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Estimation of Genetic Parameters of Some Yield and Fiber Quality Traits in Cotton Using Triple Test Cross Analysis

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ABSTRACT

This study was done at Sakha Experimental Station; Agriculture Research Center, Kafr El-Sheikh governorate, Egypt, during three seasons (2022-2024). Triple test cross manner was employed to disclose epistasis, additive, and dominance components of genetic variability for cotton yield, its components and fiber quality traits, three testers: Giza 86, Giza 93 and their F_1 hybrid (Giza 86 x Giza 93) were crossed as male parents to ten cotton lines as female parents: Giza 89, Giza 92, Giza 94, Giza 95, Giza 96, Pima S_4, Pima S_7, Karshenky, 10229 and Australy 13. In 2024 season a randomized complete blocks design with three replications was carried to evaluate 43 genotypes including three testers, ten inbred lines, 20 single crosses and 10 three-way crosses. Results revealed significant differences due to genotypes, parents, lines, hybrids and hybrids *vs*. parents for all studied trait, while Significant the testers and lines *vs*. testers were detected for most studied traits. The mean square for the deviations total epistasis (L1i + L2i - 2L3i) revealed the presence of highly significant epistasis for all studied traits except micronaire reading. Showed that mean squares estimates due to additive × additive (i) type were found to be non significant for all the traits studied. The presence of (j+l) epistatic types appeared to be highly significant in the inheritance of all the traits studied except micronaire reading. The epistatic type (i) interactions, was larger in magnitudes than the other epistatic type (j+l) for all traits studied except boll weight, lint index and micronaire reading. Additive Variances were greater than dominance variance for all studied traits. The degree of dominance (√H/D) was less than unity suggesting the role of partial or incomplete dominance for all the studied traits.

Keywords: Cotton, triple test cross, epistasis, gene action.

1. Introduction

The success in the selection of plant breeding programme largely depends upon the availability of reliable information about the nature and magnitude of gene action presents in the material being handled by the breeder. Several biometrical methods are available for obtaining information on the nature of genetic variation. The North Carolina Design III (NCD III) of Comstock and Robinson (1952) in which homozygous parents are crossed and F_2 plants are back crosses to each of the parents provides reliable estimate of additive and dominance components, but it assumes to no epistasis. Kearsey and Jinks (1968) extended this concept and included back Crosse to the F_1 generation. This type of experiment was called Triple Test Cross by Jinks *et al.* (1969) and it is modified by many other workers (Jinks and Perkins, 1970; Perkins and Jinks, 1971 and Jinks and Virk, 1977). This method is the most efficient for detection and estimation of epistatic variation. If epistasis is present in the material investigated, one can obtain better estimation of additive and dominance components by this method by compared to the other methods (Chahal and Singh, 1974). It also provides unbiased estimates of genetic variation.

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AL-Hibbiny *et al.* (2020) In their study showed that the mean squares between L1, L2 and L3 were highly significant for all traits studied, while between L1 and L2 Families, they found significant variances for boll weight, lint percentage, lint index, fiber length and micronaire reading. Overall epistatic gene effects were highly significant differences for all studied traits except for fiber length and fiber strength. The (i) fixable type (additive × additive) was the most important epistatic effect than j and 1 non-fixable type for all traits. Both additive and dominance components were highly significant for all the studied traits. The degree of dominance was less than unity and confirmed the presence of partial dominance for all studied traits except for lint yield/plant; lint index and seed index which showed over-dominance. The Additive gene action played an important role in controlling inheritance for all traits studied than dominance one, except for lint yield/plant; lint index and seed index. Direction of dominance (r) was non-significant for most traits indicating absence of dominance directional. Due to influence of (i) type of epistatic effects for the majority of the studied traits, selection in early generations may be recommended. Genotypic correlation was positive and significant between yield traits and its components.

El-Shazly *et al.* (2024) found that the 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 epitasis (L1i + L2i - 2L3i) revealed the presence of highly significant epistasis for all studied traits. Mean squares estimates due to additive × 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 for all the studied traits. The epistatic type (i) interaction, was detected to be 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 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).

The present investigation was undertaken to detect the presence of epistasis and to estimate the additive and dominance as the genetic variation components for some quantitative traits in cotton genotypes.

