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Estimation of Genetic Variance Components by Using Triple Test Cross in Cotton (*Gosssypium barbadense* L.)

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THIS STUDY was done at Sakha Experimental Station, ARC, Egypt, during three seasons (2020-2022). 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 96(L1), S.101(L2) and their F1 hybrid(L3) were crossed as male parents to seven cotton lines as female parents. Differences were significant concerning genotypes, hybrids, parents and lines for all traits and among testers for yield traits. Total epistasis was present for all the studied traits except for micronaire reading. The (i) type of epistasis (additive x additive) was significant for yield and its component traits and fiber quality traits except for micronaire reading. While the (j+l) type (additive x dominance and dominance x dominance) was significant for seed cotton and lint yield/plant, lint% and lint uniformity index. The (i) type was higher than the (j+l) type for all the studied traits except micronaire reading. Both additive and dominance were important for controlling the studied traits except boll weight, micronaire reading and Pressely index, only additive genetic effect was important. Additive component was extremely higher than dominance component for all traits. Degree of dominance was less than unity for all studied traits, indicating partial dominance. Most of the lines did not share significant positive portion to the total epistasis for most traits. The results illustrated that the role of epistasis must be in breeder's consideration during planning a breeding program for improving economic traits in cotton.

Keywords: Cotton, Epistasis, Triple test cross.

Introduction

Cotton occupies essential role in the economics as the main fiber crop worldwide. The progress in breeding program count on the genetic variability within the studied population in addition to the nature and amount of this variability for the economic traits. Estimation of the variance components help breeders to recognize the genetic constitution of quantitative traits to work out the adequate procedures to be followed in the breeding program (Singh, 2004).

Many procedures have been submitted and used to realize the nature of gene action participated in inheritance of the quantitative traits. In cotton crop, the main target of the breeder is to develop varieties with high yield and superior fiber properties. Hence, the determination of genetic components is required to contrive appropriate breeding procedures to improve these traits. Unfortunately, the presence of epistasis (additive x additive, dominance x dominance and additive x dominance) cause prepositional estimates of the gene action components, therefore breeders demand a genetic analysis to obtain correct and precise estimates of all genetic variance components. Hence, Kearsey & Jinks (1968) postulated the triple test cross (TTC) design which is a simple extension of design III of Comstock & Robinson (1952). This design can find out epistatic effects for the quantitative traits, and when epistasis is absent, it gives estimates of additive and dominance components of genetic

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variability, moreover it accurately assess the dominance direction regardless the degree of breeding, genes frequencies and the population mating system.

Consequently, cotton breeders have been widely employed the triple test cross technique to identify the genetic basis of the various cotton traits in Egyptian cotton (*G. barbadense* L.) as reported by El-Hoseiny et al. (2012), Saleh (2013), Abou El-yazied (2014), Dawwam et al. (2016), AL-Hibbiny et al. (2020) and EL-Mansy et al. (2020) as well as in upland cotton (*G. hirsutum* L.) as reported by Singh & Chahal (2003), Bhatti et al. (2006), Sohu et al. (2010), Jayade et al. (2014) and Ali et al. (2016). These studies recorded fundamental role for epistasis in inheritance of cotton economic traits. Otherwise, both additive and dominance components of genetic variability were participated with different relative contribution of each component for the various traits.

In this work, triple test cross (TTC) analysis was utilized to: 1) Explore the existence of epistasis as well as to determine the additive and dominance variances of various traits in cotton. 2) Predict the favorable selection method for each trait to help cotton breeders to improve these traits.

Materials and Methods

Materials

The materials used in this study contained nine 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 nine 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 (2020 – 2022).

Methods

Two cotton varieties, Giza 96 and S. 101 designated as T1 and T2, respectively were used as tester genotypes. The two varieties were sown in the first season (2020) and crossed to obtain F_1 hybrid that was used as the third tester designated as T3. In the second season (2021) seven cotton lines: Giza 87, Giza 92, Giza 93, Giza 94, Giza 97, S 106 and A 101 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 2022, the experimental materials consisted of 31 genotypes including three testers (one of them is a single cross), seven inbred lines, 14 single crosses and 7 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 4m long, and 0.70m width and 50cm between hills with one plant left per hill. The normal agricultural practices were adopted through the growing seasons.

TABLE 1. Origin, pedigree and category for the fifteen parental cotton genotypes

No.	Parents	Origin	Pedigree	Category
			Lines	
L1	Giza 87	Egypt	Giza 77 x Giza 45A	Extra-long staple
L2	Giza 92	Egypt	Giza 84 x (Giza 74 x Giza 68)	" "
L3	Giza 93	Egypt	Giza 77 x S 106	" "
L4	Giza 94	Egypt	A 101 x Giza 86	Long staple
L5	Giza 97	Egypt	(Giza 89 x R 101 x Giza 86) x Giza 94	" "
L6	S 106	USA	(5934-23-2-6 x 5903-98-4-4)	" "
L7	A 101	Australia	Unknown	" "
			Testers	
T1	Giza 96 (P_1)	Egypt	[(Giza 84 x G.70) x Giza 51B)] x S.106	Extra-long staple
T2	S 101(P_2)	Egypt	Complex cross of Sea Island, Pima, Tanguis, Stoneville	Long staple
T3	P_1 x P_2 (F_1)	Egypt	$P_1 \times P_2$ (F_1)	-

Ten guarded plants from each plot were used individually to collect data for the following traits: Boll weight (BW) in grams, seed cotton yield/ plant (SCY/P) in grams, lint yield/plant (LY/P) in grams and lint percentage (L%). In addition to four fiber quality traits which were: Micronaire reading (Mic.), fiber strength (FS) as Pressely 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.

