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Identifying Superior Parents and Hybrids for Yield, Its Components and Fiber Quality in Cotton (*Gossypium barbadense* L.)

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THIS study was accomplished at 2018-2020 seasons at Sakha Experimental Station. Four Egyptian cotton varieties (Giza87, Giza92, Giza93 and Giza96) were used as lines crossed by Pima Early, PimaS-1 and PimaS-6 as testers in line x tester manner. Heterosis and combining ability were determined for yield, its components and fiber traits. Genotypes significantly differed for all traits, Giza96, PimaS-6 and Giza96xPimaS-6 gave highest yield, while Giza87, PimaS-1 and Giza96xPimaS-1 showed the best fiber traits. Giza92 showed the highest positive heterosis for yield and its components when crossed to the three testers, while Pima Early showed the highest positive heterosis for yield and its components when crossed to most of lines. GCA and SCA variances were significant as additive and non-additive gene actions were controlling the studied traits. Giza96 and PimaS-6 were the best combiners for yield and its components, while Giza87 and PimaS-1 were the best combiners for fiber traits. Giza96xPimaS-6 hybrid had the best SCA for yielding traits, while Giza96xPimaS-1 was the best for most fiber traits. Variance of SCA was greater than GCA for almost all traits as non-additive gene action was more important in controlling these traits. Giza96, PimaS-6 and their hybrid were promising for improving the yield potential, while Giza87, PimaS-1 and Giza96xPimaS-1 hybrid were promising for improving fiber quality traits in breeding programs. Giza92, Giza93, Giza96 and Pima Early were the most similar genotypes, whereas Giza87 and the cluster between Giza92 and Giza93 showed the lowest similarity. PimaS-1 and PimaS-6 grouped in one cluster.

Keywords: Cotton, Line x tester, Heterosis, Similarity.

Introduction

Cotton (*Gossypium spp*.) or the white gold is a major source of natural textile fiber and edible oil. The detailed information regarding genetic variance for yield and quality-related traits within the existing germplasm of a crop is essential for starting a crop improvement program (Ali et al., 2011). Hence, prosperous hybridization program for improved yield and fiber quality traits in cotton counts primarily on the genetic variability's nature and magnitude, which helps cotton breeders to select profitable divergent parents to be used as parents in hybridization (Shahrajabian et al., 2020). There are sundry procedures that can be utilized to estimate the desired genetic variability as well as the nature and magnitude of gene action involved in the heritage of quantitative traits.

Combining ability analysis results the indispensable information for choosing the worthy parents and cross combinations for usage in breeding program. It also differentiates between poor and good combiners and identifies the best crosses with wide environmental adaptability (Sprague & Tatum, 1942). General combining ability (GCA) is an active guide to the value of a genotype in hybrid combinations, GCA effects have been attributed to the additive and additive x additive gene actions. On the other hand, specific combining ability (SCA) is profitable for realizing the potential hybrids that have higher performance and sensible level of stability, differences in the SCA have attributed to the non-

additive (dominance or epistasis) gene action (Griffing, 1956). Therefore, GCA is profitable for selection and hybridization programs, while SCA is beneficial for the production of hybrids and heterotic effects (Jatoi et al., 2011).

Line x tester biometrical technique is a simple, crucial and vastly useful analysis that estimates large number of genotypes to pick out appropriate parents and superior crosses with concern to the economic traits, in addition, it clears nature and the magnitude of different types of gene action participated in the expression of such traits which is conclusive for selecting the worthy parents and crosses to be used in crop improvement (Kempthorne, 1957).

Therefore, the line x tester mating design has been widely utilized by cotton breeders for analysis and picking out the potential combiners in early generation for cotton yielding ability and fiber quality traits in Egyptian cotton (*G. barbadense* L.) as reported by Yehia & El-Hashash (2019), EL-Mansy et al. (2020), Mokadem et al. (2020), Amer et al. (2021), Hamed & Said (2021) and Max et al. (2021) as well as in upland cotton (*G. hirsutum* L.) as reported by Chaudhary et al. (2019), Patel et al. (2019), Manonmani et al. (2020) and Chakholoma et al. (2022).

This research aimed to evaluate the mean performance, heterosis, GCA, SCA and heritability estimates for yield, its components and fiber properties using four Egyptian cotton varieties used as females (lines) and crossed by three exotic varieties belong to *G. barbadense* as testers, as well as to adopt convenient parents and crosses utilizing the line × tester mating system.

Materials and Methods

This investigation was undertaken at Sakha Research Station, Agriculture Research Center, Kafr El-Sheakh Governorate, Egypt, in three growing seasons (2018–2020).

Materials
The genetic materials comprised seven cotton genotypes belonging to *Gossypium barbadense* L., four extra-long staple Egyptian cotton genotypes i.e. Giza 87, Giza 92, Giza 93 and Giza 96, in addition to three Pima (Egyptian-American) genotypes i.e. Pima Early, Pima S-1, and Pima S-6. Pure selfed seeds of all genotypes were obtained by Cotton Research Institute, Agric. Res. Center, Giza, Egypt. Origin, pedigree and characterization of the seven cotton genotypes used in this investigation are presented in Table 1.

TABLE 1. Origin, pedigree and characterization of the studied seven cotton genotypes

No.	Variety	Origin	Pedigree	Characterization
1	Giza 87 (L1)	Egypt	(G.77 x G.45) A	An extra-fine, extra-long staple with intermediate yielding and excellent fiber quality.
2	Giza 92 (L2)	Egypt	G.84 x (G.74 x G.68)	An extra-long staple with high yield and extra strong fiber.
3	Giza 93 (L3)	Egypt	G.77 x Pima S-6	An extra-fine, extra-long staple and strong fiber with high yield and early maturity.
4	Giza 96 (L4)	Egypt	[G.84 x (G.70 x G.51 B)] x S- 62	An extra-long staple, high yielding ability and lint %, with excellent fiber properties.
5	Pima Early (T1)	USA	Unknown	An extra-long staple, high seed cotton yield, high lint percentage and early maturity.
6	Pima S-1 (T2)	USA	Complex cross of Sea Island, Pima, Tanguis and Stoneville.	An extra-long staple, compact in growth, high yielding, early maturity, more fiber fineness.
7	Pima S-6 (T3)	USA	(5934-23-2-6 x 5903-98-4-4).	Long staple, high lint percentage, high yield, earlier maturity, smaller bolls, slightly shorter fiber length and strong and coarser fibers.

Methods

In 2018 season, pure seeds of the seven genotypes were sown on 21st of April. At flowering, hybridization was accomplished using the Egyptian genotypes (Giza 87, Giza 92, Giza 93 and Giza 96) as female parents, while the Pima genotypes (Pima Early, Pima S-1, and Pima S-6) were used as male parents in line x tester manner to produce the hybrid seeds of twelve F_1's crosses.

