



Using triple test cross analysis to estimate genetic components and genetic correlation for some quantitative traits in cotton

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Abstract

The triple test cross analysis was used to study different components of genetic variation between 75 Triple Test Cross (TTC) families and their parents, F1 and F2 in one cotton cross (Giza 94 × Australy) for yield, its components and fiber quality traits. The 75 TTC families (25 L1, 25 L2 and 25 L3) were sown at Sakha Experimental Station, Agriculture Research Center, Kafr El-Sheikh government, Egypt during 2020, 2021, 2022 and 2023 growing seasons. The results showed that mean squares between L1, L2 and L3 (TTC) was significant for all studied traits, except boll weight, micronaire reading and fiber strength, while between L1 and L2 families were found to be significant for seed cotton yield/plant, lint cotton yield/plant and lint index. Overall epistatic gene effects had significant differences for lint cotton yield/plant, fiber length and uniformity index. The (i) fixable type (additive × additive) components of epistasis were more important than (j + 1) non-fixable one in the inheritance of all studied traits, except lint index. Both additive and dominance components were significant for all the studied traits. Degree of dominance ($\sqrt{H/D}$) was less than the unity for seed cotton yield/plant, lint cotton yield/plant, seed index, fiber length, micronaire reading and uniformity index which showed over-dominance (greater than unity). Further, the correlation coefficient between the sum ($L1i + L2i$) and difference ($L1i - L2i$) was found to be negative and insignificant for all studied traits, except fiber length, fiber strength and uniformity index, which were positive and non-significant. Genotypic correlation was positive and significant between yield trait and some of its components. This could help cotton breeders to use indirect selection to increase yield productivity.

Keywords: cotton, triple test cross, epistasis, additive, dominance, genotypic correlation.

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1. Introduction

Triple test cross is a valuable design for detecting and estimating genetic components of variation for quantitative traits, particularly in self-pollinated species like cotton where epistasis plays a crucial role in breeding decisions (Singh and Singh, 1976). This design allows for the identification of epistasis effects and provides unbiased estimates of additive and dominance components, aiding breeders in making informed choices for crop improvement (Singh and Singh, 1976). The F₂ triple test cross is specifically highlighted as a method to detect epistasis and provide clear insights into genetic components (Singh and Singh, 1976). The presence of epistasis, including additive × additive, additive × dominance, and dominance × dominance interactions, is tested before implementing any breeding program using the triple test cross model (Singh and Singh, 1976). This approach ensures that breeders have a comprehensive understanding of the genetic interactions at play, allowing for more effective breeding strategies to be developed (Singh and Singh, 1976). Furthermore, the triple test cross design has been shown to be efficient in detecting epistasis and estimating genetic variance components for quantitative traits (Zhu and Zhang, 2007). This method provides breeders with a reliable technique to obtain accurate estimates of genetic components, essential for making informed decisions in crop improvement programs (Zhu and Zhang, 2007). Al-Hibbiny *et al.* (2020) cleared that overall epistatic gene effects had highly significant differences for all studied traits, except fiber length and fiber

strength. The (i) fixable type (additive × additive) was the most important epistatic effect than (j and l) non-fixable type for all traits. Both additive and dominance components were highly significant for all studied traits. Degree of dominance was less than the unity and confirmed the presence of partial dominance for all studied traits, except for lint yield/plant, lint index and seed index, which were controlled with over-dominance. The Additive gene action played an important role in controlling inheritance of all studied traits than dominance one, except for lint yield/plant, lint index and seed index. Direction of dominance (r) was non-significant for most traits, indicating absence of dominance direction. They added that influence of (i) type of epistatic effects for the majority of the studied traits selection in early generations may be recommended. Genotypic correlation was positive and significant between yield traits and its components. Isong *et al.* (2021) revealed that both additive and dominance gene effects were involved in the expression of most of the yield contributing traits. One or more types of epistatic interaction effects were prevalent for all the characters and thus played a major role in the control of the characters. For seed cotton yield per plant, the dominance × dominance interaction effect was positively significant for all the crosses, the additive × dominance effect was positively significant only in cross 1 and the dominance main effect showed negative significant in all crosses. The dominance (h) and dominance × dominance (l) effects were opposite signs in all the crosses, indicating the presence of duplicate epistasis. Giri *et al.* (2020) found that estimated mean effects (m) were highly

