37 and 57.73%), respectively. These results are in common

agreement with the results mentioned by El-Said (2016), Ibrahim (2016), Salem (2016) and Shaker *et al.* (2016). General combining ability effects (g<sub>i</sub>) of the parents in F<sub>1</sub> hybrids for yield and yield component traits were shown in Table (5). Results showed that the estimates of (G.C.A.) effects for (S.I.) were positive and highly significant in line (L<sub>1</sub>) in F<sub>1</sub> hybrids. In addition, the estimates of (G.C.A.) effects for (No.O.B. / P.), (B.W.), (S.C.Y. / P.), (L.Y. / P.), (L.%) and (L.I.) were positive and highly significant in line (L<sub>5</sub>) in F<sub>1</sub> hybrids. Results recorded that the tester (T<sub>1</sub>) showed positive and highly significant for (No.O.B. / P.), (S.C.Y. / P.), (L.Y. / P.) and (L.%) in F<sub>1</sub> hybrids. In addition, the tester (T<sub>3</sub>) showed positive and highly significant for (B.W.), (S.C.Y. / P.) and (S.I.) in F<sub>1</sub> hybrids.

**Table 4. Estimates of heterosis (H%) relative to the mid-parent (M.P.) and better parent (B.P.) for yield and yield component traits.**

No.	Genotypes	No.O.B. /P.		B.W. (g)		S.C.Y. /P. (g)		L.Y. /P. (g)		L %		S.I. (g)		L.I. (g)	
		MP.	BP.	MP.	BP.	MP.	BP.	MP.	BP.	MP.	BP.	MP.	BP.	MP.	BP.
1	L <sub>1</sub> × T <sub>1</sub>	18.56**	7.07**	2.60**	-4.90**	22.69**	19.28**	32.24**	29.15**	7.76**	7.25**	1.37**	-3.22**	14.52**	8.54**
2	L <sub>1</sub> × T <sub>2</sub>	11.97**	9.19**	3.53**	-4.42**	16.18**	9.81**	17.16**	8.18**	1.02	-1.46	2.57**	1.37**	4.14	-0.95
3	L <sub>1</sub> × T <sub>3</sub>	31.93**	14.66**	10.50**	5.81**	44.82**	21.33**	47.25**	23.64**	1.62	1.36	3.68**	3.36**	6.34*	5.55
4	L <sub>2</sub> × T <sub>1</sub>	-6.75**	-11.16**	2.42**	-3.39**	-4.77**	-14.18**	-0.76	-11.02**	4.28**	3.69*	10.31**	9.15**	18.04**	15.77**
5	L <sub>2</sub> × T <sub>2</sub>	-0.78	-12.28**	4.83**	-1.53**	3.14**	-13.63**	2.66	-15.79**	0.05	-2.49	7.34**	4.71**	7.51*	5.82
6	L <sub>2</sub> × T <sub>3</sub>	11.08**	-14.52**	4.73**	2.12**	15.46**	-12.71**	14.07**	-13.66**	-1.24	-1.40	4.32**	0.31	2.20	-2.00
7	L <sub>3</sub> × T <sub>1</sub>	20.40**	1.23	11.45**	9.78**	34.59**	14.58**	38.48**	21.89**	2.18	-1.69	9.33**	3.97**	13.48**	12.03**
8	L <sub>3</sub> × T <sub>2</sub>	36.64**	23.22**	14.64**	12.43**	56.98**	44.08**	65.44**	60.65**	4.82**	-1.09	3.80**	-4.51**	12.69**	11.66**
9	L <sub>3</sub> × T <sub>3</sub>	47.95**	38.56**	15.70**	13.47**	71.42**	63.54**	70.37**	57.73**	-0.44	-3.55**	12.77**	2.35**	12.38**	7.06*
10	L <sub>4</sub> × T <sub>1</sub>	5.28**	-3.82**	11.04**	9.99**	17.02**	7.83**	22.87**	13.80	4.96**	4.39*	3.62**	3.13**	12.09**	10.59**
11	L <sub>4</sub> × T <sub>2</sub>	5.70**	4.37**	9.70**	8.19**	15.97**	15.83**	26.55**	23.19**	9.16**	6.39**	-0.47	-3.46**	14.87**	13.75**
12	L <sub>4</sub> × T <sub>3</sub>	28.95**	10.87**	14.68**	11.86**	48.49**	30.45**	48.65**	30.79**	0.08	-0.09	4.58**	0.00	4.66	-0.22
13	L <sub>5</sub> × T <sub>1</sub>	12.22**	5.64**	13.26**	11.07**	27.26**	22.07**	36.31**	33.99**	7.00**	4.36*	2.99**	1.36**	15.04**	8.83**
14	L <sub>5</sub> × T <sub>2</sub>	6.21**	4.14**	15.65**	12.92**	22.77**	17.59**	30.93**	20.16**	6.83**	2.16	0.70*	-1.24**	12.10**	6.41*
15	L <sub>5</sub> × T <sub>3</sub>	37.87**	15.41**	13.61**	11.93**	57.10**	33.12**	63.53**	36.57**	4.43**	2.59	2.26**	-1.14**	9.85**	9.25**
L.S.D. 0.05		1.08	1.25	0.02	0.03	3.03	3.50	2.44	2.81	1.18	1.37	0.07	0.08	0.3265	0.38
L.S.D. 0.01		1.45	1.68	0.03	0.04	4.06	4.69	3.26	3.77	1.58	1.83	0.09	0.10	0.437	0.50