In 2019 growing season, F_1 seeds of 12 hybrids along with their seven parents were sown in the field on 24th of April in three replications under randomized complete block design (RCBD). The experimental plot comprised four rows, each row was 4.0m long and 0.65m wide, hills spaced 0.50m apart to give 8 hills/row, with one plant left per hill.

All recommended agronomic practices were kept constant during the growing season.

Data were recorded on individual plant basis for the following traits: Seed cotton yield/plant (SCY/p) and lint yield/plant (LY/p) in grams, lint percentage (L%= lint yield x 100/seed cotton yield), boll weight in grams (BW), number of bolls per plant (NB/p) and seed index in grams (SI). In addition to the following fiber quality traits: Micronaire reading (Mic.), fiber strength as Pressley index (Press.) measured by Stelometer, fiber length as the upper half mean length (UHM) in mm measured by the digital Fibrograph and lint uniformity index (LUI%) which is the ratio between the mean length and the upper half mean length of the fibers, expressed as a percentage.

All fiber traits were kindly measured in the laboratories of Cotton Technology Research Division, Cotton Research Institute, Agric. Res. Center, Giza, Egypt.

Statistical analysis

Data collected for parents along with their F_1 crosses were analyzed according to Singh & Chaudhary (1999) for 19 genotypes (parents and crosses), when the differences among these genotypes were significant, line x tester analysis as the procedures developed by Kempthorne (1957) was applied to partition genetic variance and to estimate the various types of gene effects for the F_1 crosses as well as to give information concerning general and specific combining ability for parents and crosses. The least significant difference test (L.S.D) as described by Singh & Chaudhary (1999) was utilized to detect the significance of the differences among means and heterosis estimates. In addition, heritability estimates in both broad-sense ($h^2b\%$) and narrow-sense ($h^2n\%$) were calculated as given by Mather (1949).

Cluster analysis exploiting Ward's method (Ward, 1963) and interval Euclidean distance, was used for evaluating the genetic distance and variance among the parental cotton genotypes based on the various studied traits. The Minitab software was used to determine the coefficient of similarity and dendrogram for Euclidean distance and single linkage for the studied genotypes.

For the better recognition about relationships among the various traits, Pearson correlation coefficient (r) was calculated according to Falconer & Mackay (1996) to estimate the degree of association among these traits, the significance of correlations was determined.

Results and Discussion

Analysis of variance

Mean squares produced from the analysis of variance for cotton yield, its components and fiber traits for the studied genotypes (seven parents along with their 12 F_1 crosses) were presented in Table 2. Results revealed highly significant differences among genotypes for all the studied traits which indicating the existence of abundant amount of genetic variability among these genotypes as the tested parents or their crosses did not act similarly for the studied traits.

Further, mean squares for the tested parents cleared highly significant differences for all traits. Moreover, mean squares for crosses were highly significant for all traits except for lint yield/plant and Pressely index which were significant, whereas, boll weight showed insignificant differences.

Mean squares of parents versus crosses showed highly significant differences in F_1 hybrids for all the studied traits except for micronaire reading and Pressely index which were significant, these results clarified the presence of the heterotic effects.

TABLE 2. Mean squares resulted from line x tester analysis for seven cotton parents and their crosses in F₁ generation for the studied traits

S.O.V	d.f	Seed cotton yield and its components						Fiber quality			
		SCY/p (g)	LY/p (g)	L %	BW (g)	BN/p	SI (g)	Mic.	Press.	UHM (mm)	LUI %
Replications	2	102.03 -	4.67 -	5.96 **	0.004 -	9.72 -	0.02 -	0.12 **	0.20 **	0.06 -	0.02 -
Genotypes	18	964.31 **	203.39 **	10.45 **	3.116 **	454.74 **	0.13 **	0.18 **	0.14 **	1.30 **	1.21 **
Parents (P)	6	1731.17 **	399.25 **	19.22 **	0.076 **	141.90 **	0.14 **	0.40 **	0.31 **	1.95 **	2.33 **
Crosses (C)	11	254.96 **	44.98 *	5.10 **	0.005 -	19.55 **	0.10 **	0.08 **	0.06 *	0.92 **	0.67 **
P. vs. C	1	4165.99 **	770.75 **	16.57 **	55.573 **	118.79 **	0.47 **	0.09 *	0.12 *	1.57 **	0.32 **
Lines (L)	3	476.89 **	74.97 *	16.21 **	0.001 -	39.41 **	0.27 **	0.09 *	0.04 -	2.48 **	0.50 **
Testers (T)	2	598.91 **	121.23 *	2.57 *	0.019 *	37.38 *	0.12 **	0.22 **	0.17 *	1.12 **	1.00 *
L x T	6	169.35 **	46.57 *	10.39 **	0.003 -	30.67 *	0.11 **	0.02 -	0.11 *	0.78 *	0.65 -
Error	36	70.29	19.67	0.69	0.004	6.75	0.02	0.02	0.02	0.11	0.28

* and ** indicate significant at 0.05 and 0.01 levels of probability, respectively.
SCY/p: Seed cotton yield per plant, LY/p: Lint yield per plant, L%: Lint percentage, BW: Boll weight, BN/p: Number of bolls per plant, SI: Seed index, Mic.: Micronaire reading, Press.: Pressely index, UHM: Upper half mean and LUI: Lint uniformity index.

Therefore, mean squares of the F₁ crosses were partitioned utilizing the line × tester analysis to: Lines (females), testers (males) and their interaction (crosses) as shown in Table 2. Mean squares for lines were significant for all traits, except for boll weight and Pressely index that were insignificant. Similarly, mean squares among testers were significant or highly significant for all the studied traits. Hence, the significance of mean squares for both lines and testers in this study reflecting the importance of general combining ability (GCA) effects with additive genes.

Concerning the interaction (line × tester), mean squares revealed significant differences for almost all of the studied traits, except for boll weight, Micronaire reading and lint uniformity index, revealing specific combining ability (SCA) with dominant gene actions. The significance of GCA for both of lines and testers as well as SCA for their crosses revealing that both additive and non-additive gene actions were participated in the expression of the studied traits (Kempthorne, 1957).

Mean performance of the tested genotypes

Mean performances for the seven parental genotypes and their 12 F₁s hybrids for the studied traits were displayed on Table 3. Results revealed that the parental lines used in this work varied significantly for all of studied traits, reflecting the different genetic back-ground for these genotypes. The highest mean performances for seed cotton yield, its components and lint uniformity index were found for the line Giza 96 as it gave 130.21g for SCY/p, 49.22g for LY/p, 37.79% for L%, 3.11g for BW, 41.92 for BN/p, and 87.75% for LUI. Giza 92 gave the highest means for SI (10.22g) and Pressely index (12.05), Giza 87 line had the best values of UHM (36.07mm) and Mic. (3.20).

