GENETIC ANALYSIS FOR YIELD AND FIBER QUALITY TRAITS IN EGYPTIAN COTTON (*Gossypium barbadense* L.)

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ABSTRACT

This work was achieved during three seasons (2018-2020) at Sakha Experimental Station, Kafr El-Sheikh Governorate, Egypt. Four Egyptian cotton varieties (Giza 92, Giza 93, Giza 96 and Giza 87) used as lines and three genotypes (C.B 58, Russ.6022 and Aust.10229) as testers in line x tester mating design. Combining ability, genetic components and heritability were estimated in F_1 and F_2 generations for yield, its components and fiber properties. Genotypes varied significantly for all traits, Giza 92, Giza 96 and Russ.6022 gave the highest yield, Giza 87 had the best fiber properties. Giza 96 x Russ.6022 cross gave the highest yield, Giza 87 x Aust.10229 had the best fiber traits. Significance of GCA and SCA indicated that additive and non-additive gene actions are controlling the studied traits. Giza 92 was the best combiner for yield and fiber strength, followed by Giza 96, while Giza 87 and Russ.6022 were the best combiners for fiber traits. Giza 92 x Russ.6022 showed the highest significant desirable SCA effects. The SCA variance was higher than GCA for most traits indicating that non-additive gene action was controlling these traits, whereas additive type was prevalence for lint% and fiber length. Broad sense heritability was low for boll weight, intermediate for fiber length and large for the rest of traits. Narrow sense heritability was low to intermediate for all traits. Giza 92 and Giza 96 and the cross Giza 92 x Russ.6022 were promising for improving yield in breeding programs.

Key words: *Egyptian Cotton, Line x Tester, Combining ability, Gene action, Heterosis, Heritability.*

INTRODUCTION

The main target of cotton (*Gossypium* Sp.) breeding program is introducing new lines or varieties with higher yield potential and better fiber quality than the commercial varieties. The first procedure in efficacious breeding program is choice of beneficial genotypes as parents to be used in efficient hybridization programs.

Combining ability proposed by Sprague and Tatum (1942) is an effective biometrical approach that refers to the ability of a genotype to transfer strong expression of a trait to its hybrids, also it distinguish between good and poor combiners and develop best hybrid with wide environmental adaptation, thereby helps breeders to pick out proper parents for hybridization, it also distinguish the eminent specific cross combinations.

General combining ability (GCA) is an efficient indicator for the value of genotypes in hybrid combinations, good GCA is the ability of a genotype to produce hybrids with high genetic quality, when crossed to many other genotypes in the population, differences in GCA effects have been ascribed to additive and additive x additive gene action. While

specific combining ability (SCA) is useful for recognition of potential hybrids with higher performance and reasonable level of stability, good SCA means that the progeny from a particular full-sib cross perform better than the expected from the GCA of parents, differences in SCA have been attributed to non-additive (dominance or epistasis) gene action (Sprague and Tatum, 1942; Griffing, 1956). Hence, GCA is beneficial for hybridization and selection programs, while SCA is advantageous for hybrid crop production (Jatoi *et al*., 2011).

Selection of parental genotypes that will be used for augmenting yield and fiber quality traits is a ticklish step in cotton breeding program. Parents are picked for their mean performance and GCA effects. Parents with high mean performance and positively significant GCA effects are generally desired for all plant attributes except earliness traits, seed index and fiber fineness. Furthermore, the crosses developed by hybridization must be analyzed for their performance, SCA effects and standard heterosis over a check genotype to adopt the breeding procedures to be followed for these crosses (Gnanasekaran and Thiyagu, 2021).

The line x tester analysis is a simple and influential mating design that evaluates large number of genotypes for detecting suitable parents and superior crosses for the traits under concern, in addition to the information concerning the nature and proportion of gene action participated in the expression of these traits which is very decisive for choosing the eligible parents and crosses for crop improvement (Kempthorne, 1957).

Cotton breeding scientists have been widely exploited the line x tester design for improving cotton yield, its components and fiber properties in Egyptian cotton (*G. barbadense* L.) as recorded by: Orabi *et al*., 2017; Sultan *et al*., 2018; Yehia and El-Hashash, 2019; Mokadem *et al*., 2020; Hamed and Said, 2021 and Max *et al*., 2021. as well as in upland cotton (*G. hirsutum* L.) as recorded by: Baloch *et al*., 2016; Basal *et al*., 2017; Khokhar *et al*., 2018; Unay *et al*., 2019, Chapara *et al*., 2020 and Gnanasekaran and Thiyagu, 2021

The aims of the present research were to assess the mean performance, GCA, SCA, heritability and heterosis estimates for yield, yield components and fiber quality traits among four Egyptian extra-long staple varieties that

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were used as female parents (lines) and pollinated by three exotic varieties as testers, in addition to identify favorable parents and crosses in F_1 and F_2 generations for the studied traits by exploiting line $\times$ tester mating system.

MATERIALS AND METHODS

The present study was accomplished at Sakha Experimental Research Station, Agriculture Research Center, Kafr El-Sheakh Governorate, Egypt, through three successful growing seasons (2018–2020). The genetic materials included seven cotton genotypes belonging to *Gossypium barbadense* L., four Egyptian extra-long staple varieties i.e. Giza 92, Giza 93, Giza 96 and Giza 87, in addition to C.B 58 and Russ. 6022 (Russian varieties) as well as Aust. 10229 (Australian strain)**.**

Pure selfed seeds of all genotypes were obtained from Cotton Research Institute, Agric. Res. Center, Giza, Egypt. In 2018 season, pure seeds of these genotypes were sown on 21st of April according to line x tester mating system. The four Egyptian genotypes: Giza 92, Giza 93, Giza 96 and Giza 87 were used as lines (females), while, the three exotic genotypes: C.B 58, Russ.6022, and Aust.10229 were used as testers (males) to produce the hybrid seeds of twelve F_1's crosses.

In 2019 season, parents and F_1 seed were sown on 24th of April and crossing were repeated in the same manner to produce F_1 seeds again, while F_1 plants were self-pollinated at flowering period to produce the F_2's seeds. In 2020 season, seeds of the seven parents and their twelve crosses in both F_1 and F_2 generations were sown on 28th of April in randomized complete block design with three replications. The experimental plot included four rows for parents and F_1 hybrids and six rows for F_2 hybrids, each row was 4.0 m long and 0.65 m wide, hills were spaced 0.40 m apart to give 10 hills/ row, with one plant left per hill. All normal cultural practices were adopted for plants during the three growing seasons.

