



Genetic Parameters of Some Quantitative Traits in Cotton Using Triple Test Cross Analysis

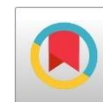
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ABSTRACT: The current study was conducted at Sakha Agricultural Research Station Kafr El-Sheikh Governorate Egypt, during (2021-2023) growing seasons. Triple test cross analysis was employed to disclose epistasis, additive, and dominance components of genetic variability for yield components and fiber quality traits, using three testers as male with ten lines as female parents. Results demonstrated significant differences for each of genotypes, parents, lines, testers, hybrids, lines vs. testers and hybrids vs. parents for most studied traits. The mean square for the deviations total epistasis ($L_{1i} + L_{2i} - 2L_{3i}$) revealed the presence of highly significant epistasis for all studied traits. Mean squares estimates due to additive \times additive (i) type were found to be non significant for all studied traits. The presence of (i + j) epistatic types appeared to be highly significant in the inheritance of all the studied traits. The epistatic type (i) interaction, was detected to be much larger in magnitudes than the other epistatic type (i+ j) for all studied traits, except for seed index. Additive values were greater than dominance genetic variance for all studied traits except for boll weight and micronaire reading. The degree of dominance $\sqrt{H/D}$ was less than unity suggesting the role of partial or incomplete dominance for all the studied traits, except for boll weight and micronaire reading which showed over dominance (greater than unity).

Keywords: Cotton, *Gossypium barbadense* L., Triple test cross, Gene interactions and Epistasis.

INTRODUCTION:

Estimating the genetic components of the studied traits of any cotton population is important for planning an appropriate and effective breeding program. The early attempts to partition the genetic variance were done by (Fisher, 1918), classified the genetic variance into three components, additive, dominance and epistasis. Which, developed by Hayman and Mather (1955), where they indicated that epistasis can also classified to three components additive \times additive, additive \times dominance and dominance \times dominance. Triple Test Cross technique (Kearsey and Jinks, 1968) provides un-ambiguous estimates for epistasis and in the lack of epistasis, un-biased estimation of additive and non-additive components also remains unaffected by differences in allele frequencies, degree of inbreeding as well as correlation. Successful breeding program is limited by the portion of genotypic variance due to additive gene effect as well as additive \times additive epistatic interaction; because these two types of gene effect can only be retained by subsequent inbreeding. While if non-additive gene portion is larger than additive ones, the improvement of the characters studied required intensive selection through later generations; when there were significantly epistatic effects, the possibility of obtaining

desirable segregates through inter-mating in early generations can led to breaking undesirable linkage group or by adoption of recurrent selection for rapid improvement (Esmail, 2007).

Al-Hibbiny *et al.*, (2020) revealed that fixable type was most important epistatic effect than non-fixable type for all studied traits. For all of the studied traits, both additive and dominant components were significant. Lint cotton yield/plant, lint index and seed index were confirmed the presence of over-dominant, although, the degree of dominance was less than unity, confirming the occurrence of partial dominance for all studied traits. Except for lint yield/plant, lint index, and seed index, additive gene action was more essential in influencing inheritance than dominance one.

Hassan *et al.*, (2022) showed that (i) type of epistasis (additive \times additive) showed significantly for some yield components and fiber quality traits, except for micronaire reading. While, (additive \times dominance) as well as (dominance \times dominance) demonstrated significant for seed cotton yield / plant, lint cotton yield/plant, lint percentage and uniformity index. The (i) type as compared to (j+l) type showed higher values for all the studied traits, with the exception of micronaire reading. Both additive and dominance were important for controlling the

traits, except boll weight, micronaire reading and pressley index, which controlled with additive genetic effect. On the other side, additive component was higher than dominance component for all traits. Degree of dominance for all studied traits was less than unity, indicating partial dominance.

El-Shazly et al., (2023) The results revealed that all genotypes, parents, crosses, and parents vs. crosses mean squares were extremely significant for all tested features, with the exception of micronaire reading in the crosses. The findings demonstrated that additive effects had a comparatively minor role in the emergence of these traits as compared to non-additive effects. The results indicated that the hybridization programme would be effective in improving the majority of the attributes studied.