L<sub>1</sub>, L<sub>2</sub>, L<sub>3</sub>, L<sub>4</sub>, L<sub>5</sub>, T<sub>1</sub>, T<sub>2</sub> and T<sub>3</sub> are (Giza 90, [(G.83 × G.80) × G.89] × Australy, (G.91 × G.90) × G.80, [(G.83 × G.80) × G.89] × (G.83 × Daltabain 703), Giza 95, INB I, BBB and 10229, respectively.

\*, \*\* Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.

**Table 5. General combining ability effects (g<sub>i</sub>) of five parental lines and three testers in F<sub>1</sub> for yield and yield component traits.**

Genotypes	No.O.B. /P.	B.W. (g)	S.C.Y. /P. (g)	L.Y. /P. (g)	L %	S.I. (g)	L.I. (g)
L <sub>1</sub>	0.16	0.014**	1.24	-0.56	-0.46	0.22**	0.01
L <sub>2</sub>	-0.55*	-0.09**	-9.18**	-6.87**	-1.34**	0.31**	-0.16*
L <sub>3</sub>	2.25**	0.04**	10.85**	5.27**	0.43	-0.16**	0.00
L <sub>4</sub>	-3.92**	-0.0324**	-15.00**	-6.00**	0.02	-0.21**	-0.13
L <sub>5</sub>	2.05**	0.06**	12.08**	8.16**	1.34**	-0.15**	0.27**
C.D. 0.05	0.51	0.01	1.43	1.15	0.56	0.03	0.15
C.D. 0.01	0.68	0.01	1.91	1.54	0.75	0.04	0.21
T <sub>1</sub>	3.48**	-0.08**	4.81**	3.94**	0.82**	-0.21**	0.09
T <sub>2</sub>	-1.76**	-0.05**	-9.53**	-4.43**	-0.27	-0.10**	-0.14*
T <sub>3</sub>	-1.71**	0.13**	4.71**	0.49	-0.54*	0.31**	0.05
C.D. 0.05	0.40	0.01	1.11	0.89	0.43	0.02	0.12
C.D. 0.01	0.53	0.01	1.48	1.19	0.58	0.03	0.16

L<sub>1</sub>, L<sub>2</sub>, L<sub>3</sub>, L<sub>4</sub>, L<sub>5</sub>, T<sub>1</sub>, T<sub>2</sub> and T<sub>3</sub> are (Giza 90, [(G.83 × G.80) × G.89] × Australy, (G.91 × G.90) × G.80, [(G.83 × G.80) × G.89] × (G.83 × Daltabain 703), Giza 95, INB I, BBB and 10229, respectively.

\*, \*\* Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.

Specific combining ability effects (s<sub>ij</sub>) of the parents in F<sub>1</sub> hybrids for yield and yield component traits are presented in Table (6). Results indicated that the estimates of (S.C.A.) effects in F<sub>1</sub> hybrids the cross (No. 5) recorded positive and significant or highly significant for most

studied traits. While, the cross (No. 11) showed positive and significant or highly significant for (L %) and (L.I.) in F<sub>1</sub> hybrids. These results are in agreement with these previously reported by Monicashree *et al.* (2017), Sivya *et al.* (2017) and Makhdoom *et al.* (2019).