On the opposite, Giza 87 line showed the lowest values for the traits: SCY/p (84.73g), LY/p (28.29g), L% (33.35%), BW (2.92g), BN/p (28.90), SI (9.58g) and 86.75% for LUI, in addition, the line Giza 92 showed the worst Mic. (3.87) and UHM (33.99mm), while Giza 93

showed the lowest value for Press. (11.52).

On the other hand, the tested testers showed that the highest mean performances were found for Pima S-6 for the traits: BW (3.32g), BN/p (49.43), SCY/p (151.25g), LY/p (60.07g), L% (39.75%) and Press. (11.40). While Pima S-1 showed the highest mean values for SI (10.22g) and LUI (86.90%) as well as the best Mic. (lowest reading) that reached 3.85, while Pima Early tester gave the highest value for UHM (35.27mm).

On the contrary, Pima Early tester showed the worst values for the traits, BW (3.20g), BN/p (38.87), SCY/p (127.96g), LY/p (49.44g), SI (9.90g), Press. (11.07) and LUI (84.95%). While

Pima S-1 showed the lowest values of L% (37.40) and UHM (34.37mm), the worst value of Mic. (4.20) was obtained by Pima S-6.

Concerning F₁ hybrids, results showed that Giza 96 x Pima S-6 hybrid gave the best mean performance for the traits: BW (3.35g), LY/p (57.75g) and L% (39.97%); while the cross Giza 92 x Pima S-6 gave the highest values for BN/p (46.38), SCY/p (153.60g) and Press. (11.88). Giza 96 x Pima S-1 hybrid showed the best mean performance for the traits: Mic. (3.42) and LUI (87.40%), while Giza 96 x Pima Early hybrid had the highest UHM (36.10mm) and the hybrid Giza 92 x Pima S-1 had the highest SI (10.52g).

TABLE 3. Mean performance of seven cotton genotypes and their 12 hybrids in F₁ generation for the studied traits

| Genotypes | Seed cotton yield and its components | | | | | | Fiber quality | | | |
	SCY/p (g)	LY/p (g)	L %	BW (g)	BN/p	SI (g)	Mic.	Press.	UHM (mm)	LUI %
G.87 (L1)	84.73	28.29	33.35	2.92	28.90	9.58	3.20	11.79	36.07	86.75
G.92 (L2)	102.38	35.15	34.33	3.03	34.88	10.22	3.87	12.05	33.99	86.95
G. 93 (L3)	105.93	36.08	34.08	2.94	33.63	9.94	3.60	11.52	35.11	87.10
G. 96 (L4)	130.21	49.22	37.79	3.11	41.92	9.98	3.40	11.60	35.95	87.75
Pima E. (T1)	127.96	49.44	38.73	3.20	38.87	9.90	4.10	11.07	35.27	84.95
Pima S-1 (T2)	143.92	53.90	37.40	3.28	43.39	10.22	3.85	11.33	34.37	86.90
Pima S-6 (T3)	151.25	60.07	39.75	3.32	49.43	10.06	4.20	11.40	34.42	86.20
L1 x T1	124.12	47.36	36.63	3.24	38.28	9.94	3.60	11.61	35.85	86.65
L1 x T2	127.78	47.30	35.99	3.30	38.69	10.01	3.48	11.70	35.58	86.75
L1 x T3	137.11	55.16	36.63	3.29	41.71	9.90	3.60	11.59	35.55	86.60
L2 x T1	130.76	51.67	37.11	3.25	40.25	10.25	3.83	11.50	35.16	85.90
L2 x T2	142.29	51.57	37.15	3.30	43.12	10.52	3.60	11.81	34.36	86.45
L2 x T3	153.60	57.07	37.62	3.31	46.38	10.35	3.93	11.88	34.24	85.80
L3 x T1	132.22	50.18	36.74	3.21	41.20	10.07	3.80	11.42	35.77	87.15
L3 x T2	135.25	49.26	36.58	3.34	40.35	10.35	3.53	11.69	35.29	86.55
L3 x T3	141.33	52.88	38.26	3.29	43.02	10.20	3.70	11.61	35.50	85.90
L4 x T1	140.77	48.81	39.49	3.27	43.09	10.08	3.60	11.53	36.10	85.95
L4 x T2	146.28	57.57	39.14	3.28	44.53	10.24	3.42	11.68	35.49	87.40
L4 x T3	152.12	57.75	39.97	3.35	45.41	10.17	3.83	11.64	35.51	86.27
LSD 0.05	**13.88**	**7.34**	**1.38**	**0.11**	**4.30**	**0.22**	**0.20**	**0.26**	**0.56**	**0.88**
LSD 0.01	**18.62**	**9.85**	**1.85**	**0.14**	**5.77**	**0.29**	**0.27**	**0.34**	**0.75**	**1.18**

G= Giza, E= Early, L= Line, T= Tester.

SCY/p: Seed cotton yield per plant, LY/p: Lint yield per plant, L%: Lint percentage, BW: Boll weight, BN/p: Number of bolls per plant, SI: Seed index, Mic.: Micronaire reading, Press.: Pressely index, UHM: Upper half mean and LUI: Lint uniformity index.

On the contrary, the lowest values were recorded for Giza 87 x Pima Early hybrid concerning BN/p and SCY/p as it gave 38.28 and 124.12g, respectively, Giza 87 x Pima S-1 hybrid showed the worst mean performance for the traits: LY/p and L% as it gave 47.30g and 35.99%, respectively. While Giza 87 x Pima S-6 hybrid showed the lowest SI (9.90g). Moreover, Giza 92 x Pima S-6 hybrid gave the worst values for the traits: Mic., UHM and LUI (3.93, 34.24mm and 85.80%, respectively). Giza 93 x Pima Early hybrid had the lowest values for BW (3.21g) and Press. (11.42).

In conclusion, it may be summed that Giza 87 and Giza 93 lines when crossed to the three testers: Pima Early, Pima S-1 and Pima S-6 did not produce any advantageous hybrid for all of the studied traits, as they yielded the worst values for seven out of the ten evaluated traits. Whereas Giza 92 and Giza 96 lines when crossed to the same testers produced beneficial hybrids which gave the highest values for all of the studied traits, Giza 96 ranked first and followed by Giza 92 line.

Our results were in accordance with previous studies that resulted significant genotypic differences among cotton varieties and their F_1 hybrids either in Egyptian cotton by Yehia & El-Hashash (2019), Mokadem et al. (2020), Amer et al. (2021) and Max et al. (2021) or in upland cotton by Patel et al. (2019), Manonmani et al. (2020), Gnanasekaran & Thiyagu (2021) and Chakholoma et al. (2022).

Genetic diversity among cotton genotypes

Cluster analysis in cotton clarifies more information about interrelationships among genotypes and displaying graphical assess for genetic diversity. Therefore, hierarchical cluster analysis exploiting Ward's method and interval Euclidean distance was used to assess the genetic distance and diversity among the tested cotton genotypes based on the various studied traits.