The present investigation was undertaken to detect the presence of epistasis and to estimate the additive and dominance components of

genetic variation of some quantitative traits in cotton.

MATERIALS AND METHODS:

Study Area

Triple test cross (TTC) experiment was conducted out during three growing seasons (2021 to 2023) at Sakha Agricultural Research Station Kafr El-Sheikh Governorate Egypt.

Genetic materials and experimental procedures

Ten cotton lines included wide genotypes, Giza 80 (L₁), Giza 86 (L₂), Giza 87 (L₃), Giza 88 (L₄), Giza 90 (L₅), Giza 92 (L₆), 10229 (L₇), Pima S₇ (L₈), Karshenky (L₉) and Pima S₆ (L₁₀) were crossed to 3 testers; Giza 94 (T₁), Giza 96 (T₂) and their F₁ hybrid (T₃). The origin, pedigree and category of these genotypes were presented in (Table 1). Thus the experimental materials comprised of 13 parental genotypes, 20 single cross including T₁ and T₂, and 10 three-way crosses involving T₃.

Table 1. Origin, pedigree and category for the thirteen parental cotton genotypes

Parents	Origin	Pedigree	Category	
Lines				
L ₁	Giza 80	Egypt	Giza 66 x Giza 73	Long staple
L ₂	Giza 86	Egypt	Giza 75 x Giza 81	Long staple
L ₃	Giza 87	Egypt	Giza 77 x Giza 45	Extra-long staple
L ₄	Giza 88	Egypt	(Giza 77 x Giza 45) B	Extra-long staple
L ₅	Giza 90	Egypt	G. 83 x Dendera	Long staple
L ₆	Giza 92	Egypt	(Giza 84 x Giza 74) x Giza 68	Extra-long staple
L ₇	10229	Russian	(Imported genotype)	Long staple
L ₈	Pima S ₇	American-Egyptian Variety	(6614-91-9-3 x 6907-513-509-501).	Long staple
L ₉	Karshenky	Russian	Unknown	Long staple
L ₁₀	Pima S ₆	American-Egyptian Variety	(5934-23-2-6) x (5903-98-4-4)	Long staple
Testers				
T ₁	Giza 94	Egypt	10229 x Giza 86	Long staple
T ₂	Giza 96	Egypt	(Giza 84 x (Giza 70 x Giza 51b)) x S62	Extra-long staple
T ₃	Giza 94 x Giza 96 (F ₁)	Egypt	Giza 94 x Giza 96	

During 2023 growing season, the 43-genotype evaluated in a randomized complete block design (RCBD) with three replications. Each replicate contained three rows for each genotype. Row was 4 m long, and 0.70 m width and 40 cm between hills with one plant left / hill. All agricultural practices were adopted through the growing seasons.

Ten guarded plants from each plot were used individually to collect data for the following traits: seed cotton yield (g) / plant (SCY/P), lint cotton yield (g)/ plant (LCY/P), lint percentage (L %), boll weight (g) (BW), seed index (g) (SI), lint index (g) (LI), micronaire reading (MR), pressley index (PI), 2.5% span length (mm) (UHM) and Uniformity index (UI%), these traits were estimated at the Cotton Technology Laboratories, Cotton Research Institute, ARC, Giza, Egypt.

Statistical and genetic analysis:

Analysis of variance was done as outlined by **Singh and Chaudhary (1999)** Epistasis detection was carried out according to the method outlined by **Kearsey and Jinks (1968)** and is based on the genetic model;

$$L_{ijk} = M + G_{ij} + R_k + E_{ijk}$$

Where,

L_{ijk} = Phenotypic value of cross between tester i and line j in k replication.

M = Overall mean of all single and three way crosses.

G_{ij} = Genotypic value of cross between tester i and line j.

R_k = Effect of kth replication.

E_{ijk} = Error.

