

Relationship Between Combining Ability, Genetic Components And Genetic Diversity Using Triple Test Cross

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Abstract

Background: The target of this study is to investigate the relationship between genetic components, combining ability and genetic diversity among twenty six cotton crosses derived from a cross between thirteen contrasting inbred lines with two testers in three replications using modified triple test cross model.

Results: All the genotypes showed highly significant differences for twelve yield and fiber quality traits reflecting genetic variability between lines, testers and crosses. Giza 86 is considered as a good combiner for yield and its components traits, while Giza 45 is the best combiner for fiber fineness and fiber strength, which classified in unique cluster. Most of the combinations having significant SCA effects were belonging to genetically diverse parents. The mean squares for the deviations revealed the presence of significant epistasis for all the studied traits except, seed index and fiber reflectance. While, significant mean squares were shown for sums and differences except lint index for additive and uniformity ratio and fiber reflectance for dominance. The fixable type (i) of epistasis was larger than non-fixable (i + l) type for the inheritance of the studied traits. The traits had significant mean squares for both fixable and non-fixable gene action, also showed significant GCA and SCA among 15 parents and 26 cotton crosses, respectively. Additive genetic component was larger than dominance for all the studied traits. So, most of the studied traits had significant GCA and degree of dominance was less than unity for all the studied traits, indicating partial or incomplete dominance. The correlation coefficient between the sums and difference were found to be insignificant indicating the genes with positive and negative effects were equally distributed among the genotypes.

Conclusions: Genetic correlation between three genetic components revealed that both additive and epistasis play a great role among some studied traits suggesting common genetic pool. Thus, selection based on additive gene action based on indirect selection could improve cotton yield. The genotypes which have large genetic diversity could produce significant general or specific combining ability which may be reflecting its genetic behavior.

Introduction

Cotton is the most important commercial fibre crop playing key role in economic, political and social development of the world. The Egyptian cotton breeding program (*Gossypium barbadense* L.) is depending on producing pure lines to release new varieties. The main emphasis of breeding program is to develop new varieties with high yield potential and superior fiber quality traits. Since genetic improvement process never ends. Cotton yield is a polygenic trait and based on its components (El-Mansy et al., 2014). Cotton yield components may link or segregate independently, so the cotton breeder should investigate the genetic control and behavior for yield, its components and fiber quality traits.

The success of any breeding program based on the available data about genetic variation in the studied population. So, the plant breeders used many biometrical techniques to estimate or measure genetic variation and classified to its components. The available results or data provide genetic information about the inheritance of the economic quantitative traits (Jayade et al., 2014). Finally, the plant breeders know how to manage and lead breeding program. Fisher was the first one classified genetic variation into additive (D), dominance (H) and epistasis (i) components (Sing and Narayanan, 2013).

Also, understand combining ability effects is essential for efficient breeding program. Combining ability define as the estimation of the genotypes value on the basis of their offspring performance in some definite mating designs. General combining ability (GCA) is associated with additive gene effects; while specific combining ability (SCA) is related to dominance and epistatic effects if it is present (Fasahat et al 2016). The GCA of a line can be used in plant breeding as a measure of its breeding value. Also, GCA considered a good indicator for the relative value of the parental lines or frequency of favorable alleles and its genetic divergence, which help to select the superior parental lines. The differences between pure lines in GCA are due to the additive or additive \times additive gene interactions (if epistasis is present), while the differences in the SCA of combinations are related to non-additive, often dominant epistatic interactions (Sing and Narayanan, 2013).

Triple test cross (TTC) designed by **KeARSEY and JINKS, 1968** which is one of the best matting design for detecting and estimating the fixable and non-fixable genetic components for quantitative traits. Therefore, classified epistasis to its components (additive \times additive and additive \times dominance), which should be studied precisely before starting any breeding program. The output analysis could help plant breeder to choose the best breeding or selection procedures to be followed for breeding program improvement. Also, provide more knowledge about genetic correlation between the three genetic components (additive, dominance and epistasis), which occurs between traits, that can help breeder to increase selection efficiency by using favorable trait combinations to minimize the retarding effect of negative correlations between different traits. So many Egyptian cotton breeders used TTC analysis to understand the genetic basis of cotton yield and fiber quality traits Soliman et al., 2008; El-Lawendey et al., 2010; Saleh 2013 and Mahros, 2016.

Genetic diversity is the foundation to release new cotton varieties. It is essential to the plant breeder to detect and know more information about genetic diversity and select the more diverse parents for hybridization breeding program to increase transgressive segregation. The accumulation knowledge about genetic diversity and genetic inheritance or control of the quantitative traits could help plant breeder to increase

population variability combined with selection to favorable alleles. So, many Egyptian cotton breeder study genetic diversity among Egyptian cotton genotypes Abd El-Moghny et al., 2015 a and b.

The aim of the study is to create 26 ($13G_i \times L_1$ and $13G_i \times L_2$) cotton crosses using 13 cotton lines (G_i) and two testers (L_1 and L_2) to obtain useful information about the relationship between genetic component (fixable and non-fixable), combining ability and genetic diversity. Also, the study will extend to estimate genetic correlations between genetic components by using modified triple test cross analysis for twelve quantitative cotton traits.

Materials And Methods

The genetic materials used in the present investigation were involved fifteen cotton genotypes derived from three origins belong to *Gossypium barbadense* L. Origin, pedigree and category of these genotypes are presented in Table 1. The selfed seeds of these genotypes were kindly supported from the Cotton Breeding and Cotton Maintenance Departments; Cotton Research Institute, Agriculture Research Center, Giza, Egypt. The present investigation was carried out at Sakha Experimental Station; Agriculture Research Center, Kafr El-Sheikh government; Egypt, during the three growing seasons of 2017–2019.

The selfed seeds of the fifteen cotton genotypes were evaluated for twelve quantitative yield and fiber quality traits during the growing seasons 2017 to obtain more information about the highest and lowest performing cotton genotypes to be used as testers to construct modified triple test cross (TTC) population. The experimental design was randomized complete blocks design (RCBD) with three replications. Each replicate consists of four rows for each genotype.

In the growing season of 2018, each of the thirteen cotton genotypes ($G_i = 1$ to 13) were crossed to the two testers Alexandra 4; (L_1) and Bahtim (L_2) to produce 26 F_1 crosses; consists of $13L_1 (G_i \times L_1)$ and $13L_2 (G_i \times L_2)$, respectively where $G_i = 1$ to 13.

In the growing season of 2019, the seeds of 26 families ($13L_1 + 13L_2$) with their fifteen parental genotypes were sown in a randomized complete blocks design (RCBD) with three replications each replicate was consists of four rows for both parents and their F_1 crosses. Row was 4.0 m long; the distance between rows 0.7 m and within plants 0.4 m to insure 10 plants per row. Hills were thinned to keep a constant stand of one plant per hill at seedlings stage. All agronomic cultural practices were applied as usually recommended for ordinary cotton fields.

At harvest the inner eight individual plants of the fifteen parental cotton genotypes with their derived 26 hybrids were harvested from each row and ginned in order to, estimate six agronomic traits. The data were recorded on boll weight (BW) in grams as the average weight of ten bolls per plant, seed cotton yield per plant (SCY) in grams, lint yield per plant (LY) in grams, lint percentage (L%), seed index (SI) and lint index (LI) in grams. Also, six fiber quality traits; fiber length (FL), fiber strength (FS), fiber fineness (FF), uniformity ratio (UR%) yellowness (+ b) and fiber reflectance (Rd) were estimated at Cotton Technology Laboratory, Cotton Research Institute, Agricultural Research Center, Giza, Egypt.