Data matrix for the similarity coefficients and Euclidean distance between the seven parental genotypes was shown in Table 4 and Fig. 1. Genotypes assorted in same cluster (intra-cluster) were predicted to be genetically similar more than genotypes assorted in different clusters (inter-cluster).

The similarity coefficient for the seven parental genotypes ranged from 65.12 between the cluster that comprised three genotypes (Giza 87, Giza 92 and Giza 93) and the cluster contained the other four genotypes (Giza 96, Pima Early, Pima S-1 and Pima S-6) up to 94.66 between the Egyptian varieties Giza 92 and Giza 93. While the level of genetic distance ranged from 4.100 between the Egyptian varieties Giza 92 and Giza 93 to 20.015 between Giza 87 and the cluster contained Giza 92 and Giza 93. This range of similarity and genetic distance among these genotypes reflected the presence of considerable extent of genetic variability and offer an opportunity to enhance the cotton attributes through crossing technique.

Cluster analysis assorted the seven cotton genotypes into six main groups according to the genetic similarity level which contributed the ten studied traits as shown from the Dendrogram presented in Fig.1. It's clear that three Egyptian genotypes (Giza 92, Giza 93 and Giza 96) in addition to the American genotype Pima Early were the most similar genotypes with narrow genetic distance (less than 5) and similarity level exceeded 90, while the other two American genotypes (Pima S-1 and Pima S-6) were grouped in one cluster with genetic distance reached 11.595 and similarity level of 84.91. Whereas the genotype Giza 87 and the cluster between Giza 92 and Giza 93 had the lowest similarity (76.75) that mainly ascribed to Giza 87.

TABLE 4. Genetic similarity coefficient and genetic distance between seven parental cotton genotypes based on Euclidean distance

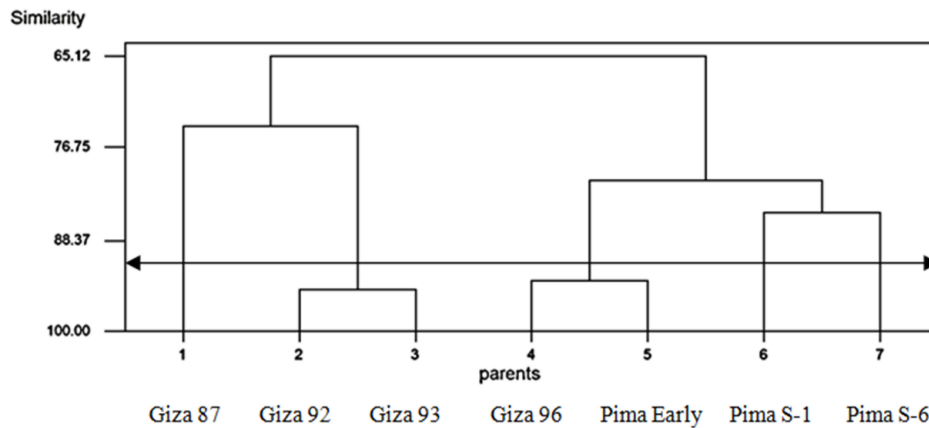| Step	Clusters joined	No. of obs. in new cluster	Similarity level	Distance level
1	2 , 3	2	94.66	4.100
2	4 , 5	2	93.57	4.938
3	6 , 7	2	84.91	11.595
4	4 , 6	4	80.88	14.689
5	1 , 2	3	73.95	20.015
6	1 , 4	7	65.12	26.797

Fig.1. Dendrogram for the seven parental cotton genotypes using average linkage (within groups)

Our findings were in accordance with those recorded by El-Fesheikawy et al. (2019), Amer (2020), EL-Mansy et al. (2020) and Max et al. (2021) who emphasized the high genetic similarity and the low distance between Egyptian cotton genotypes and the necessity to enrich the genetic pool and broaden the genetic base of the Egyptian cotton to increase the efficiency of the breeding program.

Heterosis

Heterosis which is the deflection of F_1 mean performance comparative to the mid-parents (MP) in percentage, and it point to the preponderance of F_1 hybrid above its parents for the studied traits. However, positive heterosis is desired for all the studied traits, except for Micronaire value that require negative heterosis for superiority. Significant heterotic effects in the desired direction were recorded in all studied traits for most hybrids as presented in Table 5.

Concerning seed cotton yield/plant (SCY/p), MP heterosis showed that eight hybrids in F_1 possessed significant or highly significant positive values which ranged from 9.91% for L3 x T3 hybrid to 21.12% for L2 x T3 hybrid. The rest four hybrids (L3 x T2 and L4 with the three testers) gave insignificant MP heterosis for this trait.

Regarding to lint yield/plant (LY/p), MP heterosis showed that eight hybrids in F_1 had significant or highly significant positive values which ranged from 14.66% for L4 x T2 hybrid to 24.85% for L1 x T3 hybrid. While, four hybrids (L3 x T2, L3 x T3, L4 x T1 and L4 x T3) showed insignificant heterotic effects.

In respect of lint percentage (L%), MP heterosis was significant and positive for five hybrids (L2 x T2, L3 x T3 and L4 with the three testers) with values reached 3.57, 3.63, 3.23, 4.11 and 3.09%, respectively. While the rest of hybrids showed insignificant heterotic effects.

For boll weight, MP heterosis revealed that ten hybrids showed highly significant positive values, one hybrid (L4 x T1) had significant and positive heterosis, while one hybrid (L4 x T2) showed insignificant value. Significant values ranged from 3.44% for L4 x T1 hybrid to 7.83% for L3 x T2 hybrid.

In regard to boll number/plant, two hybrids i.e. L1 x T1 and L3 x T1 had highly significant MP heterosis of 12.69 and 13.64%, respectively, in addition, two hybrids i.e. L2 x T2 and L2 x T3 showed significant values of 10.20 and 10.03%, respectively, whereas the rest of hybrids showed insignificant heterosis. With reference to seed index (SI), results showed that seven hybrids possessed significant or highly significant positive heterosis which ranged from 1.92% for L2 x T1 hybrid to 2.90% for L2 x T2 hybrid. The rest five hybrids (L1 x T2 and L1 x T3, L3 x T1, L4 X T1 and L4 x T2) showed insignificant MP heterosis for this trait.

It might be concluded that Giza 92 line showed the highest values of positive heterosis for cotton yield and its components when crossed to the three tested testers followed by Giza 87 line that ranked second in this respect. On the other hand Pima Early tester showed the highest values of positive heterotic effects for cotton yield and its components when crossed to three out of the four tested lines.