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 & 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 & 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.

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, seven values (i=1 to 7) were estimated to test overall epistasis (Jinks & Virk, 1977) as described by Singh & Chaudhary (1999) as follows:

Total epistasis was estimated as uncorrected genotypes sums of square [$\sum (L_1i + L_2i - 2L_3i)/ 7$] at 7 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 =[$\sum(L_1i + L_2i - 2L_3i)/21$] and (j + l) type that measures additive x dominance and dominance x dominance part for 6 degrees of freedom = [Total epistasis – (i) type].

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 =[($\sum(L_1i - L_2i - 2L_3i)/r$], the resulted value of each genotype for a trait was tested using a t-test with 14 degrees of freedom as follows: t = Mean / S_E, where: S_E= (error mean square /r) $^{1/2}$.

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 & 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 (Table 2)

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	$\delta^2e + 2r\delta^2s$
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	$\delta^2e + 2r\delta^2d$
Error	(n-1)(r-1)	MSe	δ^2e

The observed mean squares were substituted into the equations as follows:

$\delta^2s = (MSs - MSe)/2r$; $\delta^2s = (1/4)\ D$
$D = 4(MSs - MSe)/2r$

$\delta^2d = (MSd - MSe)/2r$; $\delta^2d = (1/4)\ H$
$H = 4(MSd - MSe)/2r$

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.

Degree and direction of dominance and types of genes exhibiting dominance

Mean degree of dominance was calculated according to Singh & 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).

Results and Discussion

The analysis of variance for the various studied traits is given in Table 3. Results revealed significant differences for each of genotypes, parents and lines for all of the studied traits in addition to significant differences among testers for the yield and its components traits and fiber length which denote the presence of abundant genetic variation among these genotypes. Moreover, mean-square of hybrids were also significant for all tested traits, indicating the existence of adequate heterogeneity in the triple test cross progenies for disclosing the new genetic recombinations.

On the other hand, lines vs. testers exhibited significant differences for all the studied traits that point out to the importance of both additive and non-additive types of gene action for controlling these traits. Further, hybrids vs. parents showed significant differences for all the studied traits. The same findings for significant differences between cotton varieties and their crosses were recorded by Abou El-yazied (2014), Dawwam et al. (2016), El-Mansy et al. (2020), Said et al. (2021) and Amer (2022). These results denoted the adequacy for going on to the modified triple test cross (TCC) analysis.

Mean performances of the studied genotypes

Data concerning the mean performance of the tested genotypes (9 parents, 15 single cross and 7 three-way crosses) are exhibited in Table 4.

The nine parental genotypes showed wide range for the studied traits, regarding yield and its component traits, among the parental genotypes, L5 (Giza 97) had the best values as it gave 3.61g, 219.16g, 90.67g and 41.33%, for boll weight, seed cotton yield/plant, lint yield/plant and L%, respectively, as well as 87.46% for lint uniformity index, followed by L4 (Giza 94) that gave 3.39g, 190.58g, 76.01g and 39.85%, as well as 87.36%, respectively, for the aforementioned traits. Conversely, L1(Giza 87) gave the lowest values for yielding traits as it gave 2.57g, 67.88g, 22.33g and 32.88%, for boll weight, seed cotton yield, lint yield/plant and L%, respectively, as well as 85.70% for lint uniformity index, while the rest of parents had intermediate values.

With regard to fiber quality traits, Giza 96 (T1) had the lowest micronaire reading (desirable) that was 3.16, whereas L5 (Giza 97) gave the worse value (4.44). Giza 92 (L2) gave the highest fiber strength expressed as Pressely index (11.96), whereas L7 (A. 101) had the lowest value (10.24). For fiber length expressed as the upper half mean, L1 (Giza 87) gave the highest value, 36.43mm, whereas L7 (A. 101) had the lowest value (32.39mm).

The tested hybrids showed wide spectrum for each of the studied traits, regarding yield and its component traits, the three-way crosses L5 x F1 (Giza 97 x (Giza 96 x S. 106)) gave the best values as it had 3.58g, 198.55g, 81.52g and 41.15%, for boll weight, seed cotton yield/plant, lint yield/plant and L%, respectively, followed by the single cross L5 x T1 (Giza 97 x Giza 96) that gave 3.55g, 196.65g, 80.50g and 40.94%, respectively, for the aforementioned traits. Contrarily, the single cross L1 x T2 (Giza 87 x S 106) gave the lowest

values for yield and its component traits as it gave 2.82g, 105.45g, 34.61g and 32.78%, for boll weight, seed cotton yield/plant, lint yield/plant and L%, respectively. The rest of hybrids showed intermediate values for these traits.