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

No.	Parents	Origin	Pedigree	Category
Lines (G_i)				
P ₁	Karshenky	Russia	Unknown	Long staple
P ₂	Suvin	India	Sujata x Vincent	Long staple
P ₃	Ashmouni	Egypt	Ashmouni	Long staple
P ₄	Giza 45	Egypt	Giza 28 x Giza 7	Extra long staple
P ₅	Giza 70	Egypt	Giza 59A x Giza 51B	Extra long staple
P ₆	Giza 76	Egypt	Menoufi x Pima	Extra long staple
P ₇	Giza 77	Egypt	Giza 70 x Giza 68	Extra long staple
P ₈	Giza 80	Egypt	Giza 66 x Giza 73	Long staple
P ₉	Giza 81	Egypt	Giza 67 x 5844A	Long staple
P ₁₀	Giza 88	Egypt	(Giza 77 x Giza 45) B	Extra long staple
P ₁₁	Giza 89	Egypt	Giza 75 x 6022	Long staple
P ₁₂	Giza 89 x S6	Egypt	((Giza 75 x 6022) x S6)	Long staple
P ₁₃	Giza 86	Egypt	Giza 75 x Giza 81	Long staple
Testers (L₁ and L₂)				
L ₁	Alexandria 4	Egypt	Unknown	Long staple
L ₂	Bahim	Egypt	Unknown	Long staple

Biometrical analysis:

Before proceeding to modified triple test cross analysis, the recorded data were subjected to analysis of variance according to **Gomez and Gomez, 1984** to determine significant differences among genotypes. The variation among parental cotton genotypes (G_i) and their crosses (L₁) and (L₂) was partitioned into two sources to general combining ability (GCA) and specific combining ability (SCA) effects were calculated in accordance with the procedure suggested by Kempthorne, 1957.

The detection of epistasis was done according to the method outlined by Jinks et al., 1969 and 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 treatment means were subjected to analysis of variance according to the modified TTC method (**Ketata et al., 1976**) as illustrated by Sharma, 1988 and **Khattak et al., 2002**. The analysis of variance of (L₁, L₂, G_i) and (L₁, L₂) sets of families have been carried out for every trait separately. This method tests epistasis based on the variance between (L_{1i} + L_{2i} - G_i) for i = 1, 2... 13, where L₁ is the mean of the cross of the ith

line with tester L_1 and L_2 , respectively. The crosses mean of the i^{th} line with tester L_2 ; and G_i is the mean of the i^{th} line. While, the within (L_{1i} and L_{2i}) types of families are appropriate for testing the significance of additive ($L_{1i} + L_{2i}$) and dominance ($L_{1i} - L_{2i}$) gene effects. For test epistasis significant thirteen values of ($L_{1i} + L_{2i} - G_i$), $G_i = 1$ to 13 with 12 degrees of freedom was used to test overall epistasis. The overall epistasis was partitioned into (i) type of epistasis (additive x additive) and (i + j) type (additive x dominance) gene interactions (Jinks and Virk, 1977). Also, the mean squares due to sums ($L_{1i} + L_{2i}$) and differences ($L_{1i} - L_{2i}$) for 12 degrees of freedom were used to detect significant of both additive and dominance gene effects.

The direction of dominance (F) was computed from covariance of sums ($L_{1i} + L_{2i}$) / differences ($L_{1i} - L_{2i}$) which equal = -1/8. The correlation coefficient of sums / differences was used to test significance of F-value. The estimation of additive (D), dominance (H) and epistasis genetic components were obtained to detect the direction of dominance. The degree of dominance was calculated as $(H/D)^{1/2}$. Genetic correlation for genetic components was calculated between additive (r_D), dominance (r_H) and epistasis (r_i). Correlation coefficients were computed from ($L_{1i} + L_{2i}$), ($L_{1i} - L_{2i}$) and ($L_{1i} + L_{2i} - G_i$), respectively.

Cluster analysis using multivariate analysis based on yield, its components and fiber quality traits using averaged linkage (within groups) was calculated as outlined by Johnson and Wichern 1998 to investigate genetic dissimilarity between fifteen parental cotton genotypes. The dissimilarity coefficient and dendrogram were done by using SPSS software.

Results And Discussion

The improvement of any breeding program depending on how much information is available to the plant breeders about the crop and their target traits. Hybridization is an important source to induce genetic variability, so cotton breeders use different mating models to pass favorable alleles to the next progeny. The plant materials used in this study consists of fifteen cotton genotypes belonging to *Gossypium barbadense* L., and their twenty six cotton crosses. Analysis of variance (ANOVA) for all the agronomic and fiber quality traits was used to detect the variability between genotypes (Table 2) which revealed highly significant differences for genotypes, crosses, parents, lines and testers for all the studied traits indicating the presence of considerable variability among these genotypes and showed existence worth of variations between the two testers (L_1 and L_2) which resulted into the expression of high mean performance of their F_1 crosses. Also, provide precise estimates of additive and dominance variance as reported by **Kearsey and Jinks 1968**. However, line vs. tester showed highly significant differences for all the studied traits except uniformity ratio, yellowness and fiber reflectance, showing the importance of both additive and nonadditive variance gene effects. The same results for different cotton crosses belonging to *Gossypium barbadense* L., obtained by AL-Hibbiny, 2015; Mahrous, 2018; **Sultan et al., 2018 and Yehia and El-Hashash, 2019**. These results could be adequate for proceeding a further biometrical analysis by means using modified triple test cross (TCC).

The phenotypic mean values of backcrosses L_1 , L_2 and parents (G_i) exhibited significant differences for most studied traits (Tables 3 and 4). Generally, backcrosses to the second tester (Bahtim) showed higher mean values for six yield traits. Such values were varied from line to other, the backcross of the two testers with Giza 86 surpassed all the other genotypes for all yield traits followed by the Indian genotype (Suvin) and the Egyptian variety Giza 80. These results might reflect the conspicuous genetic constitution of the Egyptian varieties Giza 86 and Giza 80 as well as the Indian one which might possess much potential to improve yield traits.

The reverse trend was observed for fiber quality traits since backcrosses with L_1 tended to improve most fiber quality traits, which showed decrease values of micronaire reading (desirable values) and increased fiber length, fiber strength and uniformity ratio. The Egyptian lines Giza 45 and Giza 77 surpassed other lines when used as common parents in TTC and recorded desirable fiber quality values over the two testers. Similar conclusions were reported by El-Mansy et al., 2010 and 2012.

Generally, the twenty six cotton crosses showed a wide range of variability for all the studied traits represent two categories for fiber quality long and extra-long staple category. The two yield traits; seed cotton yield and lint yield for the $13(G_1 \times L_2)$ was larger than the other $13(G_1 \times L_1)$ among all crosses.

Table 2
Analysis of variance for the triple test crosses for all the studied traits

Mean Squares							
Yield and its components							
S.O.V	d.f	Boll weight g	Seed cotton yield g	Lint yield g	Lint %	Seed index g	Lint index g
Replications	2	0.057	84.272	10.938	0.279	0.364	0.146
Genotypes (G _i) + (G _i x L ₁) + (G _i x L ₂)	40	0.244**	1380.051**	203.240**	11.331**	1.509**	1.440**
Parents (G _i + L ₁ + L ₂)	14	0.177**	390.143**	55.683**	14.889**	2.306**	1.999**
P vs. C	1	0.009	354.628	4.717	21.272**	0.562*	2.783**
Crosses (13G _i x L ₁) + (13G _i x L ₂)	25	0.292**	1975.416**	293.813**	8.940**	1.101**	1.073**
Lines (G _i)	12	0.370**	1727.074**	271.623**	14.770**	1.205**	1.863**
Testers (L ₁ + L ₂)	1	0.919**	24284.637**	3513.490**	7.253**	0.000	0.324*
Gi vs. L _i	12	0.161**	364.656**	47.697**	3.252**	1.088**	0.345**
Error	80	0.029	99.885	13.817	0.545	0.138	0.063
Fiber quality traits							
SOV	d.f	Fiber fineness	Fiber length mm	Fiber strength	Uniformity ratio %	Yellowness	Fiber reflectance
Replications	2	0.018	0.188	0.186	0.018	0.270	2.218
Genotypes (G _i) + (G _i x L ₁) + (G _i x L ₂)	40	0.431**	0.807**	7.241**	0.431**	4.080**	22.886**
Parents (G _i + L ₁ + L ₂)	14	0.367**	0.821**	9.214**	0.367**	6.307**	32.038**
P vs. C	1	0.777**	0.470*	13.580**	0.777**	3.264**	21.893
Crosses (13G _i x L ₁) + (13G _i x L ₂)	25	0.453**	0.813**	5.883**	0.453*	2.865**	17.800**
Lines (G _i)	12	0.478**	0.783**	7.504**	0.478**	5.220**	33.587**
Testers (L ₁ + L ₂)	1	1.468**	0.525*	0.003	1.468	6.606**	0.431
Gi vs. L _i	12	0.344**	0.868**	4.752**	0.344	0.199	3.461
Error	80	0.058	0.120	1.051	0.058	0.185	4.616