Data were recorded on individual plant basis for the following traits

Boll weight in grams (BW); seed cotton yield (SCY/P) and lint yield/plant (LY/P) in grams; lint percentage (L%= lint yield x 100/ seed cotton yield); fiber fineness as 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; length 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:

The prime step in line x tester analysis is implement analysis of variance for genotypes (parents and crosses), if the differences among them were significant, line x tester analysis can be performed. So the analysis of variance was achieved according to Singh and Chaudhary (1985), then line x tester analysis as suggested by Kempthorne (1957) was used for partitioning the genetic variance of the F_1 and F_2 top-crosses due to lines, testers and their interactions and providing information about general and specific combining ability of the parents and crosses, as well as the estimates of various types of gene effects. The significance of differences among means and the significance of heterosis were determined using the least significant difference test (L.S.D) as described by Singh and Chaudhary (1985). Heritability was estimated in broad ($h^2_b\%$) and narrow ($h^2_n\%$) senses according to the formula proposed by Mather (1949).

RESULTS AND DISCUSSION

Analysis of variance

Mean squares resulted from the analysis of variance for yield, yield components and fiber quality traits for the tested genotypes (seven parents and their 12 crosses in F_1 and F_2 generations) are presented in Table (1). Results showed significant or highly significant genotypic differences for all the studied traits in both F_1 and F_2 generations revealing the presence of sufficient genetic variability among genotypes as the parents or crosses did not behave the same for the studied traits. In addition, mean squares due to parents were also significant for all the studied traits in F_1 and F_2 generations; moreover, mean squares due to crosses were significant for all traits in both generations (except for Mic. in F_1 generation). Mean squares

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Table 1. Mean squares from line x tester analysis for seven cotton parents and their crosses in F_1 and F_2 generations for the studied traits

Source Of Variance	d.f	BW (g)		SCY/plant (g)		LY/plant (g)		Lint %	
		F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Reps	2	0.002	0.053	9.72	25.41	4.48	10.75	0.53	0.76
Genotypes	18	0.042**	0.102**	1002.4**	1236.7**	185.56**	215.66**	7.92**	10.40**
Parents (P)	6	0.036**	0.089**	1481.8**	1544.5**	267.72**	296.56**	9.88**	12.87**
Crosses (C)	11	0.021**	0.072**	593.4**	616.8**	91.46**	123.41**	8.08**	10.55**
P vs. C	1	0.045**	0.105**	1834.2**	1871.7**	527.60**	576.91**	25.34**	11.82**
Lines (L)	3	0.032*	0.064**	824.7**	982.3**	141.99**	177.56**	11.00**	13.54**
Testers (T)	2	0.022**	0.120**	1292.1	1361.6**	195.19**	218.86**	3.05**	2.74
L x T	6	0.010	0.038**	178.30**	273.21**	142.12*	214.27**	2.01*	3.46**
Error	36	0.004	0.015	24.93	50.06	21.37	28.82	1.21	1.77
Source Of Variance	d.f	Mic.		Press.		UHM (mm)		LUI %	
		F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Reps	2	0.09	0.082	0.031	0. 053	1.186	0.935	0.019	0.434
Genotypes	18	0.124**	0.170**	0.083**	0.110**	3.520**	4.434**	1.577**	1.898**
Parents (P)	6	0.201**	0.263**	0.093**	0.128**	7.579**	10.117**	1.873**	2.634**
Crosses (C)	11	0.053**	0.081**	0.071**	0.095**	1.421**	1.867**	1.578**	1.786**
P vs. C	1	0.032**	0.075**	0.091	0.116**	0.007	0.016*	0.103**	0.210**
Lines (L)	3	0.091	0.127**	0.170**	0.218**	4.329**	5.732**	0.525**	0.797
Testers (T)	2	0.081	0.116**	0.057**	0.083**	0.448**	0.618**	4.936**	6.311**
L x T	6	0.023*	0.044	0.033	0.061	0.462	0.632	0.433**	0.525**
Error	36	0.014	0.043	0.022	0.043	0.402	0.490	0.282	0.311

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

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of parents versus crosses were significant in F_1 and F_2 hybrids for almost all of the studied traits which clarify the presence of the heterotic effects.

Accordingly, mean squares of the crosses in F_1 and F_2 generations were partitioned using line × tester analysis to: lines (females), testers (males) and line x tester interaction (crosses) as presented in (Table 1). Results revealed that, the mean squares among lines were significant for almost all traits in F_1 and F_2 generations (except for Mic. in F_1generation and LUI% in F_2 generation). Mean squares among testers were also significant for most of the studied traits in both generations (except for SCY and Mic. in F_1 generation and L% in F_2 generation), the significant mean squares for lines and testers indicating the importance of general combining ability (GCA) with additive genes.

Regarding the line × tester interaction, mean squares were significant for most traits (except for BW in F_1 and Mic. in F_2 as well as Press. and UHM in both generations), indicating specific combining ability (SCA) with dominant genes (Kempthorne, 1957). Significance of GCA for lines and testers as well as SCA for crosses indicating the participation of both additive and non-additive gene action in the expression of the studied traits.

Mean performance of genotypes

Mean performance for the seven parents and their 12 crosses in F_1 and F_2 generations for yield and yield component as well as fiber traits are presented in Table (2). Results showed that the parental genotypes used in this work varied significantly for all of studied traits, reflecting the different genetic back ground for these parents. The highest mean performance was found for the line Giza 92 for BW (3.03 g), SCY/P (147.11 g), LY/P (54.39 g) and Press. (11.92), while the line Giza 96 had the best means for L% (39.22%) and LUI% (87.75%), the line Giza 87 had the best values of UHM (36.57 mm) and Mic. (3.30).

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Table 2. Mean performances of seven cotton parents and their 12 crosses in F_1 and F_2 generations for the studied traits