With reference to fiber quality traits, the three-way crosses L1 x F1 (Giza 87 x (Giza 96 x S. 106)) showed the best values as it had 3.14, 11.77 and 35.81 for the traits micronaire reading, Pressely index and fiber length, respectively, while the hybrid L4 x F1 (Giza 94 x (Giza 96 x S. 106)) had the best value for length uniformity index (87.11%), whereas L4 x T1 (Giza 94 x Giza 96) gave the worse value of micronaire reading (3.98), L7 x T2 (A 101 x S 106) gave the worse values for Pressely index and fiber length (10.72 and 33.31 mm, respectively), L1 x T1 hybrid had the lowest uniformity index (85.42%).

Disclosing of epistasis

Analysis of variance for disclosing the presence of epistasis or non-allelic interactions for the studied traits is displayed in Table 5. The existence of epistasis was confirmed by the significance of ($L_1i + L_2i – 2L_3i$) variance.

Total epistasis was observed for all the studied traits except for micronaire reading that showed absence of epistatic effects.

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

S.O.V	d.f	Yield and its component traits			
		BW (g)	SCY/ P (g)	LY/ P (g)	L%
Replications	2	0.054*	138.04	32.87	3.07*
Genotypes	30	0.17**	3175.94**	719.50**	19.92**
Hybrids (H)	20	0.12**	2175.03**	537.52**	19.38**
Parents (P)	9	0.30**	5286.04**	1136.86**	22.93**
Lines (L)	6	0.36*	7795.28**	1654.94**	29.29**
Testers (T)	2	0.15**	356.13*	143.17*	12.56**
P_1+ P_2 Vs. F_1	1	0.11*	72.51*	19.91**	0.94
P_1 Vs. P_2	1	0.16**	615.58*	259.79*	23.88*
L Vs. T	1	8.77*	14630.06**	2060.48**	963.82**
H Vs. P	1	0.10**	4203.05**	602.76**	3.54**
Error	60	0.01	184.28	29.46	0.77
S.O.V	**d.f**	**Fiber quality traits**			
		Mic.	**FS (Press.)**	**FL (mm)**	**UI%**
Replications	2	0.024	0.047	0.064*	0.122
Genotypes	30	0.367**	0.547**	2.780**	0.751**
Hybrids (H)	20	0.178*	0.341*	1.851**	0.581**
Parents (P)	9	0.741**	0.997**	4.988**	1.133*
Lines (L)	6	0.515*	1.415*	7.229**	1.558*
Testers (T)	2	0.039	0.060	0.710*	0.115
P_1+ P_2 Vs. F_1	1	0.008	0.035	0.486*	0.003
P_1 Vs. P_2	1	0.067	0.073	0.771*	0.227
L Vs. T	1	1.407**	86.62**	749.06**	455.47**
H Vs. P	1	0.787**	0.631*	1.501**	0.729*
Error	60	0.018	0.044	0.201	0.189

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

BW: Boll weight, SCY/P: Seed cotton yield/plant, LY/P: lint yield/plant, L%: lint percentage, Mic.: Micronaire reading, FS: Fiber strength as Pressely index, FL: Fiber length and UI%: Uniformity index.