significant for all traits, indicating quantitative inheritance of these traits. Out of the seven traits under study five traits showed significance for at least one scaling test. Additive and dominant gene effects were significant for seed cotton yield with larger magnitude of dominance effects than additive ones. Dominance, additive \times dominance, and dominance \times dominance, were significant for boll weight, seed cotton yield and seed index. Hassan *et al.* (2022) showed that total epistasis was present for all the studied traits, except for micronaire reading. The (i) type of epistasis (additive \times additive) was significant for yield and its component traits and fiber quality traits, except for micronaire reading. While the (j + l) type (additive \times dominance and dominance \times 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. Hence, the current study aims to detect epistasis along with estimation of additive and dominance genetic components for yield, yield components and fiber quality traits in cotton cross (Giza 94 \times Australy) through 75 F2 TTC families. The information obtained through present study would help in understanding the genetic basis of these studied traits and making breeding strategy for the development of high yielding or valuable germplasm in cotton. Also, detect the interrelationships among various traits through computing the genotypic correlation and partitioning it to epistasis, additive and dominance correlations.

2. Materials and methods

This investigation was carried out at Sakha Agricultural Research Station,

Agriculture Research Center, Kafr El-Sheikh government, Egypt, during four successive summer growing seasons, 2020, 2021, 2022 and 2023. In 2020 growing season, two cotton varieties belong to *Gossypium barbadense* L. *i.e.*, Giza 94 and Australy were crossed to produce F1 generation, which was planted during 2021 growing season at the same time, self-pollination was done to obtain F2 population. Twenty-five plants were randomly selected from F2 population which used as males (lines) and backcrossed to three testers P1 (Giza 94), P2 (Australy) and F1 (Giza 94 \times Australy) to generate 25 L1i (P1 \times F2), 25 L2i (P2 \times F2) and 25 L3i (F1 \times F2) families, respectively as suggested by Kearsey and Jinks (1968) during the growing season of 2022. The 75 triple test cross (TTC) families were evaluated in a randomized complete block design (RCBD) with three replications in 2023 growing season. Each replicate consists of three rows for each family. The row was 7 m long, with 70 cm between rows and 40 cm between plants within row. Hills were thinned to one plant per hill at seedling stage. All the normal agronomic practices were conducted as usual in the ordinary cotton fields. The data were scored on eight guarded plants from each row in each replication for the six yield and its components traits *i.e.*, boll weight (BW) in grams as the average weight of five opening bolls/plant, seed cotton yield/plant (SCY/P), lint cotton yield/plant (LY/P), lint percentage (L %), seed index (SI) and lint index (LI) in grams. As well as four fiber

quality traits *i.e.*, fiber length (FL) in mm, fiber strength (FS) as Presley index, micronaire reading (Mic) and uniformity index (UI), which were estimated at Cotton Technology Laboratory, Cotton Research Institute, Agricultural Research Center, Giza, Egypt.

2.1 Statistical analysis

Triple test cross analysis was used as the method proposed by Jinks and Perkins, 1970 to detect epistasis (i) and to test and estimate both additive (D) and dominance (H) components of genetic variance based on general formula:

$$L_{ijk} = \mu + G_{ij} + R_k + E_{ijk}$$

Where, L_{ijk} = Phenotypic value of cross between tester i and line j in k replication. μ = 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 k th replication. E_{ijk} = Error.

2.2 Test of epistasis

For detection of epistasis, the contrast ($L_{1i} + L_{2i} - 2L_{3i}$) was computed (where, $i = 1$ to 25) from the three replicates. The epistasis sum of squares for 25 degree of freedom was partitioned into two items; 'i' type of epistasis (additive x additive interaction) with 1 degree of freedom and the other items with 24 degrees of freedom testing for 'j' and 'l' types of epistasis (additive x dominance and dominance x dominance interactions, respectively).

2.3 Detection and estimation of additive (D), dominance (H) and direction of dominance

The mean squares due to sums ($L_{1i} + L_{2i}$) and differences ($L_{1i} - L_{2i}$) for 24 degrees of freedom was used to detect both additive (D) and dominance (H) components of genetic variation. The estimation of D and H were obtained according to Jinks and Perkins (1970). The direction of dominance (F) was obtained from covariance of sums ($L_{1i} + L_{2i}$) / differences ($L_{1i} - L_{2i}$), which equals $-1/8$. Correlation coefficient of sums / differences was used to test the significance of F value (Jinks *et al.*, 1969). The obtained 25 values for each ($L_{1i} + L_{2i} - L_{3i}$), ($L_{1i} + L_{2i}$) and ($L_{1i} - L_{2i}$) comparisons for every trait were used to compute epistasis, additive and dominance genetic correlations, respectively (Jinks and Perkins, 1970). Also, degree of dominance was calculated as $(H/D)^{1/2}$.