Genotypes	B.W (g)		SCY/plant (g)		LY/plant (g)		L%	
Parents:								
Giza 92	3.03		147.11		54.39		37.00	
Giza 93	2.89		102.38		37.28		36.42	
Giza 96	2.91		120.66		47.34		39.22	
Giza 87	3.01		84.73		28.19		33.35	
C.B 58	3.00		109.37		40.33		36.87	
Russ. 6022	3.09		142.31		54.28		38.14	
Aust.10229	3.33		139.82		53.58		38.42	
Crosses	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
G. 92 x C.B 58	3.23	3.35	140.46	162.08	54.21	62.88	38.61	38.79
G. 92 x	3.21	3.19	154.24	162.22	59.84	61.61	38.45	37.15
G. 92 x A.10229	3.22	3.16	157.74	149.14	59.30	54.81	37.59	36.85
G. 93 x C.B 58	3.14	3.42	109.65	108.53	43.01	40.56	39.23	37.36
G. 93 x	3.22	3.11	152.70	145.50	57.52	52.63	37.59	36.17
G. 93 x	3.09	3.05	132.27	129.55	50.25	48.59	37.97	37.56
G. 96 x C.B 58	3.25	3.44	132.81	157.43	52.83	63.33	39.75	40.22
G. 96 x	3.15	3.03	161.16	165.96	65.30	67.06	40.52	40.41
G. 96 x	3.06	3.14	142.34	137.41	57.74	54.11	38.77	39.38
G. 87 x C.B 58	3.13	3.14	110.42	109.74	39.40	37.43	35.44	35.07
G. 87 x	3.05	3.00	113.10	110.36	40.17	39.02	35.53	35.34
G. 87 x	3.01	2.99	118.84	112.45	42.36	39.60	35.62	35.20
$LSD_{0.05}$	**0.23**	**0.24**	**16.07**	**23.35**	**6.36**	**8.55**	**1.81**	**1.32**
$LSD_{0.01}$	**0.31**	**0.32**	**21.55**	**31.31**	**8.53**	**11.47**	**2.43**	**1.77**
Genotypes	Mic.		Press.		UHM (mm)		LUI %	
Parents:								
Giza 92	3.87		11.92		35.90		86.95	
Giza 93	3.50		11.48		35.50		87.10	
Giza 96	3.60		11.60		35.83		87.75	
Giza 87	3.30		11.79		36.57		86.75	
C.B 58	4.10		11.40		33.90		84.95	
Russ. 6022	3.85		11.80		34.03		86.90	
Aust. 10229	4.30		11.70		33.95		86.20	
Crosses	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
G. 92 x C.B 58	3.53	3.53	11.70	11.25	34.50	34.10	85.90	86.15
G. 92 x	3.58	3.73	11.42	11.30	35.30	35.28	86.90	87.40
G. 92 x A.10229	3.50	3.47	11.35	11.60	34.90	34.65	86.05	86.45
G. 93 x C.B 58	3.50	3.60	11.75	11.55	35.75	34.90	87.15	87.55
G. 93 x	3.53	3.60	11.40	11.70	36.35	36.21	86.55	87.00

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G. 93 x	3.40	3.50	11.60	11.80	36.00	35.18	86.10	86.35
G. 96 x C.B 58	3.47	3.58	11.33	11.20	34.77	34.42	85.95	86.70
G. 96 x	3.46	3.63	11.53	11.40	35.03	35.30	86.90	87.30
G. 96 x	3.40	3.50	11.56	11.67	34.80	34.37	86.27	86.80
G. 87 x C.B 58	3.17	3.30	11.80	11.73	34.87	34.60	87.10	86.60
G. 87 x	3.20	3.33	11.85	11.93	35.57	35.17	86.77	87.47
G. 87 x	3.03	3.20	11.92	11.96	35.46	34.97	86.60	87.03
LSD$_{0.05}$	**0.19**	**0.36**	**0.40**	**0.42**	**0.67**	**0.69**	**0.88**	**0.76**
LSD$_{0.01}$	**0.25**	**0.48**	**0.53**	**0.57**	**0.90**	**0.92**	**1.18**	**1.02**

G.= Giza, Rus.= Russian, A.= Australian.

Contrarily, Giza 93 line gave the lowest BW (2.89 g), Press. (11.48) and UHM (35.50 mm), while the line Giza 87 showed the lowest means of SCY/P (84.73 g), LY/ P (28.19 g), L% (33.35%) and LUI (86.75%), in addition, Giza 92 line showed the lowest fiber fineness as it gave the highest Mic. reading (3.87).

Results for testers showed that the highest mean performance was found for Russ.6022 for the traits SCY/P (142.31 g), LY/P (54.28 g), Mic. (3.85), Press. (11.80), UHM (34.03 mm) and LUI (86.90%). While Aust.10229 tester gave the highest values for BW and L% (3.33 g and 38.42%, respectively). On the contrary, C.B. 58 tester showed the worst values for the traits, BW (3.00 g), SCY/P (109.37 g), LY/P (40.33 g), L% (36.87%), Press. (11.40), UHM (33.90 mm) and LUI (84.95%). While the worst value of Mic. (4.30) was obtained by Aust.10229.

Concerning the studied crosses, results of BW showed that the best mean performance was given by the cross Giza 96 x C. B 58 as it gave 3.25 and 3.44g in F_1 and F_2 generations, respectively; whereas the lowest values were recorded for Giza 87 x Aust.10229 as it gave 3.01 and 2.99 g in F_1 and F_2, respectively. For SCY, LY and L%, the cross Giza 96 x Russ. 6022 gave the highest values for the three traits (161.16 g, 65.30 g and 40.52%, respectively in F_1 as well as 165.96 g, 67.06 g and 40.41%, respectively in F_2 generation), whereas, the cross Giza 87 x C.B 58 had the lowest values for the three traits (110.42 g, 39.40 g and 35.44%, respectively in F_1 as well as 109.74 g, 37.43 g and 35.07%, respectively in F_2 generation).

Regarding fiber quality traits, the cross Giza 87 x Aust. 10229 gave the best values of Mic. (lowest reading) with values reached 3.03 and 3.20

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in addition to Press. as it had 11.92 and 11.96 in F_1 and F_2 generations, respectively. Whereas, the worst values of Mic. (highest reading) were observed for the cross Giza 92 x Russ. 6022 as it gave 3.58 and 3.73, respectively while for Press. the worst values were recorded for the cross Giza 96 x C.B 58 (11.33 and 11.20, respectively in F_1 and F_2 generations. With regard to fiber length as UHM, the best values were recorded for the cross Giza 93 x Russ. 6022 that had the longest fibers (36.35 and 36.21 mm, in F_1 and F_2 generations, respectively), whereas the worst values were recorded by the cross Giza 92 x C.B 58 as it gave 34.50 and 34.10 mm in F_1 and F_2 generations, respectively. For LUI, the cross Giza 93 x C.B 58 gave the highest values (87.15 and 87.55 %, respectively in both F_1 and F_2 generations), whereas, the lowest values were obtained by the cross Giza 92 x C.B 58 as it gave 85.90 and 86.15% in both F_1 and F_2 generations, respectively.

In general, it may be summed that Giza 92 line had the highest yielding potential and fiber strength, followed by Giza 96 line and the tester Russ. 6022 in the yielding ability, while Giza 87 line ranked first for fiber fineness and fiber length. The cross Giza 96 x Russ. 6022 gave the highest yielding ability, while the cross Giza 87 x Aust. 10229 had the best values for fiber fineness and fiber strength and the cross Giza 93 x Russ. 6022 had the best fiber length. The results were in harmony with the previous works that recorded significant differences among parental cotton genotypes and their crosses in F_1 and/or F_2 generation as obtained in Egyptian cotton by: Orabi *et al*., 2017; Yehia and El-Hashash, 2019; Amer, 2020, Mokadem *et al*., 2020; Ramadan, 2021 and Max *et al*., 2021 as well as in upland cotton by: Baloch *et al*., 2016; Basal *et al*., 2017; Khokhar *et al*., 2018; Bankar *et al.,* 2020 and Gnanasekaran and Thiyagu, 2021

Heterosis

Heterosis expressed as the deviation of F_1 mean performance relative to both mid and better-parents in percentage, and it refers to the superiority of the F_1 hybrid over its parents in the studied traits. In general, positive heterosis is desirable for all studied traits, except micronaire reading that demand negative heterosis for superiority. Significant heterosis in desired direction was observed for all studied traits in most crosses as in Table (3).