TABLE 4. Mean performance of the tested genotypes for the studied traits

Genotypes	Yield and its component traits					Fiber quality traits		
	BW (g)	SCY/ P (g)	LY/ P (g)	L%	Mic.	FS (Press.)	FL (mm)	UI%
L1 x T1	2.97	117.56	39.48	33.62	3.17	11.57	35.76	85.42
L2 x T1	3.11	162.74	59.48	36.51	3.32	11.73	35.47	86.40
L3 x T1	3.28	134.31	49.31	36.66	3.30	11.44	35.23	86.88
L4 x T1	3.41	185.73	73.50	39.61	3.98	11.10	34.17	87.04
L5 x T1	3.55	196.65	80.50	40.94	3.70	11.03	33.85	86.41
L6 x T1	3.21	154.72	53.77	34.73	3.55	11.02	34.37	86.39
L7 x T1	3.23	152.90	55.51	36.27	3.64	10.96	33.86	85.99
L1 x T2	2.82	105.45	34.61	32.78	3.32	11.52	35.52	85.65
L2 x T2	2.95	156.59	54.19	34.62	3.51	11.66	35.11	86.11
L3 x T2	3.08	134.28	46.73	34.73	3.44	11.41	34.90	86.62
L4 x T2	3.26	174.68	64.77	37.03	3.76	10.95	33.82	85.58
L5 x T2	3.37	197.72	75.61	38.24	3.89	10.95	33.56	86.18
L6 x T2	3.03	141.36	50.10	35.42	3.62	10.91	33.88	86.48
L7 x T2	3.09	147.18	49.66	33.72	3.76	10.72	33.31	85.97
L1 x T3	3.05	118.37	41.08	34.80	3.14	11.77	35.81	86.09
L2 x T3	3.16	160.81	60.22	37.45	3.49	11.75	35.47	85.97
L3 x T3	3.30	143.95	54.80	38.04	3.30	11.45	35.19	86.46
L4 x T3	3.45	185.56	75.71	40.81	3.91	11.06	34.26	87.11
L5 x T3	3.58	198.55	81.52	41.15	3.79	11.04	34.09	86.32
L6 x T3	3.24	155.21	60.23	38.81	3.68	11.04	34.50	86.42
L7 x T3	3.27	151.30	59.37	39.26	3.66	10.91	33.91	86.12
L1 (G. 87)	2.57	67.88	22.33	32.88	3.34	11.69	36.43	85.70
L2 (G. 92)	2.82	143.79	50.67	35.22	3.92	11.96	35.77	86.13
L3 (G. 93)	3.10	104.70	36.12	34.61	3.56	11.44	35.30	86.93
L4 (G. 94)	3.39	190.58	76.01	39.85	4.34	10.56	33.44	87.36
L5 (G. 97)	3.61	219.16	90.67	41.33	4.44	10.54	32.93	87.46
L6 (S. 106)	2.99	134.92	46.28	34.28	4.02	10.50	33.58	86.47
L7 (A. 101)	3.05	123.22	43.57	35.35	4.29	10.24	32.39	85.80
T1 (G. 96)	3.35	152.21	59.18	38.88	3.16	11.29	34.56	86.42
T2 (S. 106)	3.03	131.95	46.02	34.89	3.37	11.07	33.84	86.03
T3 (T1 x T2)	3.46	149.03	56.25	37.68	3.19	11.33	34.77	86.27
LSD 0.05	0.17	22.17	8.86	1.43	0.22	0.34	0.73	0.25
LSD 0.01	0.23	29.49	11.79	1.90	0.29	0.46	0.97	0.32

G= Giza, F1= first generation of T1 x T2 hybrid.

BW: Boll weight, SCY/P: Seed cotton yield/plant, LY/P: lint yield/plant, L%: lint percentage, Mic.: Micronaire reading, FS: Fiber strength as Pressely index, FL: Fiber length and UI%: Uniformity index.

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	Yield and its component traits			
		BW (g)	SCY/P (g)	LY/P (g)	L%
Total epistasis ($L_1i + L_2i - 2L_3i$)	7	1.90*	383.01**	411.95**	89.57*
(i) type of epistasis	1	1.316*	1682.34**	2576.64**	546.47**
(j + l) type of epistasis	6	0.003	166.46*	51.16*	13.42*
i type x replications	2	0.329	420.58*	644.16**	136.62*
(j + l) type x replications	12	0.052	1073.28**	117.09*	4.22
Total epistasis x replications	14	0.104	980.04*	192.38	23.14
Source of variation	**d.f**	**Fiber quality traits**			
		Mic.	FS (Press.)	FL (mm)	UI%
Total epistasis ($L_1i + L_2i - 2L_3i$)	7	0.057	0.115*	0.937*	2.015*
(i) type of epistasis	1	0.0001	0.448*	5.572**	1.943*
(j + l) type of epistasis	6	0.066	0.060	0.135	1.506*
i type x replicates	2	0.00001	0.112	1.438*	0.377
(j + l) type x replicates	12	0.096	0.262	0.483	2.727
Total epistasis x replicates	14	0.083	0.240	0.619*	2.391*

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

BW: Boll weight, SCY/P: Seed cotton yield/plant, LY/P: lint yield/plant, L%: lint percentage, Mic.: Micronaire reading, FS: Fiber strength as Pressely index, FL: Fiber length and UI%: Uniformity index.

These outcomes illustrate that cotton breeder cannot achieve a clear image about the genetic system that control most of the studied traits if the breeding procedure assumed the absence of epistasis. Our findings were in the same line with Sohu et al. (2010), Jayade et al. (2014), Dawwam et al. (2016), AL-Hibbiny et al. (2020) and EL-Mansy et al. (2020) who recorded the presence of epistasis for all or most of cotton traits which were boll weight, seed cotton and lint yield per plant, lint%, seed index, lint index, fiber length, fiber strength, micronaire value and uniformity ratio; whereas, other studies recorded absence of total epistasis in cotton traits which were seed and lint cotton yields, lint%, seed index, boll weight, fiber length, fiber strength and micronaire value (El-Hoseiny et al., 2012; Saleh, 2013; Abou El-yazied, 2014).

In this respect, Ketata et al. (1976) and Khattak et al. (2001) reported that the presence or absence of epistasis count on both of the genetic capacity of genotypes and the environmental conditions around plants because the genotype x environment interactions may affect the epistasis.