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

Table 3

Phenotypic mean performance for thirteen cotton genotypes (G_i), tester one (L_1) with their 13($G_i \times L_1$) and tester two (L_2) with their 13($G_i \times L_2$) crosses for the studied yield and its component traits

Genotypes	Boll weight			Seed cotton yield			Lint yield		
	BW			SCY			LY		
	g			g			g		
	P	($G_i \times L_1$)	($G_i \times L_2$)	P	($G_i \times L_1$)	($G_i \times L_2$)	P	($G_i \times L_1$)	($G_i \times L_2$)
Karshenky	2.600	2.567	2.411	92.07	61.43	84.97	31.00	20.30	30.23
Suvin	3.078	2.500	3.267	106.17	63.80	107.97	37.07	23.67	37.87
Ashmouni	2.611	2.433	2.789	80.27	49.97	64.27	29.97	19.00	25.27
Giza 45	2.622	2.078	2.556	88.27	43.47	84.57	29.13	14.63	29.20
Giza 70	2.278	2.722	2.911	79.93	49.07	110.80	27.43	17.63	41.47
Giza 76	2.667	2.833	2.933	81.50	67.60	99.53	27.37	24.37	36.13
Giza 77	2.956	2.978	2.656	85.80	93.73	119.70	30.80	35.40	45.50
Giza 80	3.033	2.956	3.078	66.03	57.53	86.83	26.67	21.77	34.93
Giza 81	3.178	3.200	3.144	76.13	69.80	81.87	28.97	26.17	31.40
Giza 88	3.011	2.833	3.356	107.23	68.37	119.93	39.90	23.77	44.90
Giza 89	2.678	2.522	2.911	90.50	89.17	142.17	33.43	34.27	53.53
Giza 89 x S6	2.789	2.467	3.033	85.57	67.93	91.27	31.47	25.70	34.23
Giza 86	3.044	3.156	3.022	101.97	79.27	126.03	40.20	30.93	47.43
Alexandria 4 (L_1)	2.722			78.27			28.97		
Bahtim (L_2)	2.756			91.47			30.87		
Mean	2.80	2.71	2.93	87.41	66.24	101.53	31.55	24.43	37.85
Overall mean	2.81			85.18			31.29		
LSD 0.05	0.231			13.58			5.05		
LSD 0.01	0.329			19.37			7.21		
Genotypes	Lint percentage			Seed index			Lint index		
	L%			SI			LI		
	g			g			g		
	P	($G_i \times L_1$)	($G_i \times L_2$)	P	($G_i \times L_1$)	($G_i \times L_2$)	P	($G_i \times L_1$)	($G_i \times L_2$)
Karshenky	33.724	33.171	35.587	9.800	9.533	9.733	4.989	4.739	5.376
Suvin	34.855	37.072	35.103	11.133	9.133	11.333	5.958	5.379	6.129
Ashmouni	37.232	38.117	39.279	10.333	10.133	10.000	6.130	6.243	6.470
Giza 45	33.018	33.758	34.534	11.133	8.333	9.600	5.488	4.245	5.064
Giza 70	34.383	35.928	37.407	8.467	10.467	10.200	4.432	5.868	6.096
Giza 76	33.499	36.003	36.312	8.600	10.133	9.600	4.337	5.696	5.473
Giza 77	35.916	37.781	37.970	8.667	10.733	9.867	4.859	6.518	6.040
Giza 80	40.306	37.833	40.236	10.333	10.133	9.433	6.981	6.167	6.352
Giza 81	38.038	37.482	38.332	10.700	10.400	9.867	6.568	6.235	6.138
Giza 88	37.204	34.649	37.440	10.467	10.000	10.067	6.201	5.310	6.026

Genotypes	Boll weight			Seed cotton yield			Lint yield		
	BW			SCY			LY		
	g			g			g		
	P	(G _i x L ₁)	(G _i x L ₂)	P	(G _i x L ₁)	(G _i x L ₂)	P	(G _i x L ₁)	(G _i x L ₂)
Giza 89	36.895	38.417	37.665	9.000	9.633	9.467	5.260	6.008	5.720
Giza 89 x S6	36.800	37.869	37.517	10.200	10.733	10.200	5.941	6.543	6.126
Giza 86	39.461	39.021	37.647	9.933	10.667	10.667	6.474	6.818	6.438
Alexandria 4 (L₁)	37.087			9.467			5.379		
Bahtim (L₂)	33.706			9.700			4.714		
Mean	36.14	36.70	37.31	9.81	10.00	10.00	5.58	5.83	5.96
Overall mean	36.31			9.93			5.78		
LSD at 0.05	1.003			0.523			0.340		
LSD at 0.01	1.431			0.746			0.486		

Table 4
Phenotypic mean performance for thirteen cotton genotypes (G_i), tester one (L_1) with their 13($G_i \times L_1$) and tester two (L_2) with their 13($G_i \times L_2$) crosses for all the studied fiber quality traits

Genotypes	Fiber fineness			Fiber length			Fiber strength		
	FF			FL			FS		
	P	($G_i \times L_1$)	($G_i \times L_2$)	P	($G_i \times L_1$)	($G_i \times L_2$)	P	($G_i \times L_1$)	($G_i \times L_2$)
Karshenky	3.4	3.1	3.2	31.267	32.633	32.200	9.633	9.833	9.367
Suvin	3.8	3.3	4.1	31.467	32.833	31.600	9.000	9.100	10.233
Ashmouni	3.8	3.9	4.1	31.067	32.300	30.867	9.500	9.533	9.533
Giza 45	3.1	3.5	3.3	34.900	34.033	34.633	10.633	10.500	10.000
Giza 70	3.6	3.5	4.4	34.900	35.233	34.433	9.333	10.567	10.100
Giza 76	3.1	4.1	3.6	34.467	35.833	35.600	9.100	11.033	9.200
Giza 77	3.0	3.4	4.1	34.700	35.433	34.800	10.233	10.467	9.567
Giza 80	4.0	3.9	3.6	31.000	31.933	34.867	9.567	10.267	9.700
Giza 81	3.5	4.1	4.1	31.700	34.633	32.900	9.800	9.600	9.700
Giza 88	3.8	3.4	4.0	34.600	32.433	35.200	9.867	9.300	9.633
Giza 89	3.9	3.7	4.0	30.033	33.533	32.533	9.300	9.333	9.300
Giza 89 x S6	3.7	3.6	4.5	32.767	34.767	32.333	9.200	10.033	10.833
Giza 86	4.2	4.1	4.1	33.100	33.433	33.900	10.000	9.500	9.767
Alexandria 4 (L_1)	4.0			32.100			10.733		
Bahtim (L_2)	3.6			32.267			9.867		
Mean	3.63	3.66	3.93	33.08	33.77	33.76	9.71	9.93	9.76
Overall mean	3.74			33.51			9.80		
LSD at 0.05	0.328			1.393			0.471		
LSD at 0.01	0.467			1.988			0.672		
Genotypes	Uniformity ratio			Yellowness			Fiber reflectance		
	UR%			+b			Rd		
	P	($G_i \times L_1$)	($G_i \times L_2$)	P	($G_i \times L_1$)	($G_i \times L_2$)	P	($G_i \times L_1$)	($G_i \times L_2$)
Karshenky	94.3	91.5	92.2	10.167	10.667	10.067	71.6	67.367	67.533
Suvin	89.9	89.2	90.3	9.133	10.300	10.267	72.3	70.233	68.700
Ashmouni	87.9	90.2	88.0	9.367	10.200	9.600	74.2	70.667	70.200
Giza 45	86.8	90.0	91.4	9.567	9.833	9.033	73.0	72.267	71.467
Giza 70	89.9	91.4	92.2	9.133	11.100	10.433	71.3	67.933	66.200
Giza 76	90.9	93.8	93.8	8.767	10.000	8.867	73.2	72.333	72.167
Giza 77	91.3	93.3	92.9	12.667	11.467	10.567	67.0	68.233	68.000
Giza 80	89.0	90.8	93.2	12.567	12.300	12.233	63.6	66.367	65.167
Giza 81	90.3	92.1	90.8	9.467	11.033	10.500	71.6	69.467	71.333
Giza 88	89.7	90.7	93.2	12.100	12.600	11.667	64.8	64.567	66.600
Giza 89	91.3	91.2	89.2	8.400	9.767	9.333	71.5	72.767	71.900

Genotypes	Fiber fineness			Fiber length			Fiber strength		
	FF			FL			FS		
	P	(G _i x L ₁)	(G _i x L ₂)	P	(G _i x L ₁)	(G _i x L ₂)	P	(G _i x L ₁)	(G _i x L ₂)
Giza 89 x S6	88.6	92.8	90.4	9.000	10.067	10.067	71.5	69.200	71.667
Giza 86	88.2	90.1	89.4	8.900	10.233	9.367	73.1	69.800	72.200
Alexandria 4 (L ₁)	88.7			11.167			68.1		
Bahtim (L ₂)	91.9			11.200			67.4		
Mean	89.92	91.31	91.31	10.11	10.74	10.15	70.27	69.32	69.47
Overall mean	90.80			10.32			69.72		
LSD at 0.05	2.507			0.584			2.919		
LSD at 0.01	3.577			0.833			4.165		

Combining ability (GCA)

The ultimate to choice parents for any breeding program is generally based on phenotypic performance of parents and their F₁s. However, GCA and SCA effects were more informative than phenotypic performance, since it also revealed the type of gene action, which could help plant breeder to devise breeding or selection strategies.