2. Materials and Methods

2.1. Materials

The materials used in this study contained of twelve cotton genotypes derived from various origins and belong to *Gossypium barbadense* L. The origin, pedigree and category of these genotypes were presented in Table (1). Selfed seeds of the twelve genotypes were received from Cotton Breeding Department, Cotton Research Institute, Agricultural Research Center (ARC), Giza, Egypt. The field work was conducted at Sakha Experimental Station; ARC, Kafr El-Sheikh governorate, Egypt, during three growing seasons (2022 – 2024).

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

Parents	Origin	Pedigree	Category
Giza 89	Egypt	(G.75 x R.6022)	Long staple
Giza 92	Egypt	Giza 84 x (Giza 74 x Giza 68)	Extra Long staple
Giza 94	Egypt	10229 x G.86	long staple
Giza 95	Egypt	(G83 x (G75 x 5844) x G80	long staple
Giza 96	Egypt	(Giza 84 x (Giza 70 x Giza 51b)) x S62	Extra Long staple
Pima S_4	America	{(P 32 x S1 10-8) x Pima S2}	Long staple
Pima S_7	America	(6614-91-9-3 x 6907-513-509-501).	Long staple
Karshenky	Russian	Unknown	Long staple
10229	Russian	Unknown	Long staple
Australy 13	Australian	Unknown	Long staple
Giza 86 (P_1)	Egypt	G. 75 x G. 81	Long staple
Giza 93 (P_2)	Egypt	Giza 77 x Pima S_6	Long staple
P_1 x P_2 (F_1)	Egypt	Giza 86 x Giza 93	Long staple

2.2. Methods

Two cotton varieties, Giza 86 and Giza 93 designated as (T1) and (T2), respectively were used as tester genotypes. The two varieties were sown in the first season (2022) and crossed to obtain F_1 hybrid that was used as the third tester designated as (T3). In the second season (2023) ten cotton lines: Giza 89, Giza 92, Giza 94, Giza 95, Giza 96, Pima S_4, Pima S_7, Karshenky, 10229 and Australy 13 were used as female parents and pollinated by the three testers (T1, T2 and T3) in the entire triple test cross combinations.

In the growing season of 2024, the experimental materials consisted of 43 genotypes including three testers (one of them is a single cross), ten inbred lines, 20 single crosses and 10 three-way crosses were planted in a randomized complete block design (RCBD) with three replications. Each replicate contained four rows for each genotype, the row was 4 m long, and 0.70 m width and 40 cm between hills with one plant left per hill. The normal 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 per plant (SCY/P), lint cotton yield per plant (LCY/P) in grams, lint percentage (L %), boll weight (BW), seed index and lint index (SI). In addition to four fiber quality traits which were: Micronaire reading (Mic.), fiber strength (FS) as Pressley index, fiber length (FL) as the upper half mean in mm, and lint uniformity index (UI%), these traits were estimated at the Cotton Technology Laboratories, Cotton Research Institute, ARC, Giza, Egypt.

2.3. Statistical analysis

The triple test cross (TTC) model explained by Ketata *et al.* (1976) that use number of different lines to be crossed with the testers T1, T2 and T3 instead of number of individual plants from F_2 as elucidated by Kearsey and Jinks (1968) to explore the presence of epistasis and to determine the additive and dominance components of genetic variability as well as degree and direction of dominance for various traits.

The analysis of variance was done as outlined by Singh and Chaudhary (1999) to estimate the significance of treatments and to partition the treatment effect as well as to determine the significance of variances among each of hybrids, parents, lines, testers, $P_1 + P_2$ *vs*. F_1, P_1 *vs*. P_2, lines *vs*. testers and hybrids *vs*. parents for the studied traits through the TTC manner.

2.4. Test for epistasis

Test of significance of the difference (L_1i + L_2i – 2L_3i (i =genotypes)) gives information for the presence of epistasis. So, ten values (i=1 to 10) were estimated to test overall epistasis (Jinks and Virk, 1977) as described by Singh and Chaudhary (1999) as follows:

Total epistasis was estimated as uncorrected genotypes sums of square [∑ (L_1i + L_2i – 2L_3i)/ 10] at 10 degrees of freedom. Resultant total epistasis was partitioned into two components i.e. (*i*) type that measures additive part of epistasis for 1 degree of freedom = [∑(L_1i + L_2i – 2L_3i)/30] and (*j* + *l*) type that measures additive x dominance and dominance x dominance part for 9 degrees of freedom = [Total epistasis – (*i*) type].