The total epistasis can be divided to two types of interactions which are: The fixable (i) type (additive x additive) and the non-fixable (j and l) type (additive x dominance and dominance x dominance). Data presented in Table 5 explained that the (i) type was significant for all of yield and its component traits as well as fiber quality traits except for micronaire reading that revealed insignificant i type of interaction. On the other hand, mean squares of the (j + l) type of interactions were significant for seed cotton yield/plant, lint yield/plant, lint % and lint uniformity index.

The (i) type of epistasis or the fixable type showed higher values than the (j+l) type or the non-fixable type for all the studied traits except micronaire reading. These results illustrated that the traits with significant and higher additive component of epistasis (i type) can be improved through direct selection in the early segregated generations.

The interactions between replications and total epistasis were significant for the traits seed cotton yield, fiber length and uniformity index, while interactions between replications and (i) type of epistasis were significant for seed cotton yield, lint yield, lint% and fiber length, moreover, interactions between replications and (j+l) type of epistasis were significant for seed and lint cotton yields indicating

the environmental effects on these traits, whereas the traits boll weight, micronaire reading and fiber strength were insensitive to the environment 'replications' (El-Mansy et al., 2020).

Consequently, the role of epistasis must be in consideration during planning a breeding program for improving economic traits. Epistasis is an important component as well as the main components (additive and dominance) for genetic variance that cannot be estimated precisely if epistasis ignored.

These results were in the same line with other studies who found significant (i) or (additive x additive) type of epistasis for boll weight, seed cotton and lint yield per plant, lint%, seed index, lint index, fiber length, fiber strength, micronaire value and uniformity ratio (El-Lawendey et al., 2010; Saleh, 2013; Abou El-yazied, 2014; AL-Hibbiny et al., 2020; El-Mansy et al., 2020), contrarily other studies found insignificant (i) type of epistasis for seed and lint cotton yields, lint%, seed index, boll weight, fiber length, fiber strength and micronaire value (Bhatti et al., 2006; El-Hoseiny et al., 2012). On the other hand, Bhatti et al. (2006), Saleh (2013) and El-Mansy et al. (2020) recorded significant non-allelic type of epistasis (j+l), contrary, El-Hoseiny et al. (2012), Abou El-yazied (2014), AL-Hibbiny et al. (2020) found insignificant (j+l) type for most traits studied. Furthermore, AL-Hibbiny et al., 2020 and El-Mansy et al., 2020 found that the (i) epistatic type was larger in magnitude as compared to the (j+l) type, which clarified that the fixable component of epistasis was more important than the non-fixable one in controlling the studied traits.

The contribution of each line to the epistasis comparison ($L_1i + L_2i - 2L_3i$) were evaluated for the investigated traits and shown in Table 6 to point lines which interacted with both of L_1 and L_2 to generate significant deviations. The results indicated differences in magnitude and sign for the individual epistasis deviations for the investigated traits, this indicating that epistatic deviations varied between cotton crosses and among the tested seven inbred lines.

TABLE 6. Individual epistatic deviations of seven cotton lines for the studied traits

Lines	Yield and its component traits			
	BW (g)	SCY/P (g)	LY/P (g)	L%
L1 (Giza 87)	-0.318*	-13.728*	-8.070	-3.190
L2 (Giza 92)	-0.267*	-2.283	-6.764	-3.775
L3 (Giza 93)	-0.233	-19.314*	-13.568	-4.672
L4 (Giza 94)	-0.238	-10.720	-13.159	-4.977
L5 (Giza 97)	-0.233	0.259	-5.823	-3.112
L6 (S. 106)	-0.248	-14.341*	-16.583*	-7.457*
L7 (A. 101)	-0.216	-2.527	-13.571	-8.525*
LSD 0.05	0.405	58.282	19.250	3.656
LSD 0.01	0.567	81.707	26.987	5.125
	Fiber quality traits			
	Mic.	FS (Press.)	FL (mm)	UI%
L1 (Giza 87)	0.212	-0.454	-0.335	-1.117
L2 (Giza 92)	-0.137	-0.063	-0.361	0.563
L3 (Giza 93)	0.130	-0.046	-0.253	0.577
L4 (Giza 94)	-0.091	-0.071	-0.528	-1.595
L5 (Giza 97)	0.009	-0.097	-0.770	-0.053
L6 (S. 106)	-0.191	-0.144	-0.756	0.044
L7 (A. 101)	0.080	-0.146	-0.661	-0.294
LSD 0.05	0.553	0.910	1.236	2.938
LSD 0.01	0.775	1.276	1.732	4.118

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

BW: Boll weight, SCY/P: Seed cotton yield/plant, LY/P: lint yield/plant, L%: lint percentage, Mic.: Micronaire reading, FS: Fiber strength as Pressely index, FL: Fiber length and UI%: Uniformity index.

However, the positive sign of epistasis deviation might be denoting the considerable contribution of parents than that of F_1, whereas, the negative sign indicates the greater contribution of F_1 than its two parents.