3. Results and Discussion

3.1 Analysis of variance

The analysis of variance of the triple test cross families of Giza 94 x Australy, for all the studied traits are presented in Table (1). The results showed that the differences between L1, L2 and L3 (TTC) were significant for all the studied traits, except boll weight, micronaire reading and fiber strength, while between L1 and L2 families it was found to be significant for seed cotton yield/plant, lint cotton

yield/plant and lint index, indicating the presence of high segregations in F2. These results might reflect that the parents (F2 Plants) involved in the backcrosses were genetically diverse and that diversity could be transmitted to their progenies. On the other hand, mean squares between L2 families were significant for all the studied traits, except seed index, fiber length, fiber strength and uniformity index, while was significant between L1 for only fiber length and between L3 for only lint percentage. Al-Hibbiny *et al.* (2020) found that mean squares between L1, L2 and L3 were highly significant for

all studied traits, while between L1 and L2 families found to be significant for boll weight, lint percentage, lint index, fiber length and micronaire reading. Also, mean squares between L1 families were significant and highly significant for lint percentage, seed index, fiber length and micronaire reading, and between L2 were significant and highly significant for all the studied traits, except seed cotton yield, lint cotton yield and fiber strength and uniformity index, while was significant and highly significant between L3 for all the studied traits, except boll weight and lint index.

Table (1): Analysis of variance of 75 triple test cross families for all the studied traits in the cotton cross (Giza 94 × Australy).

S.O.V.	D.F	Boll weight	Seed cotton yield/plant	Lint cotton yield/plant	Lint percentage	Seed index
Between L1, L2, L3	74	0.078	5444.979*	805.586*	8.161**	0.882*
Between L1	24	0.036	2754.932	468.333	3.095	0.308
Between L2	24	0.107*	7849.307**	1118.102**	11.046**	0.569
Between L3	24	0.057	3990.052	666.084	8.431*	0.588
Residual	2	0.487	26332.740	2776.457	31.086	15.073
Within L1, L2, L3	216	0.075	3921.635	604.623	6.008	0.633
Between L1, L2 Families	49	0.070	5193.913*	777.030*	6.926	0.429
Within L1, L2 Families	144	0.007	617.101	96.404	0.848	0.060
S.O.V.	D.F	Lint index	Fiber length	Micronaire reading	Fiber strength	Uniformity index
Between L1, L2, L3	74	74	0.938**	2.909**	0.118	0.422
Between L1	24	24	0.342	2.191*	0.046	0.457
Between L2	24	24	1.152**	1.156	0.273**	0.213
Between L3	24	24	0.404	1.065	0.021	0.202
Residual	2	2	11.929	54.701	0.278	5.146
Within L1, L2, L3	216	216	0.582	1.556	0.096	0.553
Between L1, L2 Families	49	49	0.732*	1.639	0.156	0.328
Within L1, L2 Families	144	144	0.074	0.165	0.013	0.033

L1 = backcross to Giza 94, L2 = backcross to Australy and L3 = backcross to F1. * and ** are the significance at 0.05 and 0.01 level of probability, respectively.

3.2 Mean performance of L1, L2 and L3 TTC families

The mean performance values of L1, L2 and L3 TTC families for all the studied traits are presented in Table (2). The obtained results showed that the means of

the backcrosses L1i, L2i and L3i families exhibited significant differences for most studied traits. The backcrosses to Giza 94 (L1) showed higher mean values than backcrosses to Australy (L2) for boll weight, lint percentage, seed index, lint index, micronaire reading, fiber strength

and uniformity index, while backcrosses to Australy (L2) showed the best mean values of backcrosses than Giza 94 (L1) for seed cotton yield/plant, lint cotton yield/plant and fiber length. On the other hand, the backcrosses to F1 (L3) showed higher mean values than backcross to Australy (L2) for boll weight, lint percentage, seed index, lint index and micronaire reading, also showed higher mean values than backcross to Giza 94 (L1) for seed cotton yield/plant, lint cotton yield/plant and

micronaire reading. These results indicated that the backcross to Giza 94 (L1) appeared to improve most yield and fiber traits than of backcross to Australy (L2), while the backcross to Australy (L2) appeared to improve both cotton yield/plant and lint cotton yield/ plant. Such results might confirm the high yielding traits and fiber quality of these two genotypes *i.e.*, Giza 94 (L1) and Australy (L2) which might be useful for improving yield traits and fiber quality in any breeding program.