Table 3. Heterosis relative to mid-parent (MP) and better-parent (BP) for the studied traits in F_1 generation

Crosses	BW (g)	SCY/P (g)	LY/P (g)	L%	Mic.	Press.	UHM (mm)	LUI%
Mid-parent (MP) heterosis								
G. 92 x C.B 58	1.33**	-2.09	-3.47*	-1.51*	1.67**	0.36**	0.07	-0.06
G. 92 x Rus.6022	4.82**	26.11**	31.28**	4.15**	-2.81**	-3.72**	-2.17**	-0.03
G. 92 x A.10229	2.05**	42.84**	42.91**	-0.32*	0.41*	-3.88**	-1.06**	-0.61**
G. 93 x C.B 58	0.16	33.25**	33.00**	0.83**	6.49**	4.01**	4.46**	1.31**
G. 93 x Rus.6022	7.69**	-10.38	-8.13*	2.63**	2.01**	-2.08**	2.56**	-0.52**
G. 93 x A.10229	-0.56**	34.12**	33.87**	1.48**	-2.53	0.07	2.78**	-0.87**
G. 96 x C.B 58	0.08	20.98*	23.36**	2.44**	6.49**	0.43**	1.29**	-0.46**
G. 96 x Rus.6022	8.42**	8.00	14.02**	6.13**	3.36**	-1.42**	-1.81**	-0.49**
G. 96 x A.10229	-1.77**	27.45**	38.64**	8.67**	2.95**	-2.72**	0.70*	-0.81**
G. 87 x C.B 58	-2.09**	3.42	-2.51	-4.38**	-1.20**	2.62**	1.48**	1.45**
G. 87 x Rus.6022	0.05	-10.12	-9.72**	1.14**	-0.58**	-0.82**	-1.11**	-0.07
G. 87 x A.10229	-4.92**	13.14*	12.49**	-0.75*	-3.69**	-0.68**	-0.10*	0.14**
LSD$_{0.05}$	**0.20**	**17.32**	**6.78**	**1.57**	**0.19**	**0.34**	**0.86**	**0.76**
LSD$_{0.01}$	**0.27**	**23.23**	**9.09**	**2.10**	**0.26**	**0.46**	**1.15**	**1.02**
Better-parent (BP) heterosis								
G. 92 x C.B 58	-3.99**	-4.52	-6.42*	-6.74**	-1.29**	-1.82**	-6.25**	-1.21*
G. 92 x Rus.6022	3.72**	24.05**	28.98**	3.92**	-3.03**	-4.20**	-4.08**	-0.06
G. 92 x A.10229	-2.56**	14.02**	16.20**	-2.16*	-5.17**	-4.76**	-5.16**	-1.04*
G. 93 x C.B 58	-7.10**	15.41**	9.30*	-5.24**	0.15	3.63**	-1.52**	0.06
G. 93 x Rus.6022	4.21**	-22.95**	-21.43**	2.03*	-1.39**	-3.39**	1.24**	-0.63
G. 93 x A.10229	-7.07**	22.68**	27.98**	-1.16	-12.50**	-0.85	-0.83	-1.38**
G. 96 x C.B 58	-6.95**	12.70**	8.09**	-3.97**	0.10	-0.43	-5.76**	-2.05**
G. 96 x Rus.6022	5.18**	-0.21	4.36	5.24**	0.01	-2.26**	-4.42**	-0.97*
G. 96 x A.10229	-7.97**	10.06**	23.49**	5.56**	-6.48**	-3.13**	-4.15**	-1.69**
G. 87 x C.B 58	-7.50**	-7.84	-20.53**	-13.67**	-7.29**	0.90	-4.65**	0.40
G. 87 x Rus.6022	-1.29**	-20.52**	-23.45**	-3.65**	-3.19**	-0.85	-2.73**	-0.15
G. 87 x A.10229	-9.47**	1.95	8.71*	-7.29**	-12.75**	-1.07*	-3.95**	-0.18
LSD$_{0.05}$	**0.23**	**20.00**	**7.83**	**1.81**	**0.22**	**0.40**	**0.99**	**0.88**
LSD$_{0.01}$	**0.31**	**26.82**	**10.50**	**2.43**	**0.30**	**0.53**	**1.33**	**1.18**

*and ** Significant at 0.05 and 0.01 probability levels, respectively.

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For boll weight, MP heterosis revealed that eight crosses out of 12 F_1 crosses exhibited significant and positive heterosis, which ranged from 0.05% for the cross Giza 87 x Russ. 6022 to 8.42% for Giza 96 x Russ. 6022, while BP heterosis showed that only three crosses had positive and significant heterosis, which ranged from 3.72% for Giza 92 x Russ. 6022 to 5.18% for Giza 96 x Russ. 6022, whereas the rest of the studied crosses showed negative values. Russ. 6022 tester had the best positive heterosis for boll weight when crossed with the three lines Giza 92, Giza 93 and Giza 96.

Regarding seed cotton yield (SCY/P), MP heterosis showed that seven crosses out of 12 F_1 crosses possessed significant positive heterosis which ranged from 13.14% for the cross Giza 87 x Aust. 10229 to 42.84% for the cross Giza 92 x Aust. 10229, while six crosses showed significant and positive BP heterosis with values ranged from 10.06% for the cross Giza 96 x Aust. 10229 to 24.05 % for the cross Giza 92 x Russ. 6022.

For lint yield (LY/P), MP heterosis showed that eight crosses out of 12 F_1 crosses had significant positive heterosis ranged from 12.49% to 42.91% for the crosses Giza 87 x Aust.10229 and Giza 92 x Aust.10229, respectively; while seven crosses showed significant and positive BP heterosis with values ranged from 8.71% to 28.98% for the crosses Giza 87 x Aust.10229 and Giza 92 x Aust.10229, respectively. The tester Aust.10229 gave the higher values of positive heterosis for seed cotton and lint yields/ plant when crossed with the four tested line as compared to the other two testers, C.B 58 and Russ. 6022.

Concerning lint percentage (L%), MP heterosis showed significant and positive values for eight crosses and ranged from 0.83% for Giza 93 x C.B 58 to 8.67% for Giza 96 x Aust.10229, while, for BP heterosis four crosses out of 12 F_1 crosses had significant and positive values ranged from 2.03% for Giza 93 x Russ. 6022 to 5.56% for Giza 96 x Aust.10229. It might be concluded that Russ. 6022 tester gave the highest values of positive heterosis for L% when crossed with the three lines Giza 92, Giza 93 and Giza 87.