Results in Table 6 showed a few significant epistatic deviations for yield and its component traits, i.e. line 1 (Giza 87) for boll weight and seed cotton yield/plant, line 2 (Giza 92) for boll weight, line 3 (Giza 93) for seed cotton yield/plant, line 6 (S 106) for seed cotton yield/plant, lint yield/plant and lint% as well as line 7 (A 101) for lint%, the rest of cases and all fiber traits showed insignificant epistatic deviations.

Accordingly, most of the studied lines were inoperative and did not share a significant positive portion to the total epistasis for most of the studied traits. Line 6 (S. 106) showed the major contribution portion of negative epistatic to the total epistasis for yield and its component traits except boll weight, line 1 (Giza 87) ranked second in this respect with negative epistatic deviations for boll weight and seed cotton yield/plant. Concerning fiber quality traits, none of the studied lines were contributed significantly to maximum portion to the total epistasis as all lines showed insignificant values.

The limited line effects on the non-allelic interactions for yield potential traits cleared that epistasis were affected to some extent by the lines used in the study. Whereas the non-allelic interactions for fiber quality traits were not affected by the studied lines. Pooni et al. (1980) reported that the optimal number of lines required for disclosing epistasis by TTC technique relies on dispersal of genes in the tested parents. Therefore, ample lines and extreme diversified testers (L_1 and L_2) should be utilized in the TTC studies for disclosing epistasis and to assess additive and dominance components of variability accurately. 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. Results illustrated that additive and dominance components were evenly important for controlling all studied traits, except for boll weight, micronaire reading and Pressely index, only additive genetic effect was significant. For that reason, as gene activity in both additive and non-additive manners is involved in the expression of most studied traits, simple selection procedure in early generations may not participate significantly to the improvement of these traits. The additive components in these traits can be successfully exploited through pedigree method of selection and recurrent selection because of major contribution of additive gene effects in late generations of segregating populations. While for boll weight, micronaire reading and Pressely index direct selection in early generations might be effective for improving these traits (Singh, 2004). To exploit all type of gene effects, bi-parental inter crossing manner and/or recurrent selection may be efficacious for developing high yielding lines in advanced generations as suggested by Khattak et al. (2001).

The magnitude of additive component or fixable genes was extremely higher than dominance component for all traits due to the widespread of common alleles in testers that increases the magnitude of additive component, in this respect, Singh et al. (1997) stated that the magnitude of additive component is usually higher than dominance component for most of quantitative traits.

Similar studies in cotton resulted that both additive and dominance components of gene action were important for the inheritance of seed and lint cotton yields, lint%, seed index, boll weight, fiber length, fiber strength and micronaire value cotton traits, i.e. Abou El-yazied (2014), Jayade et al. (2014), Dawwam, et al. (2016), AL-Hibbiny et al. (2020) and El-Mansy et al. (2020). Whereas, El-Hoseiny et al. (2012) and Saleh (2013) found significant effects for the additive component but dominance effects were insignificant for lint%, seed index, boll weight, fiber length and micronaire value.

Degree of dominance $(H/D)^{1/2}$ ranged from 0.150 for lint yield/plant to 0.783 for lint uniformity index, all traits showed values less than unity, indicating partial or incomplete dominance for the studied traits. Therefore, improving these traits is possible through selection procedures to accumulate additive genes.

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	d.f	BW (g)	SCY/P (g)	LY/P (g)	L%
Sums ($L_{1i}+L_{2i}$)	6	0.428*	9915.51**	2270.23**	56.42**
Sums x replicates	12	0.017	346.74	46.73	0.751
Differences ($L_{1i}-L_{2i}$)	6	0.052	126.69**	11.96*	4.513*
Differences x replicates	12	0.012	379.07	62.29	1.387
D (additive)		0.274*	6379.18**	1482.34**	37.11*
H (dominance)		0.007	168.26*	33.56*	2.084*
Degree of dominance $(H/D)^{1/2}$		0.159	0.162	0.150	0.237
Direction of dominance ($r_{s,d}$)		0.978*	0.360	0.825*	0.674
		Mic.	**FS (Press.)**	**FL (mm)**	**UI%**
Sums ($L_{1i}+L_{2i}$)	6	0.650*	1.396*	8.226*	1.738*
Sums x replicates	12	0.035	0.161	0.483	0.504
Differences ($L_{1i}-L_{2i}$)	6	0.061	0.016	0.035*	0.930*
Differences x replicates	12	0.028	0.077	0.650	0.174
D (additive)		0.410*	0.824*	5.161*	0.823*
H (dominance)		0.022	-0.041	-0.410*	0.504*
Degree of dominance $(H/D)^{1/2}$		0.233	0.223	0.282	0.783
Direction of dominance ($r_{s,d}$)		-0.294	0.653	0.888*	0.287

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

BW: Boll weight, SCY/P: Seed cotton yield/plant, LY/P: lint yield/plant, L%: lint percentage, Mic.: Micronaire reading, FS: Fiber strength as Pressely index, FL: Fiber length and UI%: Uniformity index.