Table (2): Mean values of triple test cross families for all the studied traits of cotton cross Giza 94 × Australy.

TTC families	Boll weight	Seed cotton yield/plant	Lint cotton yield/plant	Lint percentage	Seed index
L ₁	3.375±0.022	161.855±6.061	65.187±2.499	40.199±0.203	10.904±0.064
L ₂	3.219±0.038	195.485±10.230	75.960±3.861	39.010±0.384	10.053±0.087
L ₃	3.261±0.028	164.351±7.294	65.672±2.980	40.033±0.335	10.233±0.089
TTC families	Lint index	Fiber length	Micronaire reading	Fiber strength	Uniformity index
L ₁	7.342±0.086	32.843±0.171	4.127±0.025	10.028±0.078	85.499±0.138
L ₂	6.545±0.124	33.383±0.124	4.091±0.060	9.585±0.053	84.637±0.096
L ₃	6.971±0.073	31.709±0.119	4.209±0.017	9.564±0.052	84.051±0.113

L1 = backcross to Giza 94, L2 = backcross to Australy, and L3 = backcross to F1.

3.3 Epistasis deviations

Data given in Table (3) showed the individual epistasis deviations of each F2 male for the studied traits in cotton cross (Giza 94 × Australy). Results revealed differences among the individual epistasis deviations in magnitude and sign for all the studied traits. The magnitudes for epistasis deviations were generally differed between the cotton cross and among 25 males. All traits showed negative or positive epistasis deviations. Generally, positive epistasis deviations might indicate the greater observed values of the parental test cross, and contribution of the parents was greater than F1. While

negative individual epistasis deviations could be reflected the greater means of F1 test cross compared with P1 and P2 test crosses. Similar results were previously obtained by Saleh Eman (2013), Al-Hibbiny *et al.* (2020), and Hassan *et al.* (2022).

3.4 Tests for epistasis

The existence of non-allelic interactions for economic traits might have important inferences in plant breeding. The (i) type of epistasis represents fixable, while (j + l) types show non-fixable portions of genetic variations. Genetic analyses had epistasis affects for all the studied traits (Table 4). The mean squares for the

deviation's overall epistasis ($L1i + L2i - 2L3i$) revealed the presence of significant epistasis for lint cotton yield/plant, fiber length and uniformity index.

Table (3): Individual epistasis deviations of each F_2 male for all the studied traits in the cross (Giza 94 × Australy).

Traits TTC	Boll weight	Seed cotton yield/plant	Lint cotton yield/plant	Lint percentage	Seed index
L1	-0.160	-104.000	-45.715	-1.830	0.900
L2	-0.620	-112.100	-36.840	4.107	1.500
L3	0.220	-494.500	-188.550	-0.046	1.800
L4	0.920	-103.700	-36.734	8.363	3.200
L5	0.560	-81.000	-37.293	-5.456	1.900
L6	0.220	116.700	48.197	0.704	0.700
L7	-0.020	-50.600	-15.674	2.877	-0.600
L8	0.320	-134.800	-36.279	9.078	1.200
L9	1.000	-79.500	-28.407	1.710	3.000
L10	-1.260	-268.500	-94.345	-1.007	3.500
L11	0.800	-46.900	-1.598	10.954	4.300
L12	0.800	-81.700	-19.519	10.817	1.700
L13	1.300	18.500	15.978	3.355	2.600
L14	2.100	-0.200	19.086	8.595	4.900
L15	1.280	-209.000	-43.236	14.650	4.000
L16	0.500	-72.500	-29.710	2.192	1.400
L17	0.020	-629.800	-227.436	5.355	0.400
L18	1.220	143.900	63.870	5.175	3.700
L19	1.160	42.200	26.866	8.556	5.000
L20	0.180	-198.500	-60.302	7.924	5.000
L21	0.320	-166.100	-106.918	-20.701	3.300
L22	0.480	-2.600	2.494	1.208	3.600
L23	-0.120	-44.700	-6.873	3.959	3.200
L24	0.060	-75.900	-23.645	2.854	1.200
L25	0.380	113.000	54.614	5.756	2.400
Traits TTC	Lint index	Fiber length	Micronaire reading	Fiber strength	Uniformity index
L1	-0.144	1.400	-0.200	0.400	7.600
L2	1.975	3.300	-0.200	2.200	5.200
L3	0.570	1.900	-0.200	1.900	3.000
L4	3.766	0.500	-0.200	3.700	6.100
L5	-0.216	2.500	-1.700	2.600	6.100
L6	1.018	3.600	-0.200	0.600	4.000
L7	0.169	3.200	-0.100	0.100	3.000
L8	3.303	-1.900	0.000	-1.200	1.100
L9	2.370	-6.500	0.200	-0.900	-0.700
L10	1.963	-2.700	0.300	0.200	2.700
L11	5.506	0.500	0.200	-1.600	3.600
L12	5.458	-3.700	0.400	-0.500	1.200
L13	2.706	-3.200	0.500	1.200	0.700
L14	5.187	-2.900	-0.200	0.400	2.600
L15	5.971	-5.600	0.700	2.300	0.300
L16	0.984	-2.800	-0.100	2.800	-0.600
L17	1.489	-5.700	-0.500	1.300	1.100
L18	3.373	-2.700	0.200	0.200	0.600
L19	4.522	-5.400	0.200	2.100	5.900
L20	4.667	-4.500	-0.400	0.500	0.200
L21	-4.956	-4.000	0.400	4.400	4.700
L22	2.926	-0.600	0.000	1.100	0.800
L23	2.752	-3.500	0.100	1.800	1.000
L24	1.573	-0.200	-0.700	3.300	2.400
L25	2.838	-1.500	4.200	4.300	2.000