2.5. Individual genotypic epistasis

Individual genotypic contribution for each line relative to the total epistasis was evaluated and tested for significance as described by Ketata *et al.* (1976) for those traits which had significant total epistasis as follows: Individual genotypic epistasis = [(∑(L_1i – L_2i – 2L_3i)/r], the resulted value of each genotype for a trait was tested using a t-test with 19 degrees of freedom as follows: t = Mean / S_E, where: S_E= (error mean square /r) $^{1/2}$.

2.6. Evaluation of Additive and dominance components

In the absence of epistasis, TTC method also provides means for evaluating additive (D) and dominance (H) components of variance as illustrated by Kearsey and Jinks (1968) and Jinks *et al.,* (1969). The sum of L_1i + L_2i (testers) for each genotype (line) was calculated for each replication and subjected to the analysis of variance as follows:

Table 2: The analysis of variance for sums (additive) and differences (dominance).

Sums			
Source of variation	**d.f**	**MS**	**Expected (MS)**
Replications	*r-1*	MSr	
Genotype sums (**L_1j + L_2j**)	*n-1*	MSs	δ^2e + 2rδ^2s
Error	(*n-1*)(*r-1*)	MSe	δ^2e
	Differences		
Source of variation	**d.f**	**MS**	**Expected (MS)**
Replications	*r-1*	MSr	
Genotype difference (**L_1j - L_2j**)	*n-1*	MSd	δ^2e + 2rδ^2d
Error	(*n-1*)(*r-1*)	MSe	δ^2e

The observed mean squares were substituted into the equations as follows:
δ^2s = (MSs – MSe)/2r; δ^2s = (1/4) D D = 4(MSs – MSe)/2r
δ^2d = (MSd – MSe)/2r; δ^2d = (1/4) H H = 4(MSd – MSe)/2r
Where: r= Replication; n= Genotypes; MSr, MSs, MSe= Mean squares of replications, genotypes (sums) and error, respectively; δ^2e and δ^2s= Expected mean square of error and genotypes (sums), and the same for the differences.

2.7. Degree and direction of dominance and types of genes exhibiting dominance

Mean degree of dominance was calculated according to Singh and Chaudhary (1999) as follows: Degree of dominance = $(H/D)^{1/2}$, Where (H) and (D) are the dominance and additive variance components, respectively.

While direction of dominance was detected using the correlation coefficients of sums/differences to test the significance of F value for all genotypes. Significant positive and negative correlations reflect the direction towards decreasing and increasing values of the trait, respectively (Jinks *et al.,* 1969).

3. Results and Discussion

The analysis of variance for all studied traits is given in Table (3). Results revealed significant differences for each of genotypes, hybrids, parents and lines for all studied traits, however, significant differences among testers for the yield and its components traits and fiber length, except for boll weight, micronaire reading and fiber strength for denote the presence of abundant genetic variation among these genotypes, indicating the existence of adequate heterogeneity in the triple test cross progenies for disclosing the new genetic recombination.

On the other hand, lines *vs.* testers exhibited significant differences for all the studied traits except seed index and lint index that pointed out to the importance of both additive and non-additive types of gene action for controlling these traits. Furthermore, hybrids *vs.* parents showed significant differences for all the studied traits were recorded by Abou El-yazied (2014); Dawwam, *et al.* (2016); Amer (2020); El-Mansy *et al.* (2020); Said *et al.* (2021) and Hassan *et al.* (2022). These results denoted the adequacy for going on to the modified triple test cross (TCC) analysis.

Table 3: Mean squares from the analysis of variance for the triple test crosses for all the studied traits.