The mean squares for $L_{1i} + L_{2i} - 2L_{3i}$ deviations was used for epistasis detection. The overall epistasis was partitioned into (i) type of epistasis (additive x additive) and (i + j) type due to (additive x dominance) and (dominance x dominance) gene interactions. The estimation of additive (D) as well as dominance (H) genetic components and the correlation coefficient (r) between sums ($L_{1i} + L_{2i} + L_{3i}$) and differences ($L_{1i} - L_{2i}$) were obtained to reveal the direction of dominance, according to **Jinks and Perkins (1970)**. The degree of dominance was calculated as $\sqrt{H/D}$. Where, (H) and (D) indicated to dominance as well as additive variance components, respectively.

RESULTS AND DISCUSSION

Analysis of variance for the studied traits are presented in Table (2). Results revealed significant differences for each of genotypes, parents, lines and testers for all the studied traits except, for BW at both lines and testers and UI at testers only. Moreover, hybrids showed significant mean square for all studied traits, this indicating that the parent lines and testers utilized in the current study were divergent, and that significant differences were passed down via the progenies.

Also, significant differences for lines vs. testers were observed for all the studied traits, highlighting the importance of both additive and non-additive types of gene action in influencing these traits. Furthermore, hybrids vs. parents revealed significant differences in all the studied characteristics, similar results were those obtained by (**Abou El-Yazied, 2014 ; Dawwam et al., 2016 ; El-Mansy et al., 2020 ; Amer, 2020 ; Said et al., 2021**).

Data concerning that mean performance of the tested genotypes (13 parents, 20 single crosses as well as 10 three-way crosses) are exhibited in Table (3). The L_1 (Giza 80) gave the highest values for SI and LI, while L_2 (Giza 86) gave the best means for BW, L_3 (Giza 87) recorded the highest values for PI, L_6 (Giza 92) had the best values for SCY/P, MR, 2.5% SL and UI, while, L_{10} (Pima S6) had the best means for L%. While, for testers, T_1 (Giza 94) had the highest values for BW, SI and LI, T_2 (Giza 96) gave the best values for SCY/P, LCY/P, MR, PI, 2.5% SL and UI% although, T_3 (Giza 94 x Giza 96) had the best mean for L%.

The results additionally showed best mean performances for the three-way cross $L_6 \times T_3$ (Giza 92 x (Giza 94 x Giza 96)) for SCY/P, LCY/P and PI. On the other side, the three-way cross $L_4 \times T_3$ (Giza 88 x (Giza 94 x Giza 96)) gave the highest mean values for BW, PI and 2.5% SL. The crosses $L_1 \times T_1$ and $L_3 \times T_3$ [Giza 80 x Giza 94 and (Giza 87 x (Giza 94 x Giza 96))

had the best means for BW. The three-way cross $L_1 \times T_3$ (Giza 80 x (Giza 94 x Giza 96)) gave the best values for L%, SI and LI. While, the crosses $L_6 \times T_1$ and $L_4 \times T_2$ (Giza 92 x Giza 96) and (Giza 88 x Giza 96) had the highest mean value for MR. The cross $L_6 \times T_1$ (Giza 92 x Giza 94) gave the best values for UI%.

Regarding to epistasis, analysis of variance (Table 4) revealed highly significant overall epistasis for all studied traits. Partition of total epistasis into (i) type of epistatic (additive x additive) and (i + j) types of epistasis (additive x dominance) as well as (dominance x dominance) indicated non-significant involvement of (i) type for all studied traits. On the other hand, (i + j) types of epistasis were highly significant for all studied traits. The epistatic type (i) interaction, was detected to be much larger in magnitudes than the other epistatic type (i + j) for all studied traits except for SI, indicating that fixable components of epistasis were more important than non fixable one in the inheritance of these trait. Thus, the breeder should take epistatic into account in producing genetic models for studying quantitative traits. Similar results were obtained by (**Hussain et al., 2008 ; Sohu et al., 2010 ; El-Lawendey et al., 2010 ; Saleh, 2013 ; Jayade et al., 2014 ; Dawwam et al., 2016 ; Al-Hibbiny et al., 2020 ; El-Mansy et al., 2020**).