With Regard to the fiber quality traits, micronaire reading (Mic.) which is an indicator to fiber fineness, MP heterosis showed negative (desirable) and significant values for five crosses and ranged from -0.58% to

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3.69% for Giza 87 x Russ. 6022 and Giza 87 x Aust.10229 crosses, respectively while for BP heterosis, nine crosses showed significant negative values that ranged from -1.29% to -12.75% for the crosses Giza 92 x C.B 58 and Giza 87 x Aust.10229, respectively.

Fiber strength expressed as Pressely index (Press.) showed significant and positive MP heterosis in only four crosses, the range was 0.36% for the cross Giza 92 x C.B 58 to 4.01% for the cross Giza 93 x C.B 58, while BP heterosis, only one cross (Giza 93 x C.B 58) showed significant and positive value that was 3.63%, the rest of crosses showed either insignificant positive values or negative values.

Regarding the fiber length expressed as upper half mean (UHM), MP heterosis revealed that six crosses out of 12 F_1 crosses had significant and positive values that ranged from 0.70% for Giza 96 x Aust.10229 to 4.46% for Giza 93 x C.B 58, while only one cross (Giza 93 x Russ. 6022) showed significant and positive BP heterosis with value 1.24%.

Length uniformity index (LUI%) revealed significant and positive MP heterosis in only three crosses, ranged from 0.14% for Giza 87 x Aust.10229 cross to 1.45% for Giza 87 x C.B 58 cross, while BP heterosis, all crosses showed either insignificant positive values or negative values. Similar significant heterosis in cotton plant traits were previously recorded by: Orabi *et al*., 2017; Khokhar *et al*, 2018; Orabi *et al*., 2017; Mokadem *et al*., 2020; Gnanasekaran and Thiyagu, 2021; Hamed and Said, 2021 and Max *et al*., 2021.

Combining ability effects

Significance of general combining ability (GCA) for lines and testers as well as specific combining ability SCA for crosses indicated the involvement of both additive and non-additive gene action in the expression of the studied traits in F_1 and F_2 generations.

General Combining Ability effects (GCA)

The GCA is the mean performance of a line or tester in a series of their crosses, good combiner genotype is able to produce hybrids with high expression of a particular trait. Results of GCA effects for lines and testers are present in Table 4.

Table 4. General Combining Ability (GCA) effects from line x tester analysis for parental cotton genotypes in F_1 and F_2 generations for the studied traits.

Genotypes	BW		SCY/P		LY/P		L%	
Lines :	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Giza 92	0.082**	0.044*	24.13**	17.98**	9.44**	6.70**	0.27	0.14
Giza 93	0.002	0.004	-7.22*	-7.04	-2.32	-3.45	0.32	-0.43
Giza 96	0.003	0.094**	4.69	11.28**	3.99*	7.96**	1.75**	2.55**
Giza 87	-0.086**	-0.141**	-21.61**	-22.23**	-11.11**	-11.21**	-2.33**	-2.26**
$LSD_{0.05}$	**0.034**	**0.036**	**6.56**	**7.29**	**3.52**	**4.13**	**1.04**	**0.79**
$LSD_{0.01}$	**0.046**	**0.049**	**8.49**	**9.22**	**4.56**	**5.88**	**1.40**	**1.06**
Testers :								
C.B 58	0.019*	0.211**	7.64*	5.85	3.47*	2.81	0.38	0.40
Russ. 6022	0.033**	0.109**	-2.62	1.67	-1.49	0.46	-0.37	-0.19
Aust.10229	-0.048**	-0.101*	-5.02	-7.52	-1.97	-3.27*	-0.02	-0.21
$LSD_{0.05}$	**0.017**	**0.081**	**7.01**	**11.51**	**2.92**	**3.25**	**0.90**	**0.68**
$LSD_{0.01}$	**0.028**	**0.108**	**10.41**	**15.43**	**3.75**	**4.63**	**1.21**	**0.92**
	Mic.		Press.		UHM		LUI%	
Lines:	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Giza 92	-0.044*	-0.210**	0.249*	0.256*	-0.219**	-0.389**	-0.219*	-0.142
Giza 93	-0.016	-0.057*	0.046*	0.094**	0.031	0.828**	0.031	0.025
Giza 96	0.083**	0.082**	0.115**	0.167**	-0.131*	0.183	-0.131	0.008
Giza 87	-0.122**	-0.235**	0.268*	0.278**	0.519**	0.682**	0.319**	0.108
$LSD_{0.05}$	**0.030**	**0.034**	**0.039**	**0.046**	**0.118**	**0.172**	**0.208**	**0.241**
$LSD_{0.01}$	**0.058**	**0.061**	**0.067**	**0.079**	**0.173**	**0.213**	**0.267**	**0.290**
Testers :								
C.B 58	0.099*	0.197**	0.175**	0.156*	0.022	0.193**	0.022	-0.038
Russ. 6022	-0.139**	-0.136**	-0.075	0.023	0.276**	0.182*	0.276**	0.417**
Aust.10229	0.040	-0.061	0.100*	0.153*	-0.299**	0.011	0.299**	-0.379**
$LSD_{0.05}$	**0.074**	**0.101**	**0.099**	**0.113**	**0.141**	**0.150**	**0.195**	**0.211**
$LSD_{0.01}$	**0.110**	**0.132**	**0.137**	**0.186**	**0.190**	**0.192**	**0.253**	**0.278**

*and ** Significant at 0.05 and 0.01 probability levels, respectively.

Among the seven parental lines used in this study, the highest positive GCA effects were exhibited by the line Giza 92 for the traits: BW, SCY/P, LY/P and Press. in addition to significant negative and desirable GCA for Mic. in both F_1 and F_2 generations. Giza 96 line ranked second in this respect and showed significant positive GCA for the traits: LY/P, L%

and Press. in both generations, in addition to BW and SCY/P in F_2 generation. Hence, these two lines might be considered as the best combiners. Giza 87 line showed significant positive GCA for Press. and UHM as well as significant negative and desirable GCA for Mic. in both generations in addition to LUI in F_1 generation. Whereas Giza 93 line had the lowest GCA effects for most of the studied traits and considered as the poorest combiner.

In the same connection, the GCA effects for the three testers showed that Russ. 6022 tester had significant and desirable GCA effects for the traits: Bw, Mic., UHM and LUI in F_1 and F_2 generations. C.B 58 tester showed significant and positive GCA effects for the traits: BW and Press. in F_1 and F_2 as well as SCY/p and LY/p in F_1 generation. Hence, these two testers might be considered as the best combiners. Whereas Aust.10229 tester had the lowest GCA effects for most of the studied traits and considered as the poorest combiner.

High positive GCA of the parents indicating the prevalence of additive gene action or additive x additive interaction (if epistasis is present) in inheritance of the studied traits (Khokhar *et al.*, 2018 and Max *et al*., 2021). The relative contribution of discrete parents to upgrade a specific trait in the population can be evaluated by comparing the GCA for such parents.