TABLE 5. Mid-parent (MP) heterosis in 12 F₁ hybrids for the studied traits

Genotypes	Seed cotton yield and its components						Fiber quality			
	SCY/p (g)	LY/p (g)	L%	BW (g)	BN/p	SI (g)	Mic.	Press.	UHM (mm)	LUI%
L1 x T1	16.71**	21.87**	1.64	5.83**	12.96**	2.09*	-1.37	1.60	1.51*	1.45**
L1 x T2	11.76*	15.09*	1.72	6.56**	7.02	1.11	-2.60	1.15	1.04	-0.07
L1 x T3	16.20**	24.85**	0.21	5.34**	6.49	0.76	-2.70	-0.06	0.88	0.14
L2 x T1	13.53*	22.18**	1.60	4.27**	9.17	1.92*	-3.77*	-0.50	1.54*	-0.06
L2 x T2	15.54**	15.83*	3.57*	4.73**	10.20*	2.90**	-6.70**	1.04	1.55*	-0.03
L2 x T3	21.12**	19.86**	1.57	4.49**	10.03*	2.09*	-2.48	1.32	0.12	-0.61
L3 x T1	13.06*	17.35*	0.91	4.52**	13.64**	1.53	-1.30	2.34*	1.65*	1.31**
L3 x T2	8.27	9.49	2.34	7.83**	4.78	2.66**	-5.15*	2.35*	1.59*	-0.52
L3 x T3	9.91*	9.99	3.63*	5.12**	3.57	2.03*	-5.13*	1.29	2.11**	-0.87
L4 x T1	9.05	-1.05	3.23*	3.44*	6.68	1.39	-4.00*	0.88	1.36*	-0.46
L4 x T2	6.72	14.66*	4.11*	2.76	4.39	1.40	-4.37*	1.86	1.95*	-0.49
L4 x T3	8.10	5.69	3.09*	4.20**	-0.57	1.96*	0.88	1.25	0.93	-0.81
LSD 0.05	12.02	6.36	1.19	0.09	3.73	0.19	0.18	0.22	0.48	0.76
LSD 0.01	16.12	8.53	1.60	0.12	5.00	0.25	0.24	0.30	0.65	1.02

* and ** denote significant at 0.05 and 0.01 levels of probability, respectively.

L1= G.87, L2= G.92, L3= G.93, L4= G.96, T1= Pima Early, T2= Pima S-1 and T3= Pima S-6.

SCY/p: Seed cotton yield per plant, LY/p: Lint yield per plant, L%: Lint percentage, BW: Boll weight, BN/p: Number of bolls per plant, SI: Seed index, Mic.: Micronaire reading, Press.: Pressely index, UHM: Upper half mean and LUI: Lint uniformity index.

With respect to fiber quality traits, Micronaire reading (Mic.) that is an indicator to both fiber fineness and maturity, MP heterosis showed desirable significant and negative values for six hybrids (L2 x T1, L2 x T2, L3 x T2, L3 x T3, L4 x T1and L4 x T2) and ranged from -3.77% to -6.70% for L2 x T1 and L2 x T2 hybrids, respectively. The rest six hybrids showed insignificant heterotic effects. In connection with fiber strength as Pressely index (Press.), only two hybrids (L3 x T1 and L3 x T2) showed significant positive MP heterosis, the values were 2.34 and 2.35%, respectively. The rest of hybrids showed insignificant values.

Respecting fiber length measured as the upper half mean (UHM), results concerning MP heterosis revealed that eight hybrids possessed significant positive values which ranged from 1.36% for L4 x T1 hybrid to 2.11% for L3 x T3 hybrid. The rest four hybrids (L1 x T2, L1 x T3, L2 x T3 and L4 x T3) showed insignificant MP heterosis for such trait. Lint uniformity index (LUI%) disclosed highly significant and positive MP heterosis in only two hybrids L1 x T1 and L3 x T1 with values of 1.45 and 1.31%, respectively. The rest 10 hybrids showed insignificant negative values in most cases.

It might be concluded that Giza 93 line had the most desired values of heterosis for fiber traits when crossed to the three testers followed by Giza 92

and Giza 96 lines, while Giza 87 line did not show desirable significant heterosis in most cases.

Similar significant heterotic effects in cotton traits were recorded by Khokhar et al. (2018), Chaudhary et al. (2019), Mokadem et al. (2020), Amer et al. (2021), Gnanasekaran & Thiyagu (2021) and Max et al. (2021).

Combining ability effects:

Significant mean squares for lines and testers (GCA) as well as line x tester interactions (SCA) as shown in Table 2, reflected the presence of both additive and non-additive gene actions in the expression of the studied traits.

General Combining Ability effects (GCA)

GCA was defined as the mean performance of a genotype (line or tester) in a series of its hybrids, the good combiner genotype that capable of giving hybrids with high expression of a specified trait. The relative contribution of each separate parent to enhance a trait in the population might be estimated by comparing the GCA values for the tested parents (Kempthorne, 1957).

Results concerning the estimated GCA effects for the tested lines and testers were presented in Table 6.

TABLE 6. Estimates of general combining ability (GCA) effects from line x tester analysis for seven parental cotton genotypes for the studied traits

Genotype	Seed cotton yield and its components						Fiber quality			
	SCY/p (g)	LY/p (g)	L %	BW (g)	BN/p	SI (g)	Mic.	Press.	UHM (mm)	LUI %
Lines										
G. 87	-8.97**	-2.28**	-1.19**	-0.009	-2.61**	-0.222*	-0.117*	0.001	0.29**	0.319**
G. 92	3.58**	1.22**	-0.31*	0.0003	1.08**	0.199**	0.128**	0.098*	-0.78**	-0.219**
G. 93	-2.37*	-1.44**	-0.42**	-0.005	-0.65	0.034	0.017	-0.052	0.15*	0.031
G. 96	7.75**	2.50**	1.92**	0.014*	2.17**	-0.011	-0.028	-0.047	0.33**	-0.131*
LSD 0.05	5.668	2.998	0.562	0.043	1.76	0.096	0.096	0.105	0.22	0.358
LSD 0.01	7.600	4.020	0.753	0.057	2.35	0.128	0.128	0.140	0.30	0.480
Testers										
P. Early	-6.67**	-2.71*	-0.12	-0.046*	-1.56*	-0.088*	0.047	-0.135**	0.353**	0.014
P. S-1	-0.74	-0.79	-0.49*	0.005	-0.76	0.117**	-0.153**	0.096*	-0.186	0.313**
P. S-6	7.40**	3.50**	0.61**	0.041*	2.32**	-0.029	0.106*	0.039	-0.168	-0.299*
LSD 0.05	4.91	2.59	0.48	0.037	1.52	0.083	0.083	0.091	0.194	0.229
LSD 0.01	6.58	3.48	0.65	0.050	2.04	0.111	0.111	0.122	0.260	0.307

* and ** denotes significant differences at 5% and 1% probability levels, respectively.

G= Giza and P= Pima.

SCY/p: Seed cotton yield per plant, LY/p: Lint yield per plant, L%: Lint percentage, BW: Boll weight, BN/p: Number of bolls per plant, SI: Seed index, Mic.: Micronaire reading, Press.: Pressely index, UHM: Upper half mean and LUI: Lint uniformity index.