S.O.V	**d.f**	**Seed cotton yield/plant**	**Lint cotton yield/plant**	**Lint percentage**	**Boll weight**	**Seed index**
Replications	2	32.68	6.70	0.08	0.00	0.00
Genotypes	42	1957.69**	335.36**	4.74**	0.14**	1.50**
Hybrids (H)	29	1456.87**	229.09**	2.18**	0.07**	1.12**
Parents (P)	12	2031.81**	362.57**	9.49**	0.15**	1.69**
Lines (L)	9	2113.68**	371.89**	10.05**	0.16**	2.23**
Testers (T)	2	1028.97**	287.41**	10.75**	0.04	0.12**
P_1+ P_2 *Vs.* F_1	1	1021.82**	252.02**	5.32**	0.05	0.06
P_1 *Vs.* P_2	1	695.53**	238.78**	14.42**	0.01	0.17
L *Vs.* T	1	3300.70**	428.99**	1.87**	0.28**	0.04
H *Vs.* P	1	15592.18**	3090.77**	21.94**	1.99**	10.10**
Error	84	37.71	5.93	0.13	0.01	0.02

Table 3: Cont.

S.O.V	d.f	Lint index	Micronaire reading	Fiber strength	Fiber length	Uniformity index
Replications	2	0.01	0.05	0.01	0.17	0.88
Genotypes	42	1.00**	0.35**	1.51**	9.02**	13.78**
Hybrids (H)	29	0.55**	0.33**	0.74**	4.48**	7.79**
Parents (P)	12	1.21**	0.40**	1.75**	12.25**	14.20**
Lines (L)	9	1.34**	0.45**	1.65**	10.24**	9.87**
Testers (T)	2	1.22**	0.08	0.04	6.45**	4.90**
P_1+ P_2 *Vs*. F_1	1	0.61**	0.00	0.05	5.32**	4.59
P_1 *Vs*. P_2	1	1.62**	0.17**	0.01	5.80**	3.68
L *Vs*. T	1	0.05	0.59**	6.09**	41.93**	71.78**
H *Vs*. P	1	11.43**	0.30**	20.82**	102.15**	182.40**
Error	84	0.02	0.05	0.02	0.07	0.88

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

Mean performances of the studied genotypes

Data concerning the mean performance of the tested genotypes (13 parents, 20 single crosses and 10 triple crosses) are exhibited in Table (4). For the lines; Giza 92 gave the best values for micronaire reading and fiber strength. Giza 94 had the highest means for seed index and lint index. Giza 95 recorded the highest values for lint percentage. Australy 13 had the best values for lint cotton yield/plant, while for testers (Giza 86 x Giza 93) had the best means for seed cotton yield/plant, boll weight, fiber length and uniformity index.

The results also showed that the best mean performances were found for the triple crosses; the cross (Giza 92 x (Giza 86 x Giza 93)) for boll weight, seed index and fiber strength. The triple cross (Giza 95 x (Giza 86 x Giza 93)) gave the best values for lint percentage. The triple cross (Giza 96 x (Giza 86 x Giza 93)) gave the best values for fiber length and uniformity index. The cross (pima S_4 x (Giza 86 x Giza 93)) had the best means for micronaire reading. The cross (Karshenky x (Giza 86 x Giza 93)) gave the best values for lint index. The cross (Australy 13 x (Giza 86 x Giza 93)) had the best means for seed cotton yield/ plant and lint cotton yield/ plant.

Table 4: Mean performances of the tested genotypes for the studied traits

Genotypes	Seed cotton yield/plant	Lint cotton yield/plant	Lint percentage	Boll weight	Seed index
Giza 89 x Giza 86	166.13	66.69	40.13	3.70	10.47
Giza 92 x Giza 86	144.23	58.90	40.83	3.53	11.40
Giza 94 x Giza 86	186.67	76.16	40.80	3.50	12.27
Giza 95 x Giza 86	144.90	60.37	41.67	3.37	10.40
Giza 96 x Giza 86	176.63	69.71	39.47	3.53	11.27
Pima S4 x Giza 86	130.17	52.68	40.47	3.70	10.30
Pima S7 x Giza 86	156.63	62.69	40.03	3.47	11.37
Karshenky x Giza 86	155.93	62.94	40.37	3.63	11.03
10229 x Giza 86	128.20	52.22	40.73	3.23	10.23
Australy 13 x Giza 86	191.57	76.43	39.90	3.73	10.87
Giza 89 x Giza 93	131.30	49.76	37.90	3.50	10.30
Giza 92 x Giza 93	146.90	57.00	38.80	3.47	10.93
Giza 94 x Giza 93	167.50	66.38	39.63	3.63	11.80
Giza 95 x Giza 93	152.70	62.87	41.17	3.37	10.27
Giza 96 x Giza 93	135.87	51.76	38.10	3.37	10.97
Pima S4 x Giza 93	123.47	49.31	39.93	3.67	10.40
Pima S7 x Giza 93	163.30	64.08	39.23	3.43	11.33
Karshenky x Giza 93	161.70	64.63	39.97	3.57	11.17
10229 x Giza 93	127.33	51.78	40.67	3.17	10.30