Further, parents with positive and significant values of mean performance and GCA effects may own more number of additive genes and may lead to accumulate favorable genes in a few genotypes (Gnanasekaran and Thiyagu, 2021). Therefore, in this study parents with positive and high GCA (Giza 92, Giza 96 and C.B 58 for yield potential as well as Giza 87 and Russ. 6022 for fiber properties) proved to be the best combiners that might be used in breeding programs to improve cotton yielding ability possess the ability for increasing the mean performance of traits in the population. On the contrary, parents with negative GCA effects lead mostly to the reduction of the trait. Finding results were in harmony with those reported in earlier studies by Orabi *et al*., 2017; Khokhar *et al.,* 2018; Mokadem *et al*., 2020; Gnanasekaran and Thiyagu, 2021; Max *et al*., 2021 and Ramadan, 2021.

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Specific Combining Ability effects (SCA)

The SCA is defined as the performance of certain hybrid combinations either better or poorer than the prospective on the basis of the mean performance of their parental inbred lines. Hence, SCA is useful for recognition of expected hybrids with higher performance and acceptable level of stability, differences due to SCA have been attributed to non-additive (dominance or epistasis) gene action (Sprague and Tatum, 1942 and Griffing, 1956).

The results of SCA effects of crosses in F_1 and F_2 generations for the studied traits are presented in Table (5). Variances due to SCA were significant and positive or negative for a few of yield and it's attributed traits, and most of fiber quality traits in both of F_1 and F_2 generations, disclosing the involvement of non-additive (dominance or epistasis) effects in the inheritance of these traits. Negative specific combining ability indicates unfavorable combinations of parents. Low mean performance and negative SCA effects were desirable for fiber fineness (Mic.).

Results indicated that the highest significant desirable SCA effects were recorded for the cross Giza 92 x Russ. 6022 for the traits, Mic., and LUI in both generations; SCY/p, LY/p and L%, in F_1 as well as BW and UHM in F_2. Two crosses *viz*: Giza 93 x C.B 58 and Giza 96 x Russ. 6022 ranked second in this respect. While, the cross Giza 93 x Russ. 6022 showed significant undesirable SCA effects for almost all traits in F_1 and F_2 generations.

As recorded in GCA effects, parents with positive and high GCA were Giza 92, Giza 96 and C.B 58 for yield potential as well as Giza 87 and Russ. 6022 for fiber properties; hence hybrids that showed high positive SCA effects resulted from crossing between two parents, at least one of them had high positive GCA effects.

Singh *et al.*, (2010) reported that when two good general combiner parents shows high SCA effects that may be ascribe to the involvement of additive genes. Moreover, Basal *et al.*, 2017 and Munir *et al.*, 2018 indicated that advantageous hybrids for yield and its contributing components have at least one parent with good GCA. In the same connection, Ramadan, 2021 added that such crosses that include one good

Table 5. Specific combining ability (SCA) estimates from line × tester analysis in F_1 and F_2 generations for the studied traits.

Genotypes	BW		SCY/P		LY/P		L%	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
G. 92 x C.B 58	-0.001	-0.096**	-30.73**	-2.84	11.77**	0.30	0.01	0.79**
G. 92 x Rus.6022	-0.058*	0.064*	21.55**	5.23	9.13**	1.38	0.61*	-0.26
G. 92 x A.10229	0.058*	0.031	9.19**	-2.40	2.65	-1.68	-0.61*	-0.53
G. 93 x C.B 58	-0.026	0.019	21.53**	1.57	9.09**	0.38	0.58*	-0.07
G. 93 x Rus.6022	0.037	0.024	-19.94**	-7.94*	-8.02**	-3.88*	-0.30	-0.67*
G. 93 x A.10229	-0.012	-0.044	-1.59	6.37	-1.07	3.49	-0.28	0.74*
G. 96 x C.B 58	-0.022	0.189**	5.81*	-0.77	2.08	-0.50	-0.32	-0.19
G. 96 x Rus.6022	0.066*	-0.146**	0.50	8.19*	-0.80	4.14*	-0.55	0.61*
G. 96 x A.10229	-0.043	-0.044	-6.30*	-7.42*	-1.28	-3.64	0.88**	-0.42
G. 87 x C.B 58	0.049	-0.113**	3.40	2.04	0.60	-0.19	-0.26	-0.53
G. 87 x Rus.6022	-0.045	0.057*	-2.10	-5.49	-0.30	-1.64	0.25	0.32
G. 87 x A.10229	-0.004	0.056*	-1.30	3.45	-0.30	1.83	0.02	0.21
LSD$_{0.05}$	**0.054**	**0.056**	**5.66**	**7.05**	**3.45**	**3.74**	**0.57**	**0.56**
LSD$_{0.01}$	**0.083**	**0.088**	**7.63**	**8.71**	**4.56**	**4.83**	**0.77**	**0.75**
	Mic.		Press.		UHM		LUI%	
Crosses	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
G. 92 x C.B 58	-0.015	0.003	0.036**	0.022	-0.024	0.326**	-0.406*	0.004
G. 92 x Rus.6022	-0.078**	-0.036*	0.013	0.086**	0.026	0.201**	0.340*	0.400*
G. 92 x A.10229	0.093**	-0.039**	0.039**	0.064**	-0.001	-0.528**	0.065	-0.404*
G. 93 x C.B 58	0.085**	0.069**	0.092**	0.022	-0.041	-0.090*	0.594**	0.588**
G. 93 x Rus.6022	0.022	-0.147**	-0.158**	0.014	0.209**	0.365**	-0.260	-0.367*
G. 93 x A.10229	-0.107**	0.078**	0.067**	-0.036	0.168**	0.456**	-0.335*	-0.221
G. 96 x C.B 58	-0.004	-0.019	-0.097**	0.067**	0.009	-0.196**	-0.444**	-0.196
G. 96 x Rus.6022	-0.017	0.064**	0.136**	-0.025	0.241**	0.179**	0.251	-0.050
G. 96 x A.10229	0.021	-0.044**	-0.039**	0.092**	0.232**	0.017	0.193	0.246
G. 87 x C.B 58	-0.065**	-0.053**	-0.031*	0.022	0.057*	-0.040	0.256	-0.396*
G. 87 x Rus.6022	0.072**	0.047**	0.019	0.097**	0.007	-0.015	-0.332*	0.017
G. 87 x A.10229	-0.007	0.006	0.011	0.119**	0.063**	0.056	0.076	0.379*
LSD$_{0.05}$	**0.025**	**0.029**	**0.024**	**0.042**	**0.043**	**0.070**	**0.271**	**0.311**
LSD$_{0.01}$	**0.033**	**0.037**	**0.033**	**0.057**	**0.058**	**0.094**	**0.410**	**0.443**

*and ** Significant at 0.05 and 0.01 probability levels, respectively.

and one poor general combiners may produce desirable transgressive sergeants when fixable gene complex (additive) in the good combiner parent and complementary epispastic effect in the poor combiner parent act in the same direction to maximize the desirable traits.