The individual epistatic deviations of lines are shown in Table (5). The data showed that the epistatic deviations were exhibited by L_1 (Giza 80) that had significant negative for SCY/P, LCY/P, L%, SI, LI and MR. In contrast, there were significant positive for 2.5% SL and PI. L_2 (Giza 86) was significant negative for SCY/P, LCY/P, L%, SI, LI, MR and PI. L_3 (Giza 87) was significant negative for all studied traits except, for L% and PI. Regarding L_4 (Giza 88) was negative significantly for all studied traits except, for L% and BW, while gave significant positive epistatic deviations for MR, as well as L_5 (Giza 90) was significant negative for all studied traits except, for BW and UI. On the other hand, L_6 (Giza 92) exhibited significant negative for SCY/P, LCY/P, L%, MR and PI and significant positive for BW, SI, LI and UI. Concerning, L_7 (10229) had significant negative for SCY/P, LCY/P, BW, MR and 2.5% SL but, significant positive for L%, SI, LI and UI. Regarding L_8 (Pima S7) was significant negative for all studied traits except, for L%, 2.5% SL and UI. While, L_9 (Karshenky) had significant negative for all studied traits except, for MR and 2.5% SL. whereas, L_{10} (Pima S6) had significant negative for all studied traits except, for SCY/P and significant positive for BW and SI. It is evident that all lines exhibited epistatic deviation for most studied traits. Similar results were obtained by

(Saleh, 2013 ; Abou El-Yazied, 2014 ; Jayade *et al.*, 2014 ; Al-Hibbiny *et al.*, 2020).

Analysis of variance for sums as well as differences between hybrids (Table 6) indicated that sums item ($L_{1i}+L_{2i}$) were significant for all traits except, for BW and MR. The differences in items ($L_{1i}-L_{2i}$) were significant for all traits with the exception of, BW which exhibited insignificant differences. High values of additive genetic variance were found as compared with dominance genetic variance for all studied traits except, for BW and MR. The degree of dominance ($\sqrt{H/D}$) on the other side was less than unity, suggesting the role of partial or incomplete dominance controlling for all studied traits except, for BW and MR which, showed overdominance (greater than unity). Consequently, it concluded that selection procedures in early generations based on accumulation of additive effects would be successful in improving these traits. Similar

results were obtained by (Saleh, 2013 ; Dawwam *et al.*, 2016 ; El-Mansy *et al.*, 2020). Further, the correlation coefficient between the sums ($L_{1i} + L_{2i}$) and difference ($L_{1i} - L_{2i}$) were found to be negative and insignificant for SCY/P, LCY/P and 2.5% SL. However, the other traits were positive and non-significant, these results pointed out that the genes with positive and negative dominant alleles were dispersed between testers and didn't show any proof of directional dominance for these traits. Similar results were obtained by (El-Lawendey *et al.*, 2010) demonstrated non-significant correlation coefficient of sums and differences was found for all traits, revealing that dominant genes were umbidirectional among parents. On the other hand, significant positively additive correlation among lint cotton yield/plant and each of lint index and seed index were also detected.

Table 2. Mean square estimates for the studied traits in triple test cross (TTC)