The significant positive estimates for direction of dominance ($r_{s,d}$) for the traits boll weight, lint yield/plant and fiber length indicates the direction of dominance towards fewer genes responsible for these traits. The insignificant values of dominance direction for rest of the traits clarified that such traits did not provide any confirmation for directional dominance in cotton.

For the traits, seed cotton yield/plant, lint%, Pressely index and lint uniformity index the direction of dominance ($r_{s,d}$) estimates were insignificant and positive which describe the dispersion of the dominant alleles between testers, with increasing alleles more frequently and dominant than declining alleles for these traits. Whereas, the declining alleles were more frequently dominant than increasing alleles for micronaire reading. These findings were in harmony with those recorded by El -Hoseiny et al. (2012), Abou El-yazied (2014), Dawwam et al. (2016), AL-Hibbiny et al. (2020) and El-Mansy et al. (2020).

Conclusion

Total epistasis was present for almost all of the studied traits. The (i) type of epistasis (additive x additive) was significant for almost all traits, while the (j+l) type (additive x dominance and dominance x dominance) was significant for some traits. Both additive and dominance were important for controlling most traits and the additive component was extremely higher than dominance for all traits. The role of epistasis must be in breeder's consideration during planning breeding programs for improving economic traits in cotton.

References

Abou El-yazied, M.A. (2014) Detection of epistasis and assessment genetic components in cotton (*G. barbadense* L.). *Egyptian Journal of Agricultural Research,* **92**(2), 1-10, 2014.

AL-Hibbiny, Y.I.M., Mabrouk, A.H., Gibely, Reham H.A.O. (2020) The role of non-allelic interaction in inheritance of some economic traits in *G.*

barbadense. Menoufia Journal of Plant Protection, **5**, 399 - 410.

Ali, I., Shakeel, A., Ali, A., Sadia, B. (2016) Genetic basis of variation for within-boll yield components in cotton. *Turkish Journal of Agriculture and Forestry,* **40**, 18-24.

Amer, E.A. (2022) Identifying superior parents and hybrids for yield, its components and fiber quality in cotton (*Gossypium barbadense* L.). *Egyptian Journal of Agronomy*, **44** (1), 59-73.

Bhatti, M.A., Azhar, F.M., Alvi, A.W. (2006) Triple test cross analysis of seed cotton yield and its components. *International Journal of Agriculture And Biology,* **8**(6), 820 - 823.

Comstock, R.E., Robinson, H.F. (1952) "*Estimation of Average Dominance of Genes*". Heterosis. Iowa State College Press, Ames, Iowa. Chapter 30.

Dawwam, H.A., Hendawy, F.A., Abd El-Aziz, M.A., Esmail, R.M., Khatab, A.B., El- Shymaa, H.M. (2016) Using triple test cross technique for partitioning the components of genetic variance and predicting the properties of new recombinant inbred lines in cotton (*G. barbadense* L.). *10th Inter. Plant Breed. Conf.,* 5-6 September, Fac. Agric. Menoufia Univ.

El-Hoseiny, H.A., Orabi, M.H., Sultan, A.M., El-Feki, T.A. (2012) Detection of epistasis, additive and dominance as genetic components for some cotton genotypes. *Egyptian Journal of Agricultural Research*, **90**(4), 1677-1685.

El-Lawendey, M.M., El-Mansy, Y.M., Abd El-Salam, M.E. (2010) Determination of genetic components through triple test cross in cotton (*G. barbadense* L.). *Journal of Agricultural Research. Kafr El-Shaikh University*, **36**, 240-257.

EL-Mansy, Y.M., Abdelmoghny, A.M., Gibely, Reham H.A.O., Mabrouk, A.H. (2020) Relationship between combining ability, genetic components and genetic diversity using triple test cross in cotton. *16th Int. Conf. Crop Sci. Al-Azher Univ*. 13-14 October.

Jayade, V.S., Patil, S.R., Peshattiwarand, P.D., Deotale, R.D. (2014) Simplified triple test cross analysis for yield, yield contirbting and fiber traits in cotton (*Gossypium hirsutum* L.,). *International Journal of Researches in Biosciences, Agriculture & Technology,* **2**(II), 177-187.

Jinks, J.L., Virk, D.S. (1977) A modified triple test-cross analysis to test and allow for inadequate testers. *Heredity*, **39**(1), 165-170.

Jinks, J.L., Perkins, J.M., Breeze, E.L. (1969) A general method of detecting additive, dominance and epistatic components of variation for metrical traits: II. Application to inbred lines. *Heredity*, **24**, 45-57.

Kearsey, M.J., Jinks, J.L. (1968) A general method of detecting additive, dominance and epistatic variation for metrical traits. I. Theory. *Heredity*, **23**, 403-409.

Ketata, H., Smith, E.L., Edwards, L.K., Mcnew, R.W. (1976) Detection of epistatic, additive and dominance variation in winter wheat. *Crop Science,* **16**, 1-4.

Khattak, G.S.S., Haq, M.A., Ashraf, M., Mcneilly, T. (2001) Genetic basis of variation of yield and yield components in mungbean (*Vigna radiata* L.). *Hereditas*, **134**, 211-217.