Australy 13 x Giza 93	179.83	71.03	39.50	3.60	11.27
(Giza 89 x (Giza 86 x Giza	189.20	75.36	39.83	3.63	10.40
(Giza 92 x (Giza 86 x Giza	177.97	70.42	39.57	3.67	11.80
(Giza 94 x (Giza 86 x Giza	195.23	76.52	39.20	3.47	12.00
(Giza 95 x (Giza 86 x Giza	171.20	69.28	40.47	3.60	10.27
(Giza 96 x (Giza 86 x Giza	173.13	66.65	38.50	3.63	11.50
(Pima S4 x (Giza 86 x	133.23	53.21	39.93	3.43	10.40
(Pima S7 x (Giza 86 x	176.23	69.19	39.27	3.60	11.43
(Karshenky x (Giza 86 x	164.73	66.44	40.33	3.40	11.53
(10229 x (Giza 86 x Giza	152.20	60.73	39.90	3.20	10.30
(Australy 13 x (Giza 86 x	197.17	78.81	39.97	3.63	11.50
Giza 89	103.57	37.41	36.11	3.24	9.50
Giza 92	120.57	45.47	37.74	3.13	10.90
Giza 94	163.40	64.15	39.26	3.43	12.05
Giza 95	137.77	57.19	41.52	3.11	9.83
Giza 96	123.95	45.02	36.32	3.23	10.58
Pima S4	94.73	38.59	40.72	3.32	9.78
Pima S7	148.20	58.18	39.24	3.01	10.83
Karshenky	145.40	57.47	39.52	3.27	10.53
10229	101.50	41.17	40.54	2.71	9.00
Australy 13	171.57	68.61	40.02	3.52	10.53
Giza 86	154.97	61.19	39.50	3.38	10.53
Giza 93	133.43	48.57	36.40	3.30	10.20
(Giza 86 x Giza 93)	170.30	67.84	39.83	3.52	10.57
LSD 0.05	41.73	6.57	0.15	0.02	0.03
LSD 0.01	59.43	9.35	0.21	0.02	0.04

Table 4: Cont.

Genotypes	Lint index	Micronaire reading	Fiber strength	Fiber length	Uniformity index
Giza 89 x Giza 86	7.02	4.40	10.60	36.07	87.83
Giza 92 x Giza 86	7.87	3.60	11.63	35.07	90.03
Giza 94 x Giza 86	8.45	4.37	10.40	34.90	88.10
Giza 95 x Giza 86	7.43	4.53	10.30	33.07	88.07
Giza 96 x Giza 86	7.35	3.90	10.47	36.93	86.17
Pima S4 x Giza 86	7.00	3.47	10.77	33.87	87.87
Pima S7 x Giza 86	7.59	4.03	10.47	33.90	87.93
Karshenky x Giza 86	7.47	4.40	10.67	34.43	87.80
10229 x Giza 86	7.03	4.23	10.40	34.87	86.33
Australy 13 x Giza 86	7.21	4.53	10.53	34.47	85.23
Giza 89 x Giza 93	6.29	4.10	10.90	36.67	90.40
Giza 92 x Giza 93	6.93	3.37	11.93	36.17	90.17
Giza 94 x Giza 93	7.75	4.20	10.40	34.30	91.00
Giza 95 x Giza 93	7.18	4.40	10.57	36.17	89.13
Giza 96 x Giza 93	6.75	3.87	10.70	36.23	88.73
Pima S4 x Giza 93	6.91	3.97	10.37	35.93	89.33
Pima S7 x Giza 93	7.32	4.30	10.43	36.53	90.37
Karshenky x Giza 93	7.43	4.20	10.53	35.73	90.13