S.O.V	d.f.	SCY/P (g)	LCY/P (g)	L %	BW (g)	SI (g)	LI (g)	MR	PI	2.5% SL	UI %
Replications	2	20.96	7.44	1.09	0.04	0.07	0.06	0.01	0.04	0.05	1.16
Genotypes	42	4512.60**	813.18**	8.83**	0.17**	1.43**	1.60**	0.30**	1.25**	7.41**	8.79**
Crosses (C)	29	1706.16**	305.52**	2.17**	0.06**	0.54**	0.55**	0.20**	0.92**	5.89**	7.14**
Parents (P)	12	6101.38**	944.34**	16.47**	0.22**	2.71**	2.08**	0.56**	1.83**	11.54**	12.56**
Lines (L)	9	3700.28**	419.89**	18.79**	0.20	2.31**	2.51**	0.61**	2.08**	11.60**	15.82**
Testers (T)	2	3390.54**	619.50**	1.76**	0.01	0.90**	0.93**	0.37**	0.32**	16.47**	0.05
P ₁ + P ₂ Vs. F ₁	1	4968.00**	923.20**	1.20*	0.01	0.30*	0.45**	0.43**	0.24**	0.20	0.07
P ₁ Vs. P ₂	1	157.08**	8.06**	1.92**	0.02	1.40**	1.25**	0.17**	0.33**	32.67**	0.01
L Vs. T	1	33132.96**	6314.09**	25.07**	0.80**	9.91**	0.58**	0.49**	2.60**	1.14**	8.29**
C Vs. P	1	66833.85**	13961.26**	110.54**	2.74**	11.67**	26.22**	0.16**	3.67**	2.10**	11.33**
Error	84	6.58	1.91	0.52	0.03	0.09	0.09	0.03	0.05	0.13	0.53

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

Table 3. Mean performance of the tested genotypes for the studied traits

Genotypes	SCY/P (g)	LCY/P (g)	L %	BW (g)	SI (g)	LI (g)	MR	PI	2.5% SL (mm)	UI%
Giza 80 x Giza 94	146.63	60.07	40.97	3.67	10.90	7.56	4.00	9.73	32.10	87.63
Giza 86 x Giza 94	164.30	62.77	38.20	3.55	10.70	6.62	4.07	9.83	34.83	88.17
Giza 87 x Giza 94	134.00	53.87	40.20	3.30	11.20	7.53	3.80	11.07	34.87	86.40
Giza 88 x Giza 94	154.30	64.34	41.70	3.37	10.83	7.75	4.30	10.23	33.57	87.07
Giza 90 x Giza 94	139.27	56.22	40.37	3.27	10.73	7.27	3.93	10.60	31.93	85.23
Giza 92 x Giza 94	187.77	75.22	40.07	3.53	11.13	7.44	3.40	10.83	35.03	88.67
10229 x Giza 94	168.70	68.83	40.80	3.28	10.93	7.53	3.60	11.17	33.53	87.67
Pima S7 x Giza 94	162.60	66.46	40.87	3.50	10.87	7.51	3.93	10.37	31.47	86.40
Karshenky x Giza 94	138.17	54.62	39.53	3.33	10.33	6.76	3.60	10.20	33.00	84.37
Pima S6 x Giza 94	158.83	63.85	40.20	3.60	10.17	6.84	4.17	10.27	31.57	84.03
Giza 80 x Giza 96	154.00	63.55	41.27	3.23	10.03	7.05	3.80	10.40	35.13	86.17
Giza 86 x Giza 96	170.07	68.31	40.17	3.47	10.53	7.07	3.83	9.93	34.17	87.60
Giza 87 x Giza 96	133.63	54.48	40.77	3.47	10.20	7.02	4.10	11.37	33.67	86.70
Giza 88 x Giza 96	155.07	61.67	39.77	3.57	10.37	6.85	3.60	10.77	35.87	87.50
Giza 90 x Giza 96	142.70	58.94	41.30	3.35	10.60	7.46	3.93	10.63	34.27	84.07