Pooni, H.S., Jinks, J.L., Pooni, G.S. (1980) A general method for the detection and estimation of additive, dominance and epistatic variation for metrical traits. IV. Triple test cross analysis for normal families and their self. *Heredity*, **44**, 177-192.

Said, S.R.N., Max Mariz, S., Darwesh, A.E.I., Amer, E.A. (2021) Estimation of heterosis and combining ability in F_1 and F_2 generations for yield and fiber traits in cotton. *Plant Cell Biotechnology and Molecular Biology,* **22**(69&70), 241-254.

Saleh, E.M.R. (2013) Genetic estimation of yield and yield components in cotton through triple test cross analysis. *Journal of Plant Protection and Pathology, Mansoura University,* **4**(2), 229-237.

Singh, P. (2004) "*Cotton Breeding*". New Delhi: Kalyani Publishers; p. 12.

Singh, P., Chahal, G.S. (2003) Estimates of additive, dominance and epistatic variation for yield and its component characters in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development,* **17**(2), 130-134.

Singh, R.K., Chaudhary, B.D. (1999) "*Biometrical*

Methods in Quantitative Genetic Analysis". Kalyani Pub. Ludhina, New Delhi, Revised ed. p.92-101.

Singh, U.P., Ganesh, M., Srivastva, C.P. (1997) Detection of epistasis and estimation of genetic variation applying modified tripe test cross analysis using two testers in pea (*Pisum sativum* L.). *Indian Journal of Genetics and Plant Breeding,* **57**, 138-142.

Sohu, R.S., Dilawari, M., Singh ,P., Gill, B.S., Chahal, G.S. (2010) Inheritance studies for earliness, yield and fiber traits using simplified triple test cross in G. hirsutum. *Indian Journal of Genetics and Plant Breeding,* **70**(1), 71-75.

تقدير مكونات التباين الوراثى بإستخدام تحليل الإختبار الثلاثى في القطن الباربادنس

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أجريت هذه الدراسة في محطة البحوث الزراعية بسخا التابعة لمركز البحوث الزراعية بمحافظة كفر الشيخ خلال مواسم (2020-2022 م) وكان الهدف تقدير مكونات التباين الوراثى (الإضافى – السيادى – التفوق) في القطن المصرى باستعمال نموذج التهجين الرجعي الثلاثي وتحديد نسبة مساهمة هذه المكونات فى التباين الكلى. تم تقييم الآباء والهجن الناتجة (14 هجين فردى + 7 هجين ثلاثى) فى تجربة بتصميم القطاعات كاملة العشوائية ذات ثلاث مكررات وأظهرت النتائج مايلي:

- أظهر تحليل التباين وجود فروق معنوية بين التراكيب الوراثية وكذلك بين الآباء وبين الهجن لكل الصفات المدروسة.

- أظهرت النتائج وجود معنوية للفعل الجيني التفوقي الكلى لكل الصفات المدروسة ماعدا قراءة الميكرونير وكذلك كان التفاعل الإضافى (الإضافي × الإضافي) معنوياً لكل الصفات ماعدا قراءة الميكرونير بينما كان التفاعل الإضافي × السيادي والسيادي × السيادي معنوياً لصفات محصول القطن الزهر والقطن الشعر للنبات وتصافى الحليج ومعدل انتظام الطول.

- كان التفاعل الإضافي × الإضافي اكبر من التفاعل الإضافي × السيادي و السيادي × السيادي لكل الصفات المدروسة ماعدا قراءة الميكرونير.

- أظهرت النتائج أهمية كل من الفعل الجينى المضيف والفعل الجينى السيادى لتوارث كل الصفات المدروسة ماعدا وزن اللوزة وقراءة الميكرونير ومعدل البريسلى حيث كان الفعل المضيف هو المعنوى فقط.

- كانت قيم الفعل الوراثي الإضافي اكبر من قيم الفعل الوراثي السيادي لجميع الصفات المدروسة مما إنعكس على انخفاض قيم درجة السيادة عن الواحد الصحيح لكل الصفات والتى أظهرت سيادة جزئية وبالتالى يمكن للمربى تحسين هذه الصفات من خلال الإنتخاب فى الأجيال الإنعزالية المبكرة بينما الصفات التى يلعب فى تورثها التباين السيادى دور كبير فيكون من المفيد تاخير الانتخاب الى الاجبال المتاخرة ويمكن استخدام الانتخاب المتكرر والتزاوج بين العشائر لاستغلال كلاً من المكون الاضافى وغير الإضافى من التباين الوراثى فى تحسين هذه الصفات.

- لم تظهر كل السلالات المستخدمة فى الدراسة مشاركة معنوية فى التفوق الكلى لمعظم الصفات التى تم قياسها.

- تظهر هذه الدراسة أهمية التفوق كمكون من مكونات التباين الوراثى وضرورة أخذه فى الإعتبار وعدم تجاهله بواسطة مربى القطن عند وضع برنامج يهدف الى تحسين الصفات المدروسة.