Further, partitioning of total epistasis into (i) epistatic type (additive \times additive) and (j + l) epistatic types; (additive \times dominance) and (dominance \times dominance) interactions showed that mean squares estimate due to additive \times additive (i) type were found to be

significant for all the studied traits, except boll weight, lint percentage and lint index. As well as the presence of (j + l) epistatic types appeared to be significant in the inheritance of seed cotton yield/plant, lint cotton yield/plant and uniformity index.

Table (4): Analysis of variance for testing the presence of epistasis in the triple test cross for all the studied traits in the cotton cross (Giza 94 \times Australy).

S.O.V.	D.F	Boll weight	Seed cotton yield/plant	Lint cotton yield/plant	Lint percentage	Seed index
i type of epistasis	1	0.4033	61512.992*	7205.181**	55.126	18.056*
(j + l) types of epistasis	24	0.2500	37133.279**	5904.705**	45.031	4.132
Overall Epistasis	25	0.2561	38108.468	5956.724**	45.435	4.689
Within Families L ₁ , L ₂ , L ₃	216	0.075	3921.635	604.623	6.008	0.633
S.O.V.	D.F	Lint index	Fiber length	Micronaire reading	Fiber strength	Uniformity index
i type of epistasis	1	0.2387	590.803**	3.040**	17.666*	310.490**
(j + l) types of epistasis	24	2.3536	8.373	0.484	0.879	2.581*
Overall Epistasis	25	2.2690	31.670**	0.586	1.550	14.897**
Within Families L ₁ , L ₂ , L ₃	216	0.582	1.556	0.096	0.553	1.508

* and ** are the significance at 0.05 and 0.01 level of probability, respectively.

The epistatic type (i) was detected to be much larger in magnitudes than the other epistatic type (j + l) interactions for all the studied traits, except for lint index, indicating that fixable components of epistasis were more important than non-fixable one in the inheritance of these traits. Since, epistasis plays an important role in governing most of the traits under study and result in biased estimates for the genetic variance, thus ignoring such effect led to loss information about epistasis, also the estimates of additive and dominance components would be biased. Thus, the breeder should take epistasis into account in producing genetic models for studying quantitative traits. Saleh Eman (2013) found that total epistasis was insignificant for all traits, however partitioning of the total epistasis, showed

significance of (i) types fixable part of epistasis and unfixable epistasis, dominance \times dominance and dominance \times additive for all traits, except lint percentage, fiber strength and micronaire. In self-fertilized crops like cotton, the fixable component of epistasis could be easily exploited, and it could have important implications in a breeding program. Standard hybridization and selection procedures could take advantage of epistasis if it is additive \times additive epistatic type as in most studied traits. A great importance of epistasis was also recorded in cotton by Bhatti *et al.* (2006), Esmail (2007), El-Lawendey *et al.* (2010), Sohu *et al.* (2010), Saleh Eman (2013), Jayade *et al.* (2014), Al-Hibbiny *et al.* (2020), Giri *et al.* (2020), Isong *et al.* (2021) and Hassan *et al.* (2022).