Giza 92 x Giza 96	198.97	78.12	39.27	3.53	10.57	6.83	4.30	11.40	35.10	87.47
10229 x Giza 96	163.73	66.69	40.73	3.20	10.80	7.42	4.17	10.70	33.20	86.73
Pima S7 x Giza 96	193.27	79.89	41.33	3.30	10.27	7.23	4.13	10.23	32.93	85.00
Karshenky x Giza 96	152.03	60.31	39.67	3.32	10.40	6.84	4.30	10.57	32.13	84.13
Pima S6 x Giza 96	169.30	67.44	39.83	3.25	10.23	6.78	3.90	10.23	31.17	83.53
Giza 80 x (Giza 94 x Giza 96)	195.93	82.22	41.97	3.40	11.40	8.24	4.13	9.90	33.27	86.70
Giza 86 x (Giza 94 x Giza 96)	212.83	87.34	41.03	3.50	11.10	7.72	4.17	10.17	34.63	88.00
Giza 87 x (Giza 94 x Giza 96)	184.80	75.03	40.60	3.67	10.83	7.41	4.27	11.33	35.23	88.63
Giza 88 x (Giza 94 x Giza 96)	194.67	79.75	40.97	3.47	11.40	7.91	3.67	11.67	35.97	87.80
Giza 90 x (Giza 94 x Giza 96)	181.27	75.71	41.77	3.30	11.00	7.89	4.20	11.23	34.57	84.83
Giza 92 x (Giza 94 x Giza 96)	215.33	87.85	40.80	3.33	9.87	6.80	4.33	11.67	35.07	87.43
10229 x (Giza 94 x Giza 96)	186.57	74.26	39.80	3.50	10.33	6.83	4.03	11.00	33.77	86.77
Pima S7 x (Giza 94 x Giza 96)	210.73	87.45	41.50	3.55	11.13	7.90	4.27	10.70	32.40	85.90
Karshenky x (Giza 94 x Giza 96)	184.00	74.34	40.40	3.60	10.53	7.14	3.67	11.37	32.10	84.70
Pima S6 x (Giza 94 x Giza 96)	170.90	71.27	41.70	3.28	9.87	7.06	4.13	10.60	32.10	84.13
Giza 80 (L ₁)	80.23	32.06	39.97	3.48	11.83	7.88	4.53	9.30	32.33	87.00
Giza 86 (L ₂)	79.47	28.31	35.62	3.52	10.47	5.79	4.17	10.60	35.30	87.57
(Giza 87 (L ₃))	71.47	26.99	37.77	3.13	9.50	5.76	3.77	11.77	34.50	85.07
Giza 88 (L ₄)	102.63	41.48	40.46	3.28	10.67	7.28	4.47	10.63	35.33	86.27
Giza 90 (L ₅)	72.57	29.41	40.52	3.16	10.70	7.30	4.40	9.90	30.93	82.70
Giza 92 (L ₆)	170.80	58.59	34.31	2.92	9.77	5.10	3.23	11.50	35.73	89.00
10229 (L ₇)	122.07	46.11	37.78	2.97	9.70	5.89	3.43	11.03	33.50	86.17
Pima S7 (L ₈)	157.03	59.47	37.87	3.15	11.17	6.81	4.10	9.33	30.20	81.27
Karshenky (L ₉)	109.17	38.57	35.32	3.48	10.00	5.47	3.60	10.27	33.13	84.70
Pima S6 (L ₁₀)	87.43	36.42	41.69	2.74	8.83	6.34	4.07	10.13	31.53	84.43
Giza 94 (T ₁)	150.17	60.51	40.30	2.90	9.40	6.35	3.70	9.73	31.20	86.57
Giza 96 (T ₂)	160.40	62.83	39.17	2.77	8.43	5.43	3.37	10.20	35.87	86.60
Giza 94 x Giza 96 (T ₃)	212.83	86.48	40.63	2.86	9.37	6.44	4.07	9.57	33.90	86.37
LSD _{0.05}	7.28	2.12	0.57	0.03	0.10	0.11	0.03	0.06	0.15	0.58
LSD _{0.01}	10.37	3.02	0.81	0.04	0.14	0.15	0.04	0.09	0.21	0.83