High mean performance and significant positive GCA effects for one of the parents for a trait but non-significant SCA effect for the same trait may be ascribed to the lack of co-adaptation between favorable alleles of the parents involved in the cross for this trait (Munir *et al.,* 2018; Gnanasekaran and Thiyagu, 2021). The results are in agreement with those previously reported in Egyptian cotton by: Orabi *et al*., 2017; Sultan *et al*., 2018; Al-Hibbiny *et al*., 2019; Mokadem *et al*., 2020; Hamed and Said, 2021 and Max *et al*., 2021 as well as in upland cotton by: Baloch *et al*., 2016; Basal *et al*., 2017; Chaudhary *et al*., 2019 and Gnanasekaran and Thiyagu, 2021.

Proportional contribution

Relative contribution percentages of lines, testers and (line x tester) interactions in F_1 and F_2 generations for the studied traits are presented in Table (6). The results showed that line x tester interaction contributions were higher than both of lines and testers contributions for almost all of the studied traits in both generations (except lint% and UHM). However proportion contribution of lines was higher than testers for the studied traits (except LY/plant, and Press. in F_2 and LUI in F_1), which mean that reasonable amount of variance were ascribed to the maternal effect.

The greater contribution of line x tester interactions as compared to those of lines and testers each alone clarify the importance of non-additive (dominance or epistasis) type of gene action. These findings were in accordance with those recorded by: Baloch *et al*., 2016; Khokhar *et al*, 2018; Sultan *et al*., 2018; Yehia and El-Hashash, 2019 who mentioned that line $\times$ tester proportional contribution was greater than individual contribution of both lines and testers for most traits under study. Whereas, other studies Orabi *et al*., 2017; Hamed and Said, 2021 as well as Gnanasekaran and Thiyagu, 2021 found that proportion contribution of lines was higher than testers and line x tester interaction contributions for the studied traits.

Table 6. Proportional contributions of lines, testers and their interaction in F₁ and F₂ generations for the studied traits.

Traits	Lines		Testers		Line x Tester	
	F_1	F_2	F_1	F_2	F_1	F_2
BW	25.10	21.01	16.07	20.20	58.83	58.79
SCY/P	31.61	18.61	13.85	17.19	54.54	64.20
LY/P	23.19	16.82	16.24	19.53	60.57	63.65
L%	47.53	56.92	33.84	25.45	18.63	17.63
Mic.	28.58	27.63	20.33	19.52	51.09	52.85
Press.	27.25	15.46	24.27	23.78	48.48	60.76
UHM	65.17	59.97	21.12	22.69	13.71	17.34
LUI	20.46	29.71	26.94	21.74	52.60	48.55

Genetic parameters

Recognition of the nature of gene action helps plant breeder in the selection of parents to be used in hybridization and also to define adequate breeding procedures for genetic improvement of different quantitative traits. Hence, the genetic variance components and heritability were calculated for all studied traits in F_1 and F_2 generations and presented in Table (7).

Variance of combining ability:

The results clarified that the variance due to SCA (δ^2_{SCA}) was higher in magnitude than that due to GCA (δ^2_{GCA}) for all of the studied traits (except for L% and UHM) which indicating that the non-additive gene action (dominance or epistasis) play the important role in the expression of these traits, while additive effects have a minor role. These results were confirmed by the ($\delta_{GCA}/\delta_{SCA}$) ratio which was less than the unity. These findings may be ascribed to the high selection history for the studied materials. Consequently, the studied traits could be improved by exploiting heterosis through hybrid breeding programs while selection should be delayed to later generations until genes are stabilized.

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Table 7. Partitioning of genetic variance and heritability in broad and narrow sense in F_1 and F_2 generations for the studied traits.

Genetic parameters	BW		SCY/P		LY/P		L%	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
δ^2_{GCA}	0.0004	0.0035	19.90	11.65	5.34	1.89	0.29	0.40
δ^2_{SCA}	0.0009	0.0091	89.41	72.78	56.61	18.89	0.13	0.27
$\delta_{GCA}/\delta_{SCA}$	0.667	0.620	0.472	0.40	0.31	0.32	1.52	1.20
δ^2_{G}	0.0017	0.016	129.22	96.07	67.29	22.68	0.71	1.07
δ^2_{Ph}	0.008	0.057	171.72	131.18	105.54	36.75	1.00	1.47
H^2_b	21.25	28.07	75.25	73.23	63.76	61.71	71.00	72.79
H^2_n	10.00	12.28	23.18	27.75	10.12	13.31	58.70	64.22
	Mic.		Press.		UHM		LUI%	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
δ^2_{GCA}	0.002	0.004	0.003	0.004	0.043	0.039	0.005	0.006
δ^2_{SCA}	0.005	0.009	0.008	0.008	0.037	0.023	0.122	0.138
$\delta_{GCA}/\delta_{SCA}$	0.632	0.667	0.612	0.686	1.078	1.302	0.202	0.209
δ^2_{G}	0.009	0.017	0.014	0.016	0.123	0.102	0.132	0.150
δ^2_{Ph}	0.013	0.024	0.022	0.025	0.212	0.171	0.189	0.228
H^2_b	69.23	70.83	63.64	64.00	58.02	59.65	69.84	65.79
H^2_n	30.77	33.33	31.82	32.00	40.57	46.20	5.29	5.76

δ^2_{GCA}: Variance due to GCA, δ^2_{SCA}: Variance due to SCA, δ^2_{G}: Genotypic variance, δ^2_{Ph}: Phenotypic variance. H^2_b: Broad sense heritability, H^2_n: Narrow sense heritability.

On the other hand, additive type of gene action was prevalence for the expression of the traits lint % and fiber length expressed as UHM as the δ^2_{GCA} was higher than δ^2_{SCA} and the ($\delta_{GCA}/\delta_{SCA}$) ratio was exceeded the unity. Accordingly, recurrent selection, a breeding method that increases the frequency of favorable alleles and identifies the superior combinations by repeated crossing and selection could be the best method to exploit the additive gene effects in this population. The presence of high parent heterosis suggests an additional opportunity for developing hybrid with high performance (Gnanasekaran and Thiyagu, 2021). Likewise, Munir *et al*., 2018 reported that the presence of transgressive segregants is confirmed by additive gene effects in segregating generations, traits that were controlled by additive gene effects often have high narrow-sense heritability, hence such traits could be improved through simple selection for traits in early segregating generations.

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The results were in conformity with the previous results in upland cotton of Baloch *et al*., 2016; Khokhar *et al.,* 2018; Bankar *et al*., 2020 and Gnanasekaran and Thiyagu, 2021 as well as in Egyptian cotton of Orabi *et al.*, 2017; Yehia and El-Hashash, 2019; Mokadem *et al*., 2020; Hamed and Said, 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. Contrarily, Basal *et al*., 2017 found that GCA variances were higher than SCA for some trais in F_2 and all traits in F_3 generation, moreover, Munir *et al*., 2018; Prakash *et al.*, 2018 and Unay *et al*., 2019 found that GCA variance was higher than SCA variance for some cotton traits particularly fiber properties, indicating the role of additive type of gene action for inheritance of such traits.