Estimation of general combining ability (GCA) effects of both 13 lines (G_i) and the two testers (L₁ and L₂) for all the studied traits is presented in Table 5. The results showed that the two lines Giza 77 and Giza 89 were the best general combiner when recorded significant and positive general combining ability for seed cotton yield, lint yield and lint % and Giza 88 has the same direction for boll weight, seed cotton yield and lint yield. While, Giza 86 has positive and significant general combining ability (GCA) for all the studied yield traits, so the Egyptian cotton breeders define Giza 86 as a good combiner for yield traits and its components.

On the other hand, tester one Alexandria 4 (L₁) has negative and significant general combining ability for all the studied traits and recorded inferior values for seed index (SI) and lint index (LI). While, the second tester Bahtim (L₂) showed the opposed direction for the same traits. These findings may be reflect the higher mean performance for the crosses including second tester (L₂) as a parent than the crosses had first tester (L₁) for seed cotton yield and lint traits. So, the second tester (L₂) has a greater ability to transmit his higher performance to its progeny than tester one (L₁). For fiber quality traits the parental lines Giza 45 was the best combiner for fiber fineness and fiber strength. The extra-long staple varieties Giza 70, Giza 76 and Giza 77 showed desirable values for fiber length (FL) and uniformity ratio (UR %). The same results were obtained by many Egyptian breeders **Sultan et al., 2018 and Yehia and El-Hashash, 2019** especially for Giza 86 as a good combiner.

Since, general combining ability reflects parental performance and its gene expression; additive and additive x additive gene type of epistasis if present. The significance of GCA effects for the studied traits showed the importance of fixable gene action. Thus, plant breeder may utilize good or general combiner for specific breeding purposes. The relationship among GCA effects for the studied traits (Table 6) revealed that increasing additive gene effect controlling boll weight was correlated with increasing additive ones for lint %, seed index, lint index and fiber fineness. Boll weight is the independent key for yield components and played a prime role to managing or increasing yield productivity. Since, yield is one of the most important economic traits in cotton. So, the possibility to improve yield is increasing efficiency of indirect selection for its components (El-Mansy et al., 2014).

The basis of specific combining ability (SCA) effects revealed that most of the combinations having significant SCA effects were related to genetically diverse parents. The major aim for cotton breeding program is to obtain a cross combination with high values for all yield traits. Most of the twenty six cotton cross combination surpassed in both yield and fiber quality traits (Table 7). Two combinations recorded significant positive SCA values for boll weight. The cross (Giza 77 x Alexandria 4) and (Suvin x Bahtim) recorded the best SCA for seed cotton yield and lint yield. While, the two crosses (Giza 80 x Alexandria 4) and (Giza 70 x Bahtim) which include one good and the other poor general combiner could produce desirable transgressive segregant if complex fixable gene (additive) is present in a good combiner and complementary with epistatic gene effect in the poor combiner and act in the same direction to maximize the desirable attributes. Similar conclusion was reported by El-Mansy et al., 2014 and **Sultan et al., 2018**.

The cross (Ashmouni x Alexandria 4) showed the best SCA effects for lint %. The crosses (Giza 88 x Bahtim) and (Giza 86 x Alexandria 4) recorded significant positive SCA values for lint % and lint index, respectively. The twenty six cotton crosses did not show superiority for all the studied fiber quality traits. Generally, few combinations showed desirable significant SCA effects for fiber fineness. However, only three and four crosses recorded significant positive values for fiber strength and fiber length, respectively.

Positive and significant correlation was recorded between GCA for all studied yield traits and fiber fineness. Also, the same trend between fiber length with two fiber quality traits; fiber strength and uniformity ratio % (Table 6). Also, most of yield components traits had positive and significant SCA. While, negative correlation was shown between SCA for fiber fineness and fiber length but significant and positive correlation for SCA between fiber fineness and fiber strength. These results showed that the best specific combinations were not always obtained from parents which showed good or positive general combining ability effects. These findings are inconsistent with those obtained by **Ekinci and Basbage, 2015**; Yehia and El-Hashash, 2019 and **Al-Hibiny et al., 2019**.

These results indicated that these genotypes had the capacity to transmit superior performance to its progenies. The GCA is a primarily function of additive genetic variance (D) but if epistasis is present GCA will include additive x additive type (i) of non-allelic interaction, also it's useful to select good parents for hybridization programs. Specific combining ability (SCA) is a function of dominance genetic variance (H), but if epistasis is present it will include two types of non-allelic interaction (additive x dominance and dominance x dominance) and it's useful for selecting superior cross combinations (Sing and Narayanan, 2013 and **Fasahat et al., 2016**). Therefore, the better understand of combining ability genetic basis will be guidance for cotton improvement programs.

The presence of significance general and specific combining ability effects through F_1 generations is a consequence of fluctuations for additive and dominance relationship, respectively among the parents (**Basbag et al., 2007**). The estimation of additive and dominance genetic components appeared to be biased a result of epistasis lead to kind of discrepancy in the relative importance of genetic components. Thus, the breeder should take epistasis into account in producing genetic models.

Table 5
Estimates of general combining ability effects for all the studied traits

Yield and its components						
Parents	BW	SCY	LY	L%	SI	LI
	g	g	g		g	g
Lines (G_i)						
Karshenky	-0.331*	-10.68*	-5.876*	-2.626*	-0.369*	-0.835*
Suvin	0.064	1.997	-0.376	-0.917*	0.231	-0.139
Ashmouni	-0.21**	-26.76*	-9.009*	1.693*	0.064	0.463*
Giza 45	-0.503	-19.86*	-9.226*	-2.859*	-1.036*	-1.239*
Giza 70	-0.003	-3.953	-1.592	-0.338	0.331*	0.089
Giza 76	0.064	-0.319	-0.892	-0.848*	-0.136	-0.308*
Giza 77	-0.003	22.831*	9.308*	0.871*	0.297	0.386*
Giza 80	0.197*	-11.70*	-2.792	2.030*	-0.219	0.367*
Giza 81	0.353**	-8.053*	-2.359	0.902*	0.131	0.294*
Giza 88	0.275**	10.264*	3.191*	-0.961*	0.031	-0.225*
Giza 89	-0.103	31.781*	12.758*	1.036*	-0.453*	-0.029
Giza 89 x S6	-0.070	-4.286	-1.176	0.688*	0.464*	0.441*
Giza 86	0.269**	18.764*	8.041*	1.329*	0.664*	0.735*
Testers (L₁ and L₂)						
Alexandria 4	-0.109*	-17.65*	-6.712*	-0.305*	0.000	-0.064
Bahtim	0.109*	17.645*	6.712*	0.305*	0.000	0.064
Fiber quality traits						
Parents	FF	FS	FL	UR	+b	Rd
			mm	%		
Lines (G_i)						
Karshenky	-0.65**	-0.246	0.151	-0.646	-0.078	-1.947*
Suvin	-0.079	-0.179	-1.549	-0.079*	-0.162	0.069
Ashmouni	0.221**	-0.313*	-2.182*	0.221*	-0.545*	1.036
Giza 45	-0.413*	0.404*	0.568	-0.413	-1.012*	2.469*
Giza 70	0.171	0.487*	1.068	0.171	0.322	-2.331*
Giza 76	0.054	0.271	1.951	0.054*	-1.012*	2.853*
Giza 77	-0.063	0.171	1.351	-0.063*	0.572*	-1.281
Giza 80	-0.029	0.137	-0.365	-0.029	1.822*	-3.631*
Giza 81	0.321*	-0.196	0.001	0.321	0.322	1.003
Giza 88	-0.129	-0.379*	0.051	-0.129	1.688*	-3.814*
Giza 89	0.037	-0.529*	-0.732	0.037	-0.895*	2.936*
Giza 89 x S6	0.271**	0.587*	-0.215	0.271	-0.378	1.036
Giza 86	0.287**	-0.213	-0.099	0.287*	-0.645*	1.603

* Significant at 5% levels of probability.