**Table 6. Estimates of specific combining ability effects (S<sub>ij</sub>) of each cross for yield and yield component traits.**

No.	Genotypes	No.O.B. /P.	B.W. (g)	S.C.Y. /P. (g)	L.Y. /P. (g)	L %	S.I. (g)	L.I. (g)
1	L <sub>1</sub> × T <sub>1</sub>	4.06**	-0.03**	10.06**	6.27**	0.94	-0.19**	0.13
2	L <sub>1</sub> × T <sub>2</sub>	-1.92**	-0.05**	-9.87**	-6.72**	-1.23**	0.17**	-0.22
3	L <sub>1</sub> × T <sub>3</sub>	-2.13**	0.09**	-0.18	0.44	0.29	0.024	0.08
4	L <sub>2</sub> × T <sub>1</sub>	-2.19**	0.00	-6.65**	-1.38	0.55	0.19**	0.28*
5	L <sub>2</sub> × T <sub>2</sub>	2.09**	0.03**	9.19	2.05*	-0.67	0.18**	-0.06
6	L <sub>2</sub> × T <sub>3</sub>	0.11	-0.04**	-2.53**	-0.67	0.12	-0.38**	-0.21
7	L <sub>3</sub> × T <sub>1</sub>	-2.57**	-0.02**	-9.88**	-5.53**	-0.65	-0.03	-0.20
8	L <sub>3</sub> × T <sub>2</sub>	5.23**	0.02**	18.94**	9.22**	0.68	-0.27**	0.00
9	L <sub>3</sub> × T <sub>3</sub>	-2.65**	0.00	-9.05**	-3.69**	-0.03	0.31**	0.19
10	L <sub>4</sub> × T <sub>1</sub>	-0.33	0.02**	1.10	-0.89	-0.55	0.01	-0.14
11	L <sub>4</sub> × T <sub>2</sub>	-1.02*	-0.05**	-6.99**	0.25	1.29**	-0.12**	0.27*
12	L <sub>4</sub> × T <sub>3</sub>	1.36**	0.02**	5.88**	0.64	-0.74	0.10**	-0.13
13	L <sub>5</sub> × T <sub>1</sub>	1.05*	0.02*	5.38**	1.53	-0.30	0.01	-0.07
14	L <sub>5</sub> × T <sub>2</sub>	-4.36**	0.04**	-11.26**	-4.81**	-0.06	0.04	0.00
15	L <sub>5</sub> × T <sub>3</sub>	3.31**	-0.07**	5.88**	3.28**	0.36	-0.06*	0.06
C.D. 0.05		0.89	0.02	2.48	1.99	0.97	0.05	0.27
C.D. 0.01		1.18	0.03	3.31	2.66	1.29	0.07	0.36

L<sub>1</sub>, L<sub>2</sub>, L<sub>3</sub>, L<sub>4</sub>, L<sub>5</sub>, T<sub>1</sub>, T<sub>2</sub> and T<sub>3</sub> are (Giza 90, [(G.83 × G.80) × G.89] × Australy, (G.91 × G.90) × G.80, [(G.83 × G.80) × G.89] × (G.83 × Daltabain 703), Giza 95, INB I, BBB and 10229, respectively.

\*, \*\* Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.

Estimates of heritability in broad (h<sup>2</sup><sub>b.s.</sub> %) and narrow (h<sup>2</sup><sub>n.s.</sub> %) sense and genetic components for yield and yield component traits are presented in Table (7). The results indicated that the mean square of specific combining ability were larger than those of general

combining ability for yield and its component traits. This result could be verified by the ratio of (G.C.A. / S.C.A.) which less than the unity. In this trend the magnitudes of additive (σ<sup>2</sup>A) genetic variance were lower than those of non-additive (σ<sup>2</sup>D) genetic variance for yield and its

component traits. Results clarified that the estimates of broad sense heritability in F<sub>1</sub> hybrids for (No.O.B. / P.), (B.W.), (S.C.Y. / P.), (L.Y. / P.), (L. %), (S.I.) and (L.I.) were moderate to high with values 96.25, 96.04, 97.35, 93.09, 54.70, 97.42 and 41.49%, respectively. Results claimed that the estimates of narrow sense heritability in F<sub>1</sub>

hybrids (No.O.B. / P.), (B.W.), (S.C.Y. / P.), (L.Y. / P.), (L. %), (S.I.) and (L.I.) were low to moderate with values 8.30, 40.92, 13.77, 18.64, 12.06, 21.51 and 3.70%, respectively. These results are in common agreement with the results mentioned by Khalifa *et al.* (2016) and Monicashree *et al.* (2017).