Heritability

Estimates of heritability in F_1 and F_2 generations that shown in Table (7) revealed that broad sense heritability (h^2_b%) showed low values (less than 30%) for the trait BW in both F_1 and F_2 generations; while UHM had intermediate values (from 30 to 60%), the rest of traits gave large values (exceeded 60%). Low heritability reported by crop researchers for non-additive gene action suggesting to retard the selection for a specific traits to later segregating generations (Falconer and Macky, 1996).

On the other hand, narrow sense heritability (h^2_n%) showed low values for the traits BW, SCY/p, LY/p and LUI in F_1 and F_2 generations, the low narrow sense heritability (h^2_n%) estimates were ascribed to the higher portion of dominant variance against the additive variances controlling these traits, which suggests that selection for such traits may be delayed to later filial generations to give the opportunity for occurrence recombination between desirable genes. While the traits, L%, Mic., Press. and UHM showed intermediate to high h^2_n% values, because these traits are controlled by additive gene effects and consequently had higher narrow-sense heritability and such traits could be improved through simple selection in early segregating generations (Munir *et al*., 2018). Our results are in the same line with the previous results mentioned by Baloch *et al*., 2016; Orabi *et al.*, 2017; AL-Hibbiny *et al*., 2019-a; Mokadem *et al*., 2020 as well as Hamed and Said, 2021.

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CONCLUSION

The GCA and SCA variance was significant for almost all traits indicating that both additive and non-additive gene action are controlling such traits. The line x tester interaction contributions were higher than both of lines and testers contributions for most traits in both generations. Variance due to SCA was higher than that of GCA for most traits indicating that the non-additive gene action was more important in controlling these traits, whereas additive type of gene action was prevalence for lint% and fiber length. Giza 92 line was the best combiner for most traits, while Russ. 6022 tester, was the best combiner for fiber traits. These varieties as well as Giza 92 x Russ. 6022 cross had considered as promising for improving cotton traits in breeding programs.

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التحليل الوراثى لصفات المحصول وجودة التيله فى القطن المصرى

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تهدف هذه الدراسة الى تقدير القدرة علي الائتلاف ومكونات التباين الوراثي ودرجة التوريث وقوة الهجين لصفات المحصول ومكوناته وجودة التيله في هجن الجيل الأول والجيل الثاني الناتجة من تهجين أربعة أصناف مصرية من القطن كسلالات وهي جيزة ٩٢، جيزة ٩٣، جيزة ٩٦، جيزة ٨٧ وثلاثة تراكيب وراثية اجنبيه ككشافات وهي سى بى ٥٨ ، روسى ٦٠٢٢ والسلالة استرالى ١٠٢٢٩ باستخدام طريقة تحليل السلالة × الكشاف وذلك في محطة سخا للبحوث الزراعية بمحافظة كفر الشيخ خلال ثلاثة مواسم زراعية من ٢٠١٨ الي ٢٠٢٠م. وكانت اهم النتائج المتحصل عليها كما يلي:

١. أظهرت نتائج تحليل التباين وجود فروق معنوية بين التراكيب الوراثية المستخدمه وكذلك بين الآباء والهجن وبين الآباء مع الهجن وبين السلالات والكشافات وكذلك بين السلالات مع الكشافات لمعظم الصفات المدروسة.

٢. أظهر الصنف جيزة ٩٦ (سلاله) والصنف روسى ٦٠٢٢ (كشاف) أفضل قيم لصفات المحصول ومكوناته بينما اعطى الصنف جيزة ٨٧ (سلاله) أفضل القيم لصفات جودة التيلة. وأظهر الهجين جيزة ٩٦× روسى ٦٠٢٢ أفضل القيم لصفات المحصول ومكوناته بينما أعطى الهجين جيزة ٨٧ × استرالى ١٠٢٢٩ أفضل القيم لصفات جودة التيله.

٣. أظهرت معظم الهجن المدروسة قوة هجين مفيدة كمتوسط الأبوين لمعظم الصفات المدروسة بينما كانت قوة الهجين كأفضل الأبوين معنوية وموجبه لعدد قليل من الصفات.

٤. كانت القدرة العامه على الائتلاف معنويه للسلالات والكشافات، كما كانت القدرة الخاصة على الائتلاف للسلاله × الكشاف معنويه مما يدل على اشتراك كل من فعل الجين الإضافى والسيادة فى وراثة الصفات المدروسة.

٥. أعطى الصنفان جيزة ٩٢ و جيزة ٩٦ (كسلالات) أفضل قدرة عامة علي الائتلاف لصفات المحصول ومكوناته بينما كان الصنف جيزه ٨٧ الأفضل لصفات جودة التيله، كذلك أظهر الصنف روسى ٦٠٢٢ (كشاف) أفضل قدرة عامة علي الائتلاف لصفات جودة التيله. كما أظهر الهجين جيزة ٩٢ × روسى ٦٠٢٢ أعلى قدرة خاصة علي الائتلاف في الجيلين الأول والثاني.

٦. أظهر تقدير نسبة المساهمة أن مساهمة تفاعل السلاله × الكشاف كان أعلي من مساهمة كل من السلالات والكشافات كل على حدى لمعظم الصفات المدروسة في الجيلين الأول والثاني. وكان التباين الراجع للقدرة الخاصة على الائتلاف أعلى من ذلك الراجع للقدرة العامه على الائتلاف لكل الصفات المدروسة (ماعدا صفتى التصافى وطول التيلة) فى الجيلين الأول والثانى مما يدل على أهمية فعل الجين غير الإضافى (سيادة وتفوق) فى توارث هذه الصفات، بينما كان فعل الجين الإضافى له الدور الأكبر فى توارث صفتى التصافى وطول التيله.

٧. قيم درجة التوريث بالمعني العام كانت منخفضة لصفة وزن اللوزة ومتوسطه لصفة طول التيله وعالية لباقى الصفات، بينما كانت قيم درجة التوريث بالمعني الخاص منخفضة الى متوسطه لكل الصفات المدروسة في الجيلين الأول والثاني.

٨. عموما فانه يمكن التوصية بإستخدام الأصناف جيزة ٩٢، جيزة ٩٦ و روسى ٦٠٢٢ والهجين جيزة ٩٢ × روسى ٦٠٢٢ في برامج التربية لتحسين وزيادة القدرة الإنتاجية للأصناف الجديدة ، بينما يمكن إستعمال الصنفين جيزة ٨٧ و استرالى ١٠٢٢٩ والهجين جيزة ٨٧ × استرالى ١٠٢٢٩ في برامج التربية للحصول على أصناف جديدة ذات صفات جودة عالية.