Yield and its components						
Testers (L ₁ and L ₂)						
Alexandria 4	-0.137*	0.082	0.006	-0.137	0.291*	-0.074
Bahtim	0.137*	-0.082	-0.006	0.137	-0.291*	0.074
* Significant at 5% levels of probability.						

Table 6
Correlation between general (above diagonal) and specific (below diagonal) combining ability for all the studied traits

Traits	BW g	SCY g	LY g	L% g	SI g	LI g	FF	FS	FL mm	UR %	+b	Rd
BW		0.41*	0.47*	0.54*	0.62*	0.63*	0.61*	-0.24	0.04	0.17	0.49	-0.27
SCY	0.31		0.98**	0.24	0.27	0.27	0.21	-0.32	0.20	0.11	-0.04	0.08
LY	0.25	0.97**		0.38	0.33	0.40	0.32	-0.32	0.15	0.08	0.00	0.07
L%	-0.20	-0.16	0.04		0.53*	0.92**	0.77**	-0.17	-0.33	-0.18	0.21	0.00
SI	0.59**	0.32	0.19	-0.36		0.811**	0.67**	0.05	-0.07	-0.03	0.18	-0.18
LI	0.46*	0.21	0.23	0.39*	0.71**		0.83**	-0.08	-0.25	-0.15	0.22	-0.07
FF	0.32	0.31	0.29	-0.22	0.12	-0.03		0.05	-0.16	-0.17	-0.07	0.26
FS	0.56**	0.10	0.03	-0.36	0.462*	0.19	0.57**		0.544*	0.46	-0.06	0.00
FL	-0.20	0.19	0.31	0.65**	0.01	0.47*	-0.39*	-0.26		0.85**	0.02	-0.04
UR%	0.09	0.40*	0.47*	0.48*	0.32	0.67**	-0.14	-0.17	0.78**		0.32	-0.29
+b	0.45*	-0.16	-0.19	-0.20	0.21	0.06	0.32	0.62**	-0.21	-0.12		-0.90**
Rd	-0.15	-0.26	-0.25	-0.03	-0.30	-0.34	0.02	0.32	-0.03	-0.30	-0.15	

Table 7
Estimates of specific combining ability effects for 13($G_i \times L_1$) and 13($G_i \times L_2$) cotton crosses among all the studied traits

Crosses	BW g	SCY g	LY g	L% g	SI g	LI g	FF	FS	FL mm	UR %	+b	Rd
P ₁ x L ₁	0.186	5.878	1.745	-0.90*	-0.100	-0.254	0.121	0.151	-1.29*	0.121	0.009	-0.01
P ₂ x L ₁	-0.28**	-4.438	-0.388	1.289*	-1.10*	-0.31*	-0.279*	-0.64*	0.610	-0.27	-0.27	0.841
P ₃ x L ₁	-0.069	10.495	3.578	-0.276	0.067	-0.049	0.054	-0.082	0.710	0.054	0.009	0.308
P ₄ x L ₁	-0.130	-2.905	-0.572	-0.083	-0.63*	-0.34*	0.254	0.168	-0.306	0.254	0.109	0.474
P ₅ x L ₁	0.014	-13.22*	-5.21*	-0.434	0.133	-0.049	-0.329	0.151	0.394	-0.32	0.042	0.941
P ₆ x L ₁	0.059	1.678	0.828	0.150	0.267	0.176	0.387*	0.835*	0.110	0.387	0.276	0.158
P ₇ x L ₁	0.270**	4.662	1.662	0.210	0.433	0.304*	-0.229	0.368	0.310	-0.22	0.159	0.191
P ₈ x L ₁	0.047	2.995	0.128	-0.89*	0.350	-0.028	0.271	0.201	-1.47*	0.271	-0.25	0.674
P ₉ x L ₁	0.136	11.612*	4.095	-0.120	0.267	0.113	0.121	-0.132	0.860	0.121	-0.02	-0.85
P ₁₀ x L ₁	-0.153	-8.138	-3.855	-1.09*	-0.033	-0.29*	-0.163	-0.249	-1.39*	-0.16	0.176	-0.94
P ₁₁ x L ₁	-0.086	-8.855	-2.922	0.681	0.083	0.209	-0.029	-0.065	0.494	-0.03	-0.07	0.508
P ₁₂ x L ₁	-0.175	5.978	2.445	0.481	0.267	0.273	-0.296*	-0.48*	1.210*	-0.29	-0.29	-1.15
P ₁₃ x L ₁	0.175	-5.738	-1.538	0.992*	0.000	0.255	0.121	-0.215	-0.240	0.121	0.142	-1.12
P ₁ x L ₂	-0.186	-5.878	-1.745	0.903*	0.100	0.254	-0.121	-0.151	1.290*	-0.12	-0.01	0.009
P ₂ x L ₂	0.275**	4.438	0.388	-1.28*	1.100*	0.310*	0.279*	0.649*	-0.610	0.279	0.274	-0.84
P ₃ x L ₂	0.069	-10.495	-3.578	0.276	-0.067	0.049	-0.054	0.082	-0.710	-0.05	-0.01	-0.31
P ₄ x L ₂	0.130	2.905	0.572	0.083	0.633*	0.345*	-0.254	-0.168	0.306	-0.25	-0.11	-0.47
P ₅ x L ₂	-0.014	13.222*	5.205*	0.434	-0.133	0.049	0.329**	-0.151	-0.394	0.329	-0.04	-0.94
P ₆ x L ₂	-0.059	-1.678	-0.828	-0.150	-0.267	-0.176	-0.39**	-0.83*	-0.110	-0.38	-0.27	-0.16
P ₇ x L ₂	-0.27**	-4.662	-1.662	-0.210	-0.433	-0.30*	0.229	-0.368	-0.310	0.229	-0.16	-0.19
P ₈ x L ₂	-0.047	-2.995	-0.128	0.896*	-0.350	0.028	-0.271	-0.201	1.473*	-0.27	0.258	-0.67
P ₉ x L ₂	-0.136	-11.61*	-4.095	0.120	-0.267	-0.113	-0.121	0.132	-0.860	-0.12	0.024	0.859
P ₁₀ x L ₂	0.153	8.138	3.855	1.091*	0.033	0.294*	0.163	0.249	1.390*	0.163	-0.88	0.942
P ₁₁ x L ₂	0.086	8.855	2.922	-0.681	-0.083	-0.209	0.029	0.065	-0.494	0.029	0.074	-0.51
P ₁₂ x L ₂	0.175	-5.978	-2.445	-0.481	-0.267	-0.273	0.296**	0.482*	-1.21*	0.296	0.291	1.159
P ₁₃ x L ₂	-0.175	5.738	1.538	-0.99*	0.000	-0.255	-0.121	0.215	0.240	-0.12	-0.14	1.126

* Significant at 5% levels of probability.

Test of epistasis

The analysis of variance (ANOVA) to test the presence of epistasis for twelve quantitative yield and fiber quality traits is presented in Table 8. The mean squares for the deviations ($L_{1i} + L_{2i} - G_i$) revealed the presence of significant epistasis for all the studied traits except, seed index and fiber reflectance. Farther, partitioning total epistatic effect revealed the presence of highly significant fixable type (additive × additive) (i) for all studied traits except lint yield, fiber strength and fiber reflectance. Also, the mean square of non-fixable type (additive × dominance and dominance × dominance) or (j + l) were highly significant for all the studied traits except seed index, lint index, fiber length, uniformity ratio and

fiber reflectance. The first type of epistasis additive \times additive (i) was found to be much larger in magnitude than the second type additive \times dominance (j + l) for all traits. These results indicating that fixable components type of epistasis were more important than non-fixable one for the inheritance of these traits. So, the cotton breeder could use these findings to produce pure line. The same results were reported by El-Lawendey et al., 2010 and Saleh 2013.