Table 4. Disclosing the presence of epistasis mean square for the studied traits

S.O.V	d.f.	SCY/P (g)	LCY/P (g)	L %	BW (g)	SI (g)	LI (g)	MR	PI	2.5% SL (mm)	UI%
Total epistasis ($L_{1i} + L_{2i} - 2L_{3i}$)	10	16221.50**	3148.02**	13.12**	0.37**	4.31**	3.98**	0.90**	4.10**	6.89**	6.78**
(i) type of epistasis	1	141480.80	27868.57	59.36	0.39	2.95	12.48	2.47	22.88	22.53	8.32
(i + j) type of epistasis	9	2303.80**	401.29**	7.99**	0.37**	4.46**	3.04**	0.73**	2.02**	5.15**	6.61**
i type x replications	2	35370.20	6967.14	14.84	0.10	0.74	3.12	0.62	5.72	5.63	2.08
(i + j) type x replications	18	16.43	5.79	0.92	0.13	0.19	0.22	0.15	0.24	0.54	0.50
Total epistasis x replications	20	3551.81	701.93	2.31	0.13	0.24	0.51	0.20	0.79	1.05	0.66

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

Table 5. Individual epistatic deviations of ten cotton lines for the studied traits

Lines	SCY/P (g)	LCY/P (g)	L %	BW (g)	SI (g)	LI (g)	MR	PI	2.5% SL (mm)	UI%
Giza 80	-91.23*	-40.82**	-1.70**	0.10	-1.87**	-1.87**	-0.47**	0.33*	0.70*	0.40
Giza 86	-91.30**	-43.59**	-3.70**	0.01	-0.97**	-1.76**	-0.43**	-0.57**	-0.27	-0.23
Giza 87	-101.97**	-41.71**	-0.23	-0.57**	-0.27**	-0.26*	-0.63**	-0.23	-1.93**	-4.17**
Giza 88	-79.97**	-33.49**	-0.47	0.01	-1.60**	-1.23**	0.57**	-2.33**	-2.50**	-1.03**
Giza 90	-80.57**	-36.26**	-1.87**	0.02	-0.67**	-1.05**	-0.53**	-1.23**	-2.93**	-0.37
Giza 92	-43.93**	-22.37**	-2.27**	0.40**	1.97**	0.68**	-0.97**	-1.10**	0.01	1.27**
10229	-40.70**	-12.99**	1.93**	-0.52**	1.07**	1.30**	-0.30**	-0.13	-0.80*	0.87**
Pima S7	-65.60**	-28.56**	-0.80	-0.31**	-1.13**	-1.06**	-0.47**	-0.80**	-0.40	-0.40
Karshenky	-77.80**	-33.75**	-1.60**	-0.55**	-0.33**	-0.69**	0.57**	-1.97**	0.93**	-0.90**
Pima S6	-13.67	-11.25**	-3.37**	0.28**	0.67**	-0.50**	-0.20*	-0.70**	-1.47**	-0.70*
LSD 0.05	18.99	6.70	1.06	0.15	0.22	0.25	0.18	0.28	0.62	0.58
LSD 0.01	27.95	9.86	1.56	0.22	0.32	0.37	0.26	0.41	0.91	0.85

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

Table 6. Mean square for sums and differences as well as estimates of additive, dominance, degree and direction of dominance for the studied traits

S.O.V	d.f.	SCY/P (g)	LCY/P (g)	L %	BW (g)	SI (g)	LI (g)	MR	PI	2.5% (mm)	SL	UI %
Sums ($L_{1i}+L_{2i}$)	9	3905.28**	599.23**	5.63**	0.10	0.51**	0.80**	0.04	2.36**	17.09**		28.52**
Sums x replicates	18	12.00	2.74	0.34	0.06	0.11	0.11	0.03	0.06	0.15		0.51
Differences ($L_{1i} - L_{2i}$)	9	293.63**	62.16**	3.25**	0.13	0.43**	0.51**	0.75**	0.38**	7.24**		1.38*
Differences x replicates	18	7.19	2.44	0.25	0.03	0.05	0.06	0.04	0.08	0.18		0.22
D (additive)		2595.52	397.66	3.53	0.03	0.26	0.46	0.01	1.53	11.30		18.68
H (dominance)		190.96	39.81	2.00	0.07	0.25	0.30	0.48	0.20	4.70		0.78
Degree of dominance (H/D) ^{1/2}		0.27	0.32	0.75	1.63	0.98	0.81	9.13	0.36	0.65		0.20
Direction of dominance (r)		-0.43	-0.32	0.22	0.11	0.33	0.45	0.44	0.03	-0.04		0.02

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

CONCLUSIONS

Estimating the genetic components for yield, its component as well as fiber quality properties of any cotton population is critical for developing a suitable and effective breeding programme. This study demonstrates the significance of epistasis as a component of genetic variation and the importance of cotton breeders taking it into account and not ignoring it when developing a programme aimed at improving the studied traits.