Among the seven parental genotypes used in this study, the highest positive and desirable GCA effects were exhibited by Giza 96 line for the traits: SCY/p, LY/p, L%, BW, BN/p and UHM, the values were: 7.75, 2.50, 1.92, 0.014, 2.17 and 0.33, respectively, for the aforementioned traits. Giza 92 line ranked second in this respect as it showed positive and desirable GCA effects for the traits: SCY/p, LY/p, BN/p, SI and Press. with values reached 3.58, 1.22, 1.08, 0.199 and 0.098, respectively.

Giza 87 line ranked third with significant positive GCA effects for the traits UHM and LUI with values of 0.29 and 0.319, respectively, as well as significant and desirable negative GCA for Mic. with value of -0.117, whereas it did not have any desirable GCA effects for the seed cotton yield and its component traits. While Giza 93 line did not have any significant positive GCA effects for all the tested traits, except for UHM with value of 0.15.

Hence, two lines (Giza 96 and Giza 92) might be considered as the best combiners for the yielding traits, while Giza 87 line was the best combiner for fiber traits, whereas Giza 93 line had

the worst GCA effects for almost all of the studied traits and might be rated as the poorest combiner.

On the other hand, GCA effects for the tested testers cleared that Pima S-6 tester showed significant and desirable GCA effects for the yielding traits: SCY/p, LY/p, L%, BW and BN/p with values reached 7.40, 3.50, 0.61, 0.041 and 2.32, respectively, and might be classified as the best combiner among testers for the yielding traits. Pima S-1 showed desirable significant GCA effects for all fiber quality traits except UHM and might be classified as the best combiner tester for fiber quality traits. Whereas Pima Early did not show any desired GCA effects except for UHM that showed significant positive value (0.353) and might be considered as the poorest combiner tester.

Significant positive GCA of the tested parents indicated the distinction of the additive gene action and/or additive x additive interaction (when epistasis is present) in the inheritance of studied traits (Khokhar et al., 2018; Max et al., 2021). Furthermore, parents with higher mean performance coupled with positive and significant GCA effects may possess more numeral of the

additive genes and can gather favorable genes in a few genotypes, whereas, parents with negative GCA effects lead mostly to the reduction of the trait (Gnanasekaran & Thiyagu, 2021). Therefore, in the present study, parents with positive and high GCA i.e.: Giza 96, Giza 92 and Pima S-6 for yielding ability as well as Giza 87 and Pima S-1 for fiber quality traits, were the best combiners and were recommended to be used in breeding programs to improve cotton traits.

Our findings were in harmony with those reported in earlier studies by Khokhar et al. (2018), Yehia & El-Hashash (2019), Mokadem et al. (2020), Amer et al. (2021) and Chakholoma et al. (2022)..

Specific combining ability effects (SCA)
The SCA is the performance of particular hybrid combinations (poorer or better) than the predictable based on their parents mean performances. Hence, SCA is useful for identification of prospective hybrids with high mean performances and reasonable level of stability, differences of SCA have been ascribed to the non-additive (dominance or epistasis) gene action (Sprague & Tatum, 1942;

Griffing, 1956).

Results of SCA effects for 12 hybrids concerning the studied traits were presented in Table 7. Significant positive or negative SCA variances were detected for some traits which clarify the presence of non-additive gene action (dominance or epistasis) in inheritance of these traits. Negative SCA indicates unfavorable combinations of parents. Low mean performance and negative SCA effects were desirable for Micronaire reading.

For seed cotton yield/plant, four hybrids i.e. L_2 x T_3, L_3 x T_1, L_4 x T_2 and L_4 x T_3 showed significant positive SCA values which were: 3.98, 3.62, 1.62 and 2.27, respectively, while two hybrids L_2 x T_1 and L_4 x T_1 had significant negative SCA effects with values of -3.59 and -3.88, respectively. For lint yield/ plant, four hybrids i.e. L_1 x T_3, L_3 x T_1, L_4 x T_2 and L_4 x T_3 showed significant positive SCA values that were: 2.72, 2.12, 1.51 and 2.41, respectively, while L_4 x T_1 hybrid had significant negative SCA value (-3.93). The rest of hybrids showed insignificant SCA effects.

TABLE 7. Specific combining ability (SCA) estimates from line × tester analysis for 12 cotton hybrids in F_1 generation for the studied traits

Genotypes	Seed cotton yield and its components						Fiber quality			
	SCY/p (g)	LY/p (g)	L %	BW (g)	BN/p	SI (g)	Mic.	Press.	UHM (mm)	LUI %
L1 x T1	1.12	-0.87	0.331	0.050	-1.19	0.281*	0.108	0.104	0.426**	-0.256
L1 x T2	-1.16	-1.85	-0.033	0.033	-1.30	-0.135	0.142	-0.025	-0.199	0.532*
L1 x T3	0.04	2.72*	-0.297	-0.083*	2.48	-0.146	-0.250*	-0.080	-0.227	-0.276
L2 x T1	-3.59**	0.95	-1.092*	0.016	-1.50	-0.164	-0.173*	0.223**	-0.118	-0.506*
L2 x T2	-0.39	-1.07	-0.157	-0.029	-1.67	0.337**	0.096	0.241**	-0.061	0.241
L2 x T3	3.98**	0.13	1.249*	0.013	3.17*	-0.173	0.077	-0.464**	0.179	0.265
L3 x T1	3.62*	2.12*	-0.182	-0.023	1.59	-0.149	0.175*	-0.086	-0.100	0.524*
L3 x T2	-1.98	-0.72	0.921*	0.046	1.68	0.035	0.098	0.142*	-0.044	-0.260
L3 x T3	-1.64	-1.39	-0.739*	-0.024	-3.28*	0.115	-0.077	-0.057	0.144	-0.265
L4 x T1	-3.88**	-3.93**	-2.974**	0.123**	-6.76**	-0.145	-0.181*	-0.076	0.303*	0.444*
L4 x T2	1.62*	1.51*	1.256*	-0.249**	3.08*	0.259*	0.375**	0.135*	-0.679**	-0.251
L4 x T3	2.27**	2.41**	1.718**	0.126**	3.69**	-0.114	-0.194*	-0.059	0.376**	-0.193
LSD 0.05	**5.19**	**3.23**	**0.973**	**0.077**	**1.34**	**0.162**	**0.144**	**0.133**	**0.295**	**0.413**
LSD 0.01	**6.96**	**4.41**	**1.305**	**0.103**	**2.08**	**0.204**	**0.193**	**0.195**	**0.413**	**0.605**

* and ** denote significant at 0.05 and 0.01 levels of probability, respectively.

L1= G.87, L2= G.92, L3= G.93, L4= G.96, T1= Pima Early, T2= Pima S-1 and T3= Pima S-6.

SCY/p: Seed cotton yield per plant, LY/p: Lint yield per plant, L%: Lint percentage, BW: Boll weight, BN/p: Number of bolls per plant, SI: Seed index, Mic.: Micronaire reading, Press.: Pressely index, UHM: Upper half mean and LUI: Lint uniformity index.