Jayade et al., 2014 found that standard hybridization and selection procedures could take benefit of fixable epistasis type (i) or (additive \times additive). Whereas, non-allelic types of epistasis (j + l) (additive \times dominance and dominance \times dominance) are not fixable by selection for self pollinated crops. So, the second type of epistasis is not favorable for developing pure lines but could be useful for development hybrid varieties.

The interaction of total two types (i) and (j + l) of epistasis with replications were non-significant for all the studied traits except lint index and fiber length; which indicated that this interaction was not sensitive to the environments (replications). The analysis of variance showed significant mean squares of sums ($L_{1i} + L_{2i}$) and differences ($L_{1i} - L_{2i}$); additive and dominance gene effect, respectively for all the studied traits except lint index for sums while, uniformity ratio and fiber reflectance for differences. These results provide evidence of presence of both additive and dominance gene effect controlling these traits. These results were in line with those of many researchers El-Mansy et al., 2010; 2012 and Mahros, 2016.

The data in Table 8 illustrated that four studied traits out of twelve (boll weight, seed cotton yield, fiber strength and yellowness) had significant mean squares for the both fixable and non-fixable genetic components. Two traits (lint yield and fiber fineness) had significant additive and dominance gene action plus type two of epistasis (j + l). On the other hand, four traits (lint %, lint index, fiber length and uniformity ratio) showed significant additive and dominance gene action plus type one of epistasis (i). Finally, Table 9 summarizes significant of both fixable and non-fixable gene action over twelve studied traits.

These results are in agreement with those obtained by general and specific combining ability as shown in Tables 5 and 7, respectively. The traits which had significant mean squares for both fixable and non-fixable gene action showed significant GCA and SCA among 15 parents (G_i) and 26 cotton crosses ($13G_{1i} \times L_1$ and $13G_{2i} \times L_2$). While, two traits seed index and fiber reflectance had non-significant mean squares for both dominance gene effect and specific combining ability over twenty six cotton crosses.

Estimation of both genetic components additive (D), dominance (H), degree of dominance $(H/D)^{0.5}$, direction of dominance (F) and narrow sense heritability (h^2_{ns}) are presented in Table 10. Generally, additive genetic component was larger than dominance for all the studied traits. This indicated that additive gene action play an importance role in the inheritance of these traits. So, most of the studied traits had significant general combining ability (GCA) across fifteen parents as presented in Table 5. All these findings could help the Egyptian cotton breeder to use the best selection technique based on the accumulation of additive gene effects to improve Egyptian cotton breeding program to produce pure line.

The degree of dominance $(H/D)^{0.5}$ were less than unity for all the studied traits, indicating partial or incomplete dominance and certain the fact that, most genes are homozygous and the over-dominance are rare for self pollinated crops. Also, all traits had positive sign, explain that the parent with increasing alleles is dominance than parent with decreasing alleles (El-Mansy et al., 2012 and Dawwam et al., 2016).

Further, the correlation coefficient between the sums ($L_i + L_{2i}$) and difference ($L_{1i} - L_{2i}$) additive and dominance, respectively were found to be insignificant indicating the genes with positive and negative effects were equally distributed among the genotypes including in this study. However, the correlation coefficient for lint index was positive and significant indicating that dominance effect seemed to be acting in one direction. The direction of dominance (F) for twelve yield and fiber quality traits was non-significant which showed that the dominant alleles were dispersed between testers; therefore the two testers did not show any proof of dominance directional for these traits (Table 10).

Generally, the genetic analysis indicated that both additive and non additive types of gene effects were important for most studied traits with the predominant of fixable type of epistasis. Thus for exploitation of all types of gene effects, the intermitting population or recurrent selection followed by progeny test which utilize all kinds of gene effects.

Table 8

Mean squares for analysis of variance for epistasis ($L_{1i} + L_{2i} - G_i$), sums (additive) ($L_{1i} + L_{2i}$) and differences (dominance) ($L_{1i} - L_{2i}$) for all the studied traits

Mean squares							
Yield and its components traits							
S.O.V	d.f	Boll weight g	Seed cotton yield g	Lint yield g	Lint %	Seed index g	Lint index g
i type of epistasis	1	0.460*	2095.214*	5.386	465.021**	67.954	65.788**
j + l types of epistasis	12	0.470**	1857.922**	320.144**	30.165	3.996	3.835
Total epistasis	13	0.469**	1876.175**	295.931**	63.616	8.916	8.600*
i type of epistasis x block	2	0.115	523.803	1.346	116.255	16.988	16.447*
j + l types of epistasis x block	24	0.100	472.620	58.094	41.674	5.581	2.343
Total epistasis x block	26	0.101	476.557	53.729	47.419	6.458	3.428
Additive (D) ($L_{1i} + L_{2i}$)	12	0.739**	2896.961**	453.881**	28.675**	2.210**	3.629
Within families	24	0.041	179.141	24.643	1.160	0.263	0.091**
Dominance (H) ($L_{1i} - L_{2i}$)	12	0.407**	666.526**	91.287**	6.790**	2.117**	0.621**
Within families	24	0.039	178.619	25.364	0.698	0.249	0.118
Fiber quality traits							
S.O.V	d.f	Fiber fineness	Fiber strength	Fiber length mm	Uniformity ratio %	Yellowness	Fiber reflectance
i type of epistasis	1	0.954	4.017*	185.850**	210.312**	2.515*	6.420
j + l types of epistasis	12	14.169**	30.666**	154.510	175.328	40.154**	178.444
Total epistasis	13	15.123**	34.683**	340.360**	385.640	42.669**	184.864
i type of epistasis x block	2	0.2385	1.0043	46.4625*	52.578	0.6288	1.605
j + l types of epistasis x block	24	0.2253	0.5516	5.2640	13.558	0.4181	12.215
Total epistasis x block	26	0.2263	0.5864	8.4332	16.559	0.4343	11.398
Additive (D) ($L_{1i} + L_{2i}$)	12	1.161**	1.833**	12.854**	18.252*	8.449**	48.074**
Within families	24	0.166	0.276	1.208	6.851	0.354	12.279
Dominance (H) ($L_{1i} - L_{2i}$)	12	0.526**	1.208**	10.392**	9.090	1.823**	24.036
Within families	24	0.100	0.202	2.531	5.511	0.361	15.261
* and ** significant at 5% and 1% levels of probability, respectively.							

Table 9
Summarizes of significant fixable and non-fixable gene action over all the studied traits

Traits	Additive (D) $L_{1i} + L_{2i}$	Dominance (H) $L_{1i} - L_{2i}$	Epistasis (i) $(L_{1i} + L_{2i} - G_i)$	
			i	j+l
Boll weight	+	+	+	+
Seed cotton yield	+	+	+	+
Lint yield	+	+	-	+
Lint %	+	+	+	-
Seed index	+	+	-	-
Lint index	-	+	+	-
Fiber fineness	+	+	-	+
Fiber length	+	+	+	-
Fiber strength	+	+	+	+
Uniformity ratio	+	-	+	-
Yellowness	+	+	+	+
Fiber reflectance	+	-	-	-

Table 10
Estimation of genetic components, degree of dominance and narrow sense heritability for the traits studied for all the studied quantitative traits

Yield and its components traits						
Genetic components	Boll weight	Seed cotton yield	Lint yield	Lint %	Seed index	Lint index
	g	g	g		g	g
D	0.931	3623.761	572.318	36.687	2.596	4.717
H	0.491	650.543	87.897	8.122	2.491	0.671
$(H/D)^{0.5}$	0.726	0.424	0.392	0.471	0.980	0.377
F	0.125	-1256.028	-116.742	8.097	2.084	3.302
r	0.082	-0.326	-0.207	0.210	0.348	0.794**
h^2_{ns}	0.6416	0.8284	0.8491	0.8089	0.4968	0.8653
Fiber quality traits						
Genetic components	Fiber fineness	Fiber strength	Fiber length	Uniformity	Yellowness	Fiber reflectance
			mm	Ratio %		
D	1.327	2.076	15.527	15.201	10.793	47.727
H	0.569	1.342	10.481	4.772	1.949	11.700
$(H/D)^{0.5}$	0.655	0.804	0.822	0.560	0.425	0.495
F	-0.515	1.690	-3.617	-6.469	-0.162	-1.825
r	-0.238	0.410	-0.113	-0.181	-0.015	-0.019
h^2_{ns}	0.6791	0.5868	0.5738	0.7589	0.8349	0.7452

Genetic correlation

The type and direction of association, which may occur between the studied traits, is important for selection techniques. The plant breeder should estimate genetic correlation between three types of genetic components; additive (r_D), dominance (r_H) and epistasis (r_I) (Table 11). The obtained results provide that increasing additive gene effects controlling boll weight was controlled the increasing ones controlling yield and its components traits. **Makhdoom et al., 2010** reported that boll weight is the independent key for yield components and played a prime role in managing seed cotton yield. These results are in agreement with **Farooq et al., 2014 and El-Mansy 2015**. Lint yield and lint % were additively correlated with seed index and lint index. On the other hand, fiber length has the same direction with two fiber traits; fiber strength and uniformity ratio.