10229 x Giza 93	7.06	4.10	10.57	36.43	90.23
Australy 13 x Giza 93	7.36	4.33	10.40	35.60	88.50
(Giza 89 x (Giza 86 x Giza 93))	6.89	4.27	11.40	37.30	90.17
(Giza 92 x (Giza 86 x Giza 93))	7.73	3.70	12.00	37.20	88.73
(Giza 94 x (Giza 86 x Giza 93))	7.74	4.30	11.73	37.20	90.27
(Giza 95 x (Giza 86 x Giza 93))	6.98	4.77	11.20	35.77	87.57
(Giza 96 x (Giza 86 x Giza 93))	7.20	3.87	11.23	37.50	92.57
(Pima S4 x (Giza 86 x Giza 93))	6.91	3.63	10.97	36.90	90.53
(Pima S7 x (Giza 86 x Giza 93))	7.39	4.00	10.87	37.27	90.10
(Karshenky x (Giza 86 x Giza 93))	7.80	4.33	11.07	37.17	90.37
(10229 x (Giza 86 x Giza 93))	6.84	4.27	11.03	37.43	89.93
(Australy 13 x (Giza 86 x Giza 93))	7.66	4.13	11.40	35.60	87.77
Giza 89	5.37	4.37	9.83	33.50	84.60
Giza 92	6.61	3.60	11.50	35.63	88.60
Giza 94	7.79	4.47	9.53	34.23	86.90
Giza 95	6.98	4.70	9.27	30.33	82.33
Giza 96	6.04	4.10	10.53	36.87	87.30
Pima S4	6.72	3.75	9.53	32.47	86.40
Pima S7	7.00	4.17	9.30	32.93	84.17
Karshenky	6.88	4.60	9.17	32.33	85.60
10229	6.13	4.43	9.93	32.23	86.57
Australy 13	7.03	4.73	9.13	33.30	84.67
Giza 86	6.88	4.17	10.60	34.23	87.57
Giza 93	5.84	3.83	10.70	36.20	89.13
(Giza 86 x Giza 93)	7.00	4.00	10.83	37.10	90.10
LSD 0.05	0.02	0.02	0.02	0.08	0.89
LSD 0.01	0.03	0.03	0.04	0.11	1.27

The results also revealed that the best mean performances were found for the single crosses are; the cross Giza 89 x Giza 86 for boll weight. Giza 94 x Giza 86 for seed index and lint index, Giza 95 x Giza 86 for lint percentage, Giza 96 x Giza 86 had the best means for fiber length and Australy 13 x Giza 86 for seed cotton yield/ plant and lint cotton yield/ plant. In addition to the two crosses Giza 92 x Giza 93 and Giza 94 x Giza 93 Which gave the best means for (micronaire reading and fiber strength) and uniformity index, respectively.

3.1. Disclosing of epistasis

The existence of non-allelic interactions for economic traits might have important inferences in plant breeding. The (i) type epistasis represents fixable while (j+l) types show non-fixable portions of genetic variations. Genetic analyses of the data revealed epistasis affected all the traits studied (Table 5). The mean square for the deviations of the total epistasis (L1i + L2i - 2L3i) revealed the presence of highly significant epistasis for all studied traits except micronaire reading. Further partitioning of total epistasis into (i) epistatic type (additive × additive), (j+l) epistatic types (additive × dominance) and (dominance × dominance) interactions showed that mean squares estimates due to additive × additive (i) type were found to be non significant for all the traits studied. The presence of (j+l) epistatic types appeared to be highly significant in the inheritance of all the traits studied except micronaire reading. The epistatic type (i) interactions, was detected to be much larger in magnitudes than the other epistatic type (j+l) for all traits studied except boll weight, lint index and micronaire reading, indicating that fixable components of epistasis were more important than non fixable one in the inheritance of these traits. Since, epistasis plays an important role in governing most of the traits under study and result in biased estimates for the genetic variance. Thus ignoring such effect lead to loss information about epistasis also the estimates of additive and dominance components would be biased. Thus, the breeder should take epistasis into account in producing genetic models for studying quantitative traits. Our findings were in the same line with Sohu *et al.* (2010); El-Lawendey *et al.* (2010); Saleh (2013); Jayade *et al.* (2014); Dawwam *et al.* (2016); AL-Hibbiny *et al.* (2020) and El-Mansy *et al.* (2020).