Concerning lint%, four hybrids i.e. L_2 x T_3, L_3 x T_2, L_4 x T_2 and L_4 x T_3 showed significant positive SCA values that were: 1.249, 0.921, 1.256 and 1.718, respectively, while L_2 x T_1 and L_3 x T_3 hybrids showed significant negative SCA values (-1.092 and -2.974, respectively). Regarding boll weight, two hybrids L_4 x T_1 and L_4 x T_3 showed significant positive SCA values that were 0.123 and 0.126, respectively, while L_1 x T_3 and L_4 x T_2 hybrids had significant negative SCA values (-0.083 and -0.249, respectively). The rest of hybrids had insignificant SCA values.

For number of bolls/plant, three hybrids L_2 x T_3, L_4 x T_2 and L_4 x T_3 showed significant positive SCA values that were 3.17, 3.08 and 3.69, respectively while L_3 x T_3 and L_4 x T_1 hybrids showed significant negative SCA values (-3.28 and -6.76, respectively). For seed index, three hybrids i.e. L_1 x T_1, L_2 x T_2 and L_4 x T_2 had significant positive values of SCA that were 0.281, 0.337 and 0.259, respectively.

On the other hand, fiber quality traits showed some desired SCA effects, in regard to micronaire reading, four hybrids: L_1 x T_3, L_2 x T_1, L_4 x T_1 and L_4 x T_3 had significant negative (desirable) SCA values which were -0.250, -0.173, -0.181 and -0.194, respectively, whereas L_3 x T_1 and L_4 x T_2 hybrids gave significant positive (undesirable) SCA values of 0.175 and 0.375, respectively. While the rest of hybrids showed insignificant SCA effects.

Respecting fiber strength expressed as Pressely index, four hybrids i.e. L_2 x T_1, L_2 x T_2, L_3 x T_2 and L_4 x T_2 showed significant positive SCA values which were 0.223, 0.241, 0.142 and 0.135, respectively, while L_2 x T_3 hybrid gave significant negative SCA value of -0.464.

With respect to fiber length expressed as upper have mean, three hybrids i.e. L_1 x T_1, L_4 x T_1 and L_4 x T_3 showed significant positive SCA values which were 0.426, 0.303 and 0.376, respectively, whereas the hybrid L_4 x T_2 showed significant negative SCA value of -0.679.

Concerning lint uniformity index, three hybrids i.e. L_1 x T_2, L_3 x T_1 and L_4 x T_1 had significant positive values which were 0.532, 0.524 and 0.444, respectively, whereas L_2 x T_1 hybrid had significant negative SCA value of -0.506. While the rest of hybrids showed insignificant SCA effects.

The highest significant desirable SCA effects with concern to yield and its components traits were recorded for L_4 x T_3 hybrid (Giza 96 x Pima S-6), followed by L_4 x T_2 hybrid (Giza 96 x Pima S-1). Concerning fiber quality traits, L_4 x T_1 hybrid (Giza 96 x Pima Early) showed significant desirable SCA effects for all fiber traits except Pressely index, followed by L_4 x T_3 hybrid (Giza 96 x Pima S-6) that showed desirable SCA effects for Micronaire reading and upper half mean, while L_2 x T_1 hybrid (Giza 92 x Pima Early) showed desirable SCA effects for Micronaire reading and Pressely index.

Hybrids that showed significant and desirable SCA effects resulted from crossing between two parents, at least one of them possessed high desirable GCA effects. Similarly, Basal et al. (2017) and Munir et al. (2018) indicated that superior hybrids for yield and its components had at least one parent with good GCA. In this respect, Singh et al. (2010) concluded that when two good general combiner parents produce high SCA effects that may be ascribe to the involvement of additive genes. Whereas, high mean performance coupled with significant positive GCA effects for one of the parents for a trait but their hybrid shows insignificant SCA effects for the same trait it may be due to the lack of co-adaptation between favorable alleles of the parents for this trait (Munir et al., 2018; Gnanasekaran & Thiyagu, 2021).

Our results were in accordance with those reported in Egyptian cotton by Al-Hibbiny et al. (2019), Mokadem et al. (2020), Amer et al. (2021) and Max et al. (2021) and in upland cotton by: Basal et al. (2017), Munir et al. (2018), Chaudhary et al. (2019), Gnanasekaran & Thiyagu (2021) and Chakholoma et al. (2022).

Variance of combining ability
Information concerning gene action help cotton breeder to select appropriate parents for hybridization in addition to choose the proper breeding procedures for improving the various traits. Therefore, variances of the combining ability were estimated for the studied traits and displayed in Table 8.

TABLE 8. Combining ability variances and proportional contributions of lines, testers and their interactions in F$_1$ generation for the studied traits

Traits	Combining ability variances			Proportional contributions %		
	δ^2_{GCA}	δ^2_{SCA}	$\delta^2_{GCA}/\delta^2_{SCA}$	Lines	Testers	Line x Tester
Seed cotton yield/plant	17.79	28.62	0.622	16.59	34.74	48.67
Lint yield/plant	3.49	5.29	0.660	14.23	32.42	53.35
Lint %	0.144	0.520	0.277	21.27	28.85	49.88
Boll weight	0.0013	0.0017	0.765	18.00	31.38	50.62
Boll Number/plant	0.685	1.025	0.668	19.34	23.92	56.74
Seed Index	0.0042	0.0035	1.200	23.53	50.18	26.29
Micronaire reading	0.051	0.045	1.133	29.32	24.67	46.01
Pressely index	0.0032	0.0044	0.727	31.68	15.96	52.36
Upper half mean	0.0033	0.0052	0.635	35.83	17.08	47.09
Lint uniformity index	0.064	0.112	0.571	50.29	18.53	31.18

δ^2_{GCA}: Variance due to GCA, δ^2_{SCA}: Variance due to SCA.

Results exhibited that variances due to SCA were greater than those due to GCA for all the studied traits (except for seed index and micronaire reading) which clarify that non-additive gene action (dominance or epistasis) has the important role in controlling these traits as compared to the additive gene action. These findings were confirmed by their ratio ($\delta^2_{GCA}/\delta^2_{SCA}$) that was less than the unity. These results may be attributed to the intensive selection on the studied genotypes. Consequently, the studied traits might be improved through hybrid breeding to exploit heterosis while selection has to delay to later generations until genes are settled.

Contrarily, additive type of gene action was important for controlling seed index and Micronaire reading as the δ^2_{GCA} was higher than δ^2_{SCA} and their ratio exceeded the unity. Hence, recurrent selection that increases the frequency of favorable alleles and detects superior combinations might be the best breeding method for improving these traits. In this respect, Munir et al. (2018) stated that traits which controlled by additive genes have high heritability in narrow sense, though such traits might be improved by simple selection procedures in early segregating generations.

The higher values of GCA, SCA and heterosis reflecting the great probability to select the prospective genotype for explicit traits that could be exploited for improving yield and fiber quality in cotton.