The dominance genetic correlation was positive and significant between seed index and both boll weight and lint index. While, significant and negative dominance correlation was observed between lint % and fiber strength, yellowness and fiber reflectance. Regarding the results of epistasis genetic correlation recorded positive and significant correlation only between yield and its components (seed cotton yield, lint index and seed index). Also, genetic significant and positive epistasis controls both fiber traits; fiber length and uniformity ratio.

All the findings obtained from both levels of genetic correlation prove that GCA and SCA controlled by both additive and dominance gene effect, respectively. If epistasis is present the different types of non-allelic interaction (i) or (j + l) will control both GCA and SCA, respectively. So, the results obtained from Tables 5, 7, 9 and 10 are in the same trend. These results may help cotton breeder how to improve cotton yield, which is a quantitative traits with low or moderate heritability values and additive gene effect is a fixable type. The improvement can be effective by using indirect selection for its components like; lint yield, lint % and lint index and lint % which had high narrow sense heritability 84.91%, 80.89% and 86.53%, respectively (Table 10). The advantages of triple test cross matting design are break up undesirable linkage groups to obtain new recombinant lines, provide information about fixable and non-fixable genetic components and the genetic correlation between genetic components.

Finally, from the previous results it may be concluded that the studied traits were controlled by additive and additive x additive (i) type of epistasis and most desirable correlation were due to additive gene effects and few cases of non additive type. This suggests a common genetic pool, pleiotropy or linkage. The appearance of epistasis components in early generations is not favorable to the plant breeder because selection produces will be not fruitful, so selection process should be delay to late generations. Thus recurrent selection or intermitting population may be useful in the presence of epistasis because these techniques will increase frequency of favorable alleles.

Table 11

Genotypic correlation between additive (r_D) ($L_{1i} + L_{2i}$), dominance (r_H) ($L_{1i} - L_{2i}$) and epistasis (r_i) ($L_{1i} + L_{2i} - G_i$), gene effects controlling both yield, its components and fiber quality traits

Traits	r	BW g	SCY g	LY g	L% g	SI g	LI g	FF	FS	FL mm	UR%	+b	RD
BW g	r_D	1.000	0.541*	0.616*	0.596*	0.611*	0.660**	0.562*	-0.284	0.024	0.162	-0.149	-0.291
	r_H	1.000	0.187	0.092	-0.315	0.588*	0.377	0.256	0.651*	-0.013	0.303	0.527	-0.271
	r_i	1.000	-0.422	-0.361	0.342	-0.013	-0.351	-0.055	0.155	0.062	-0.249	0.211	0.317
SCY g	r_D		1.000	0.984**	0.200	0.488*	0.341	0.184	-0.127	0.482*	0.424	-0.273	-0.140
	r_H		1.000	0.974**	-0.022	0.346	0.348	0.341	-0.007	0.186	0.450	-0.109	-0.173
	r_i		1.000	0.850**	-0.004	-0.036	0.362	-0.165	0.009	-0.043	-0.122	0.335	-0.298
LY g	r_D			1.000	0.367	0.555*	0.486*	0.294	-0.132	0.435	0.407	-0.293	-0.137
	r_H			1.000	0.190	0.189	0.360	0.293	-0.134	0.272	0.471	-0.167	-0.151
	r_i			1.000	-0.037	0.226	0.544	-0.151	0.020	0.329	0.157	0.280	-0.310
L% g	r_D				1.000	0.579*	0.937**	0.693**	-0.121	-0.231	-0.052	-0.221	-0.001
	r_H				1.000	-0.428	0.367	-0.277	-0.576*	0.451	0.223	-0.331	0.070
	r_i				1.000	0.187	-0.076	-0.184	-0.425	-0.138	-0.024	0.665*	-0.327
SI g	r_D					1.000	0.826**	0.697**	0.016	-0.070	-0.044	0.048	-0.035
	r_H					1.000	0.682*	0.032	0.432	0.020	0.332	0.164	-0.252
	r_i					1.000	0.831**	0.080	0.025	0.627*	0.372	0.013	0.253
LI g	r_D						1.000	0.774**	-0.073	-0.186	-0.065	-0.111	0.002
	r_H						1.000	-0.166	-0.008	0.366	0.517	-0.066	-0.236
	r_i						1.000	0.062	0.102	0.701**	0.431	-0.076	0.084
FF g	r_D							1.000	0.276	-0.011	-0.027	-0.203	0.258
	r_H							1.000	0.341	-0.451	-0.153	0.029	0.008
	r_i							1.000	0.431	0.266	0.254	-0.483	0.047
FS g	r_D								1.000	0.507*	0.394	0.008	0.093
	r_H								1.000	-0.197	-0.023	0.188	0.324
	r_i								1.000	0.154	0.059	-0.176	0.201
FL mm	r_D									1.000	0.82**	-0.093	-0.177
	r_H									1.000	0.81**	0.038	-0.043
	r_i									1.000	0.606*	-0.240	-0.015
UR% g	r_D										1.000	-0.256	-0.489*
	r_H										1.000	0.137	-0.202
	r_i										1.000	-0.033	-0.284

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

Traits	r	BW	SCY	LY	L%	SI	LI	FF	FS	FL	UR%	+b	RD
		g	g	g		g	g			mm			
+b	r_D											1.000	-0.110
	r_H											1.000	-0.74**
	r_i											1.000	-0.306
* and ** significant at 5% and 1% levels of probability, respectively.													

Genetic diversity

Genetic divergence studies in cotton revealed some interesting features of differentiation and adaptability such as cluster analysis which provide additional information for studying interrelationship between genotypes and giving graphical assessment of genetic variability. For this propose hierarchical cluster analysis, on the basis of Wards method and interval Euclidean distance, was applied to investigate genetic distance and diversity between the fifteen parental cotton genotypes. The data matrix of the dissimilarity coefficient on the basis of Euclidean distance is presented in Table 12. This dissimilarity coefficient was ranged from 2.93 between Giza 70 and Giza 76 to 43.45 between Giza 80 and Giza 88. This wide range of genetic distance among these genotypes reflected the presence of wide range of genetic variation and provides an opportunity to improve the cotton genetic basis by implementing crossing technique.

Cluster analysis sequestered the fifteen cotton genotypes into nine major groups on the basis of dissimilarity and contributed the studied traits as shown in Fig. 1. It's clear that the two testers were grouped into different clusters with average dissimilarity coefficient 14.2. These female parents varied in general combining ability for most studied traits. On the other side, the commercial variety Giza 86 formed a unique cluster and wide distance from the other parents (Table 13). So, the commercial variety Giza 86 was classified as the best combiner for all yield traits (Table 5). The half sense parents; Giza 89 and Giza 89 x S6 were grouped at the same cluster with narrow genetic distance. On the other side, Giza 77 grouped in a cluster and characterized as a good combiner for most yield traits.

The five genotypes (Giza 70, Giza 76, Ashmouni, Giza 81 and Alexandria 4) were grouped together with narrow genetic base. These genotypes described as poor general combiners for most studied yield traits but showed some sort of superior fiber quality traits. In this trend, **El-Mansy, 2014**, **Abd El-Moghny et al., 2015 a and b** and **Akter et al., 2019** used phenotypic performance to classified cotton genotypes into different clusters.