Table 5: Mean squares from the analysis of variance for disclosing the presence of epistasis for the studied traits in cotton.

Source Of Variation	d.f	Seed cotton yield/plant	Lint cotton yield/plant	Lint percentage	Boll weight	Seed index
(i) type of epistasis	1	45544.24	6379.37	8.64	0.04	4.64
(j + l) type of epistasis	9	1438.39**	248.52**	3.96**	0.33*	0.74**
Total epistasis (L1i + L2i– 2L3i)	10	5848.98**	861.61**	4.43**	0.30*	1.13**
i type x replications	2	11386.06	1594.84	2.16	0.01	1.16
(j + l) type x replications	18	103.04	17.03	0.34	0.11	0.10
Total epistasis x replications	20	1231.35	174.82	0.53	0.10	0.21

Table 5: Cont.

Source Of Variation	d.f	Lint index	Micronaire reading	Fiber strength	Fiber length	Uniformity index
(i) type of epistasis	1	0.22	0.02	48.90	294.53	153.68
(j + l) type of epistasis	9	0.95**	0.36	1.21**	5.07**	37.41**
Total epistasis (L1i + L2i– 2L3i)	10	0.88**	0.33	5.98**	34.01**	49.04**
i type x replicates	2	0.05	0.004	12.22	73.63	38.42
(j + l) type x replicates	18	0.10	0.16	0.21	0.09	10.28
Total epistasis x replicates	20	0.09	0.14	1.41	7.45	13.09

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

The individual epistatic deviations of lines are shown in Table (6). The data indicated that the epistatic deviations were exhibited by line Giza 89 had significant negative for lint cotton yield/plant, lint percentage, lint index, fiber strength and fiber length. Giza 92 was significant negative for boll weight, seed index, lint index, micronaire reading, fiber strength and fiber length and positive significant for lint percentage. Giza 94 was significant negative for fiber strength and fiber length, while, significant positive for lint percentage, boll weight and lint index. Concerning Giza 95 was significant negative for boll weight, micronaire reading, fiber strength and fiber length, while, significant positive for lint percentage, seed index and lint index. Regarding line Giza 96 was significant negative for boll weight, seed index, lint index, fiber strength and fiber length, while gave significant positive for lint percentage, as well as line Pima S_4 was significant negative for fiber strength and fiber length, gave significant positive for lint percentage and boll weight.

Table 6: Individual epistatic deviations of ten cotton lines for the studied traits

Lines	Seed cotton yield/plant	Lint cotton yield/plant	Lint percentage	Boll weight	Seed index
Giza 89	-80.97	-34.28**	-1.63**	-0.07	-0.03
Giza 92	-64.80	-24.93	0.50*	-0.33**	-1.27**
Giza 94	-36.30	-10.50	2.03**	0.20**	0.07
Giza 95	-44.80	-15.33	1.90**	-0.47**	0.13*
Giza 96	-33.77	-11.84	0.57*	-0.37**	-0.77**
Pima S4	-12.83	-4.43	0.53*	0.50**	-0.10
Pima S7	-32.53	-11.60	0.73**	-0.30**	-0.17**
Karshenky	-11.83	-5.31	-0.33	0.40**	-0.87**
10229	-48.87	-17.45	1.60**	0.00	-0.07
Australy 13	-22.93	-10.15	-0.53	0.07	-0.87**
LSD 0.05	119.12	19.69	0.40	0.13	0.11
LSD 0.01	175.31	28.98	0.59	0.19	0.17

Table 6: Cont.

Lines	Lint index	Micronaire reading	Fiber strength	Fiber length	Uniformity index
Giza 89	-0.47**	-0.03	-1.30**	-1.87**	-2.10
Giza 92	-0.65**	-0.43**	-0.43**	-3.17**	2.73
Giza 94	0.73**	-0.03	-2.67**	-5.20**	-1.43
Giza 95	0.65**	-0.60**	-1.53**	-2.30**	2.07
Giza 96	-0.30**	0.03	-1.30**	-1.83**	-10.23
Pima S4	0.09	0.17	-0.80**	-4.00**	-3.87
Pima S7	0.12*	0.33**	-0.83**	-4.10**	-1.90
Karshenky	-0.69**	-0.07	-0.93**	-4.17**	-2.80
10229	0.42**	-0.20*	-1.10**	-3.57**	-3.30
Australy 13	-0.74**	0.60**	-1.87**	-1.13**	-1.80
LSD 0.05	0.11	0.18	0.24	0.11	11.88
LSD 0.01	0.16	0.27	0.35	0.16	17.49