Our results were in accordance with the results in upland cotton of Khokhar et al. (2018) and Gnanasekaran & Thiyagu (2021) as well as in Egyptian cotton of Yehia & El-Hashash (2019), Mokadem et al. (2020), Amer et al. (2021) and Max et al. (2021) who found that the SCA variance was higher than GCA and non-additive gene effects were more important than additive gene effects for cotton characters. On the contrary, Basal et al. (2017), Munir et al. (2018) and Chakholoma et al. (2022) found that GCA variances were higher than SCA ones for some cotton traits specially fiber traits, indicating the importance of additive gene actions for controlling these traits.

Proportional contribution

The percentage of relative contributions for the tested lines, testers and their interactions in F$_1$ generation for the studied traits were given in Table 8. The line x tester interaction contributions were greater than lines and testers contributions for all studied traits (except for seed index and lint uniformity index) reflecting the importance of non-additive (dominance or epistasis) type of gene action in controlling these traits. On the other hand, the line's contributions were higher than tester's for fiber quality traits indicating that considerable amount of variance were attributed to the maternal effect. While the tester's contributions were greater than those of line's for yield and its components.

Our findings were in accordance with those of Khokhar et al. (2018), Yehia & El-Hashash (2019),

Mokadem et al. (2020) and Amer et al. (2021) who found that line × tester contributions were greater than individual contribution of both lines and testers for most traits. Whereas, Gnanasekaran & Thiyagu (2021) as well as Hamed & Said (2021) found that proportion contributions of lines were greater than those of testers and line x tester interactions for the studied traits.

Conclusion

Variances of GCA and SCA were significant reflecting the importance of both additive and non-additive gene actions in controlling the studied traits. Variance of SCA was greater than GCA denoting that non-additive gene action was more important in controlling the studied traits. Giza 96 line and Pima S-6 tester were the best combiners for yield and its components, Giza 87 line and Pima S-1 tester were the best combiners for fiber traits. Giza 96 x Pima S-6 hybrid had the best SCA effects. Hence these genotypes were considered as promising for improving cotton traits in breeding programs.

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تحديد الآباء والهجن المتميزة لصفات المحصول ومكوناته وجودة التيلة فى القطن

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تهدف هذه الدراسة الي تقدير قوة الهجين والقدرة علي الائتلاف لصفات المحصول ومكوناته وجودة التيلة في الهجن الناتجة من تهجين أربعة أصناف مصرية من القطن كسلالات وهي جيزة 87، جيزة 92، جيزة 93، جيزة 96 مع ثلاثة تراكيب وراثية أجنبية ككشافات وهي بيما س1 وبيما س6 باستخدام طريقة تحليل السلالة × الكشاف وذلك في محطة سخا للبحوث الزراعية بمحافظة كفر الشيخ خلال ثلاثة مواسم (2018-2020). وكانت اهم النتائج المتحصل عليها كما يلي:

1- أظهرتحليل التباين وجود فروق معنوية بين جميع التراكيب الوراثية المستعملة وكذلك بين الآباء وبعضها وبين الهجن الإثنى عشر. كما وجدت فروق معنوية عند مقارنة الآباء مع الهجن وبين السلالات وبعضها وبين الكشافات وبعضها وبين السلالات مع الكشافات لمعظم الصفات المدروسة.

2- أظهر الصنف جيزة 96 (سلالة) والصنف بيما س٦ (كشاف) والهجين جيزة96 × بيما س6 أفضل قيم لصفات المحصول ومكوناته بينما أعطى الصنف جيزة 87(سلالة) والصنف بيما س1 (كشاف) والهجين جيزة96 × بيماس1 أفضل القيم لصفات جودة التيلة.

3- أظهرت معظم الهجن المدروسة قيم معنوية ومرغوبة من قوة الهجين كمتوسط الأبوين لمعظم الصفات المدروسة، وأعطى الصنف جيزة 92 (سلالة) أفضل قيم موجبة لقوة الهجين لصفات المحصول ومكوناته عند تهجينه مع الكشافات الثلاثة المستعملة، بينما أعطى الصنف بيما س1 (كشاف) أفضل قيم موجبة لقوة الهجين لصفات المحصول ومكوناته عند التهجين مع ثلاثة سلالات من الأربعة المستعملة.

4- كانت قيم القدرة العامة وكذلك القدرة الخاصة على الإئتلاف معنوية لغالبية الصفات مما يدل على مشاركة كل من الفعل الجينى الإضافى والسيادى فى توراث الصفات المدروسة.

5- أعطى الصنفان جيزة 96(سلالة) وبيماس6(كشاف) أفضل قدرة عامة علي الائتلاف لصفات المحصول ومكوناته بينما أظهر الصنفان جيزه 87(سلالة) وبيما س1(كشاف) أفضل القيم لصفات جودة التيلة. كذلك أظهر الهجين جيزة96 × بيما س6 أفضل قيم للقدرة الخاصة على الإئتلاف لصفات المحصول ومكوناته بينما أعطى الهجين جيزة96 × بيما س1 أفضل القيم لصفات جودة التيلة.

6- كان تباين القدرة الخاصة على الائتلاف أعلى من تباين القدرة العامة على الائتلاف لكل الصفات المدروسة (ماعدا صفتى معامل البذرة وقراءة الميكرونير) مما يشير إلى أهمية الفعل الجينى غير الإضافى (سيادة وتفوق) فى توراث هذه الصفات، بينما كان لفعل الجين الإضافى الدور الأكبر فى وراثة صفتى معامل البذرة وقراءة الميكرونير.

7- أظهر تقدير نسبة المساهمة أن مساهمة التفاعل بين السلالة والكشاف كان أعلي من مساهمة كل من السلالات والكشافات لكل الصفات المدروسة فيما عدا صفتى معامل البذرة ومعدل إنتظام الطول مما يؤكد على أهمية الفعل الجينى غير الإضافى (سيادة وتفوق) فى توراث هذه الصفات.

8- إتضح من النتائج أنه يمكن إستخدام الصنفين جيزة 96وبيما س6 والهجين جيزة 96 × بيما س6 في برامج تربية القطن لزيادة القدرة الإنتاجية للأصناف الجديدة بينما يمكن إستعمال الصنفين جيزة 87 وبيما س1 والهجين جيزة 96 × بيما س1 لتحسين صفات جودة الألياف.

9- كانت نسبة التماثل الوراثى عالية (أكبر من 90%) بين الأصناف جيزة 92، جيزة 93، جيزة 96وبيما مبكر. بينما كانت نسبة التماثل الأقل (73.95%) بين الصنف جيزة 87 والعقدة بين الصنفين جيزة 92 وجيزة 93. كانت نسبة التماثل بين الصنفين بيما س1 وبيما س6 أقل منها بين الأصناف المصرية حيث بلغت 84.91% ويمثلان عقدة واحدة.