**Table 7. Combining ability and genetic components as well as estimates of heritability in broad (h<sup>2</sup><sub>b.s.</sub>%) and narrow sense (h<sup>2</sup><sub>n.s.</sub>%) for yield and yield component traits.**

	No.O.B. / P.	B.W. (g)	S.C.Y. / P. (g)	L.Y. / P. (g)	L. %	S.I. (g)	L.I. (g)
σ <sup>2</sup> G.C.A.	0.636	0.001	11.701	3.922	0.091	0.009	0.002
σ <sup>2</sup> S.C.A.	13.480	0.004	141.994	31.332	0.645	0.062	0.034
σ <sup>2</sup> G.C.A. / σ <sup>2</sup> S.C.A.	0.047	0.371	0.082	0.125	0.141	0.142	0.049
σ <sup>2</sup> A	1.273	0.003	23.402	7.844	0.182	0.017	0.003
σ <sup>2</sup> D	13.480	0.004	141.994	31.332	0.645	0.062	0.034
h <sup>2</sup> <sub>b.s.</sub> %	96.246	96.043	97.351	93.092	54.697	97.419	41.494
h <sup>2</sup> <sub>n.s.</sub> %	8.304	40.928	13.774	18.638	12.058	21.515	3.701

### CONCLUSION

Variance due to the genotypes, parents, crosses, parent vs cross, lines, testers and line × tester exhibited highly significance for most yield and yield component traits. Line × tester interaction contributed to combination variances was higher than those of lines and testers for most studied traits. Based on S.C.A. effects and heterosis values, the superior crosses were the two crosses (G.91 × G.90) × G.80 × 10229 and [(G.83 × G.80) × G.89] × (G.83 × Daltabain 703) × 10229 for most yield and yield components. These hybrids are considered the promising crossed to be used in breeding programs for produce hybrid cotton and improvement for yield and its components traits.

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تقدير القدرة على التآلف وقوة الهجين ودرجة التوريث لبعض هجن القطن المصري  
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أجريت هذه الدراسة بمحطة البحوث الزراعية بسدس والتابعة لمركز البحوث الزراعية والتي تقع بمحافظة بنى سويف بجمهورية مصر العربية فى موسمى ٢٠١٨ و ٢٠١٩ واستخدم فيها ثمانية تراكيب وراثية مختلفة من القطن تتبع النوع الباربانيس ، وقد استخدم تحليل السلالة × الكشاف لدراسة القدرة على التآلف فيما بينها ، وكذلك قوة الهجين ودرجة التوريث وكانت بعض النتائج كما يلى : أوضحت النتائج أن تباينات الأباء وهجن الجيل الأول كانت عالية المعنوية لجميع صفات المحصول. أظهرت النتائج أن تباين السلالات × الكشافات كانت عالية المعنوية لمعظم الصفات المدروسة. أشارت النتائج إلى أن الهجين رقم (١) أفضل الهجن لصفة عدد اللوز المتفتح / نبات. علاوة على ذلك كان الهجين رقم (٣) أعلى متوسط أداء بالنسبة لصفة متوسط وزن اللوزة ومعامل البذرة أما الهجين رقم (١٣) الأفضل لصفة محصول الشعير / نبات ونسبة التصافي أما الهجين رقم (١٥) الأفضل لصفة محصول القطن الزهر / نبات ومعامل الشعير. خلصت النتائج إلى أن الهجينين (جيزة ٩١ × جيزة ٩٠) × جيزة ٨٠ × ١٠٢٢٩ و [(جيزة ٨٣ × جيزة ٨٠) × جيزة ٨٩] × (جيزة ٨٣ × دلتابين ٧٠٣) × ١٠٢٢٩ أفضل الهجن بالنسبة لمعظم صفات المحصول. ومن خلال هذه الدراسة يمكن استخدام السلالات والكشافات التي أظهرت قدرة عالية على التآلف فيما بينها فى برامج التربية لإنتاج هجن جديدة ذات صفات محصولية أفضل.