3.5 Detection and estimation of additive and dominance genetic variance components

Analysis of variance for sum, additive ($L1i + L2i$) and difference, dominance ($L1i - L2i$) is presented in Table (5). The mean squares due to sums and differences was found to be significant for all the studied traits, indicating the presence of

both additive and dominance genetic variance for these traits. These results were in line with those of many researchers, such as Hendawy *et al.* (2009), El-Mansy *et al.* (2010) and (2012), Kannan *et al.* (2013), Ali *et al.* (2016), Mahros El-Shymaa (2016), Al-Hibbiny *et al.* (2020), Giri *et al.* (2020), Isong *et al.* (2021) and Hassan *et al.* (2022).

Table (5): Mean squares for sums (additive) and differences (dominance) test for the triple test cross families for all the studied traits of the cotton cross (Giza 94 × Australy).

S.O.V.	D.F	Boll weight	Seed cotton yield/plant	Lint cotton yield/plant	Lint percentage	Seed index
Between sums	24	0.125**	11370.610**	1670.578**	12.767**	0.973**
Within sums	216	0.035	2799.823	440.689	3.074	0.286
Between differences	24	0.160**	9837.868**	1502.293**	15.515**	0.779**
Within differences	144	0.042	3685.929	572.004	4.670	0.398
S.O.V.	D.F	Lint index	Fiber length	Micronaire reading	Fiber strength	Uniformity index
Between sums	24	1.113**	3.561**	0.322**	0.439*	2.491**
Within sums	216	0.394	0.552	0.068	0.248	0.506
Between differences	24	1.875**	3.133**	0.316**	0.899*	1.768**
Within differences	144	0.509	0.690	0.111	0.465	0.447

* and ** are the significance at 0.05 and 0.01 level of probability, respectively.

The TTC analysis further showed that both additive (D) and dominance (H) genetic components of variation appeared to predominantly affect for all traits (Table 6). Additive values were greater than dominance genetic variance for seed cotton yield/plant, lint cotton yield/plant, seed index, fiber length, micronaire reading and uniformity index. Also, the degree of dominance ($\sqrt{H/D}$) was less than the unity for the same traits, suggesting the role of partial or incomplete dominance in the inheritance of these traits. Consequently, it could be concluded that selection procedures in early generations based on accumulation of additive effects would be successful in improving all these traits. Similar results were previously obtained

by Bhatti *et al.* (2006), Esmail (2007), Saleh Eman (2013), Jayade *et al.* (2014), Al-Hibbiny *et al.* (2020), El-Mansy *et al.* (2020), Giri *et al.* (2020), Isong *et al.* (2021) and Hassan *et al.* (2022). Further, the correlation coefficient between the sum ($L1i + L2i$) and difference ($L1i - L2i$) was found to be negative and insignificant for all the studied traits, except fiber length, fiber strength and uniformity index, which had positive and non-significant correlation. These results indicated that the genes with positive and negative dominant alleles were dispersed between testers and did not show any proof of directional dominance for these traits. The covariance of sums and differences (F) values were negative and

insignificant for most studied traits, reflecting ambidirectional dominance. Esmail (2007) showed that the inheritance of all the studied traits was controlled by additive and non-additive genetic effects, with greater values of dominance gene effect than the additive one in most cases. Among the non-additive effect, the other fixable component, *i.e.*, additive \times additive (i) type of interaction, which had significant and constituted a major portion of the gene effects. The signs of (h) and (L) were opposite in the case of seed

cotton yield and lint yield per plant in the intrabarbadense cross suggesting duplicate type of non-allelic interaction in these traits. El-Lawendey *et al.* (2010) indicated that the correlation coefficient of sums and differences was non-significant for all characters, as well as the F-values were positive and negative, revealing that dominant genes were umbidirectional among parents. A significantly positive additive correlation between lint yield/plant and each of lint index and seed index were detected.

Table (6): Estimates of additive (D), dominance (H) components, degree of dominance $(H/D)^{0.5}$, covariance between sums, the correlation coefficient between sums (r) and differences (F) for all the studied traits in the cross (Giza 94 \times Australy).

Items \ Traits	Boll weight	Seed cotton yield/plant	