Genotypes grouped in the same cluster (intra-cluster) are expected to be genetically similar than genotypes grouped in different clusters (inter-cluster) (Table 13). These results indicated wide genetic distance among fifteen parental cotton genotypes. The highest inter-cluster distance was observed between clusters 6, 8 followed by clusters 2, 8 and 3, 2, respectively. While, the lowest genetic distance occurred between clusters 9, 5 followed by clusters 1, 4 and clusters 2, 3. So, hybridization between clusters is more useful than within clusters to increase genetic variability and obtain more transgressive segregant in early generations. The same findings were obtained by **Abd El-Moghny et al., 2015 (a)**. **Machado et al., 2002** noticed that choosing parents is very important step to obtain the best combination. The parents not only had higher genetic divergence but also have higher mean performance of parents and their F_1 s. In addition to GCA and SCA effects are more informative than mean performance values (**Abd El-Salam et al. 2010 and El-Mansy et al., 2014**).

Table 12
Genetic diversity between thirteen cotton genotypes (G_i) and the two testers (L₁ and L₂) cotton genotypes

G _i	Euclidean Distance														
	P ₁	P ₂	P ₃	P ₄	P ₅	P ₆	P ₇	P ₈	P ₉	P ₁₀	P ₁₁	P ₁₂	P ₁₃	L ₁	L ₂
P ₁₁	0.00	16.87	15.16	9.06	13.62	12.10	9.23	29.51	17.84	19.93	6.53	9.97	17.00	16.44	6.42
P ₂		0.00	27.13*	20.30	28.36	26.93	22.76	42.90	31.31	9.53	16.54	21.55	7.44	29.67	17.16
P ₃			0.00	10.11	6.94	7.14	11.22	18.65	5.70	30.61	11.95	6.45	24.14	7.11	14.45
P ₄				0.00	9.86	8.76	9.48	26.00	14.13	24.02	8.54	6.38	19.35	12.63	9.25
P ₅					0.00	2.93	9.14	18.09	7.17	31.12	12.70	8.10	26.54	6.33	13.30
P ₆						0.00	9.57	20.49	8.58	30.39	11.68	7.80	25.45	8.54	12.58
P ₇							0.00	21.60	12.26	23.61	8.58	7.15	21.06	8.95	6.83
P ₈								0.00	13.74	43.57	27.39	22.30	39.76	13.94	27.23
P ₉									0.00	33.90	15.39	10.12	28.37	5.34	16.94
P ₁₀										0.00	19.72	24.50	11.33	31.31	19.07
P ₁₁											0.00	6.15	14.28	14.09	6.62
P ₁₂												0.00	18.97	8.96	8.95
P ₁₃													0.00	26.98	16.97
L ₁														0.00	14.20
L ₂															0.00

Table 13
Average divergence values for intra (Diagonal values) and inter (Above diagonal) clusters between nine clusters for the fifteen cotton genotypes for twelve1 quantitative characteristic

Clusters	1	2	3	4	5	6	7	8	9
1	3.766	16.433	15.687	7.210	12.020	19.214	7.364	27.810	14.354
2		0.000	7.442	20.693	27.616	9.530	22.759	42.897	29.207
3			0.000	18.892	25.963	11.334	21.065	39.758	26.320
4				3.191	7.927	24.049	7.769	24.011	9.575
5					1.464	30.722	9.240	19.272	6.454
6						0.000	23.606	43.567	31.778
7							0.000	21.595	10.313
8								0.000	15.208
9									3.489

Conclusions

This investigation was designed to use modified triple test cross analysis to investigate type of gene actions and genetic correlation between most quantitative economic traits in cotton for rightful decision about effective selection procedures. Also, cotton breeder need to increase genetic diversity among new varieties and maintaining the complexity between desired traits which will present in commercial varieties. So, developing different traits combinations is a difficult process as the introgression of new genetic materials is a result of disturbing genes responsible for desired traits. The use of crosses between divergent parents could be meaning to achieve combining ability.

Abbreviations

BW: boll weight

SCY/P: seed cotton yield / plant

LY/P: lint yield / Plant

L%: lint percentage

FL: Fiber length

FF: fiber fineness (micronaire value)

FS: fiber strength (Presley index)

UR%: uniformity ratio

+b: yellowness

RD: Fiber reflectance

TTC: triple test cross analysis

GCA: general combining ability

SCA: specific combining ability

D: additive genetic variance

H: dominance genetic variance

i: epistasis genetic variance

Declarations

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Authors' contributions:-

Yasser M. El-Mansy and Ahmed M. Abdelmoghny, provided cotton germplasm and parents evaluation for the first year, data analyzed, interpreted the data, wrote the manuscript and edit for publication. Reham H. A. Gibely and Adel H. Mabrouk making 26 cotton crosses, designed parents and crosses experiment, monitored field experiment, laboratory work and help to revise the manuscript. All authors read and approved the final manuscript and have made substantive intellectual contributions to the manuscript.

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Competing interests:-

The authors declare that they have no competing interests.

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Figures

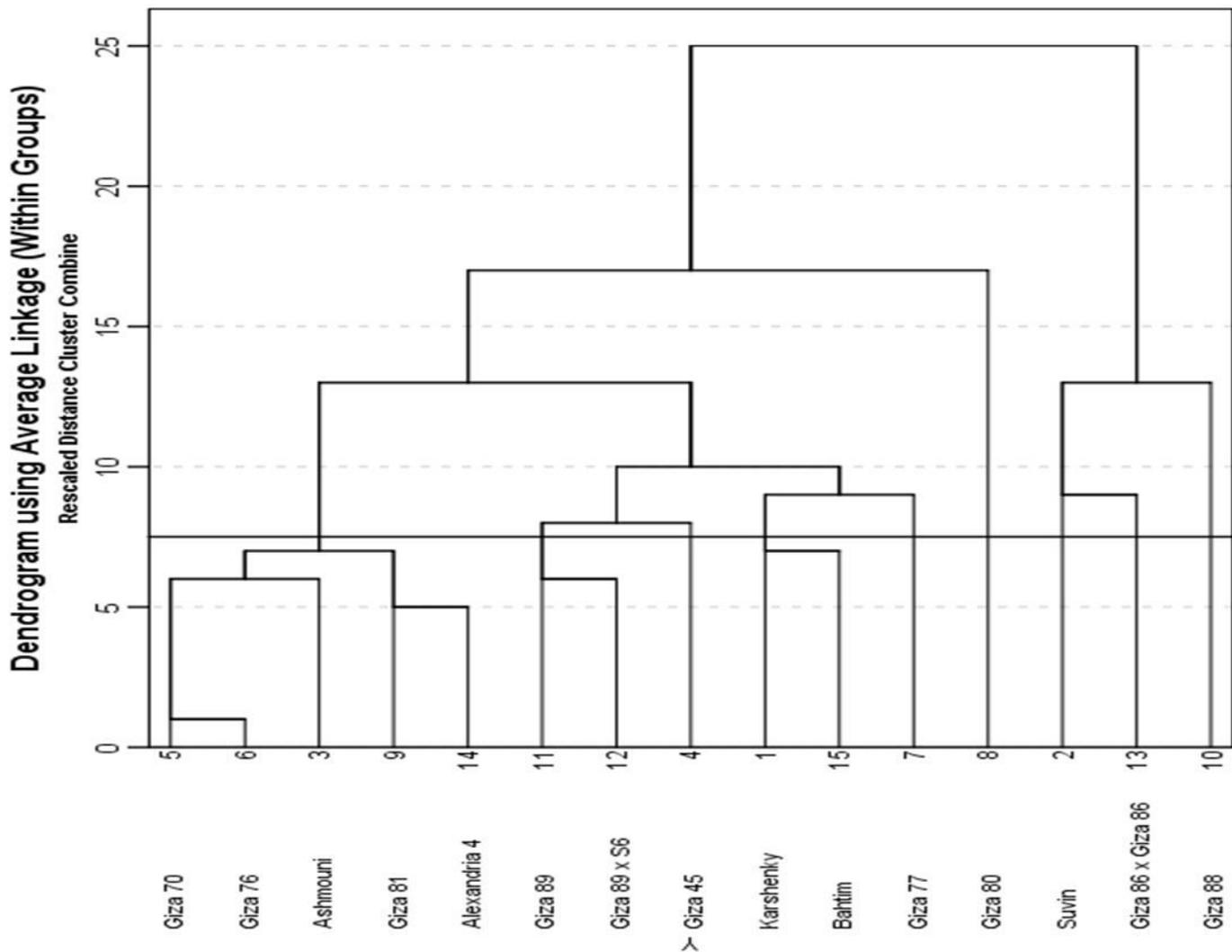


Figure 1
 Dendrogram for the fifteen cotton genotypes using average linkage (within groups)