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الملخص العربي

التقديرات الوراثية لبعض الصفات الكمية في القطن باستخدام التهجين الإختباري الثلاثي

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أجريت هذه الدراسة في محطة البحوث الزراعية بسخا - مركز البحوث الزراعية بمحافظة كفر الشيخ خلال مواسم (2021 - 2023) بهدف تقدير مكونات التباين الوراثي (الإضافي - السيادي - التفوق) لبعض صفات المحصول و خصائص جودة الألياف وتحديد أهمية هذه المكونات في التباين الكلي باستخدام نموذج التهجين الرجعي الثلاثي حيث تم التهجين بين الصنفين سوبر جيزة 94 و أكسترا جيزة 96 خلال موسم 2021 للحصول على الهجين الفردي (سوبر جيزة 94 x أكسترا جيزة 96) وفي موسم 2022 تم التهجين بين ثلاثة تراكيب وراثية ككشافات وهي سوبر جيزة 94 ، أكسترا جيزة 96 والهجين الفردي (سوبر جيزة 94 x أكسترا جيزة 96) مع عشر تراكيب وراثية كسلالات وهي جيزة 80 ، جيزة 86 ، جيزة 87 ، جيزة 88 ، جيزة 90 ، جيزة 92 ، و التركيب الوراثي 10229 ، بيما س7 ، كارشكي وبيما س6 ، كما تم تقييم 43 تركيب وراثي خلال موسم 2023 في تجربة بتصميم القطاعات كاملة العشوائية ذات ثلاث مكررات و يمكن تلخيص النتائج المتحصل عليها كما يلي:

- أظهر تحليل التباين وجود فروق معنوية بين التراكيب الوراثية والآباء والهجن والسلالات والكشافات والسلالة vs. الكشاف والهجن vs. الآباء لمعظم الصفات المدروسة.
- أظهرت النتائج وجود معنوية للفعل الجيني التفوقي الكلي لكل الصفات المدروسة وكذلك كان التفاعل الإضافي (الإضافي × الإضافي) غير معنوي لكل الصفات المدروسة بينما كان التفاعل الإضافي × السيادي و السيادي × السيادي معنوياً لكل الصفات المدروسة.
- كان التفاعل الإضافي × الإضافي أكبر من التفاعل الإضافي × السيادي و السيادي × السيادي لكل الصفات المدروسة ماعدا صفة معامل البذرة.
- كانت قيم الفعل الوراثي الإضافي أكبر من قيم الفعل الوراثي السيادي لجميع الصفات المدروسة ماعدا صفتي وزن اللوزة وقراءة الميكرونيير مما إنعكس على إنخفاض قيم درجة السيادة عن الواحد الصحيح لكل الصفات المدروسة ماعدا صفتي وزن اللوزة وقراءة الميكرونيير وبالتالي يمكن للمربي تحسين هذه الصفات من خلال الإنتخاب لهذه الصفات في الأجيال الإنعزالية المبكرة بينما الصفات التي تأثرت في توريثها بالتباين السيادي فيكون من المفيد تأخير الإنتخاب إلى الأجيال المتأخرة ولهذا فإن استخدام الإنتخاب المتكرر والتزاوج بين العشائر ربما يكون مفيد بمعنى انه يمكن ان يستغل كلاً من المكون الإضافي وغير الإضافي من التباين الوراثي في تحسين مثل هذه الصفات.
- تظهر هذه الدراسة أهمية التفوق كمكون من مكونات التباين الوراثي وضرورة أخذه في الإعتبار وعدم تجاهله بواسطة مربى القطن عند وضع برنامج يهدف الى تحسين الصفات المدروسة.