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

Regarding Pima S_7 exhibited significant negative for boll weight, seed index, fiber strength and fiber length and significant positive for lint percentage, lint index and micronaire reading. Concerning line Karshenky had significant negative for seed index, lint index, fiber strength and fiber length and significant positive for boll weight. Regarding line 10229 was significant negative for micronaire reading, fiber strength and fiber length and significant positive for lint percentage and lint index. Line Australy 13 had significant negative for seed index, lint index, fiber strength and fiber length and significant positive for micronaire reading. It is evident that all lines exhibited epistatic deviation for most studied traits. Similar results were reported by Saleh (2013); Abou El-yazied (2014); Jayade *et al.* (2014) and AL-Hibbiny *et al.* (2020).

The estimates of additive and dominance components of genetic variance as well as degree and direction of dominance for the investigated traits are exhibited in (Table 7). The absence of epistasis, the analysis of variance for sum and differences provided direct test of the significance of additive (significant of sum) and dominance components (significant of differences). The sums item ($L_{1i}+L_{2i}$) were significant for all traits except for micronaire reading. The differences in items ($L_{1i} - L_{2i}$) were significant for all traits except boll weight which exhibited insignificant differences. Additive values were greater than dominance genetic variance for all studied traits. The degree of dominance ($\sqrt{H/D}$) was less than unity suggesting the role of partial or incomplete dominance for all the traits studied. Consequently, it concluded that selection procedures in early generations based on accumulation of additive effects would be successful in improving all these traits. Similar results were previously obtained by Saleh (2013); Dawwam *et al.* (2016); El-Mansy *et al.* (2020); El-Shazly *et al.* (2023) and El-Shazly *et al.* (2024).

Table 7: Mean squares for sums and differences as well as estimates of additive, dominance, degree and direction of dominance for the studied traits.

Source Of Variation	d.f	Seed cotton yield/plant	Lint cotton yield/plant	Lint percentage	Boll weight	Seed index
Sums (L1i+L2i)	**9**	4203.67**	637.53**	7.07**	0.26**	3.95**
Sums x replicates	**18**	46.49	7.25	0.18	0.03	0.04
Differences (L1i – L2i)	**9**	913.49**	169.25**	1.61**	0.03	0.23**
Differences x replicates	**18**	62.53	10.86	0.12	0.04	0.04
D (additive) 9		2771.45	420.19	4.60	0.16	2.61
H (dominance)		567.30	105.59	0.99	-0.01	0.13
Degree of dominance (H/D)1/2		0.45	0.50	0.47	0.00	0.22
Direction of dominance (r s,d)		0.19	0.09	-0.62	0.09	0.39

Table 7: Cont.

Source Of Variation	d.f	Lint index	Micronaire reading	Fiber strength	Fiber length	Uniformity index
Sums (L1i+L2i)	**9**	1.80**	1.23	2.03**	5.61**	10.98**
Sums x replicates	**18**	0.02	0.03	0.03	0.05	0.14
Differences (L1i – L2i)	**9**	0.41**	0.19**	0.17**	4.59**	3.64**
Differences x replicates	**18**	0.03	0.02	0.02	0.08	0.29
D (additive) 9		1.19	0.80	1.33	3.71	7.23
H (dominance)		0.26	0.12	0.10	3.01	2.23
Degree of dominance (H/D)1/2		0.47	0.38	0.27	0.90	0.56
Direction of dominance (r s,d)		0.13	0.35	-0.39	0.46	0.52

* and ** indicate significant differences at 0.05 and 0.01 probability levels, respectively

Further, the correlation coefficient between the sums (L1i + L2i) and difference (L1i - L2i) were found to be negative and insignificant for lint percentage and fiber strength. However, the other traits were positive and non-significant. These results indicated that the genes with positive and negative dominant alleles were dispersed between testers and did not show any proof of directional dominance for these traits. El-Shazly *et al.* (2024) observed that the correlation coefficient between the sums (L1i + L2i) and difference (L1i - L2i) 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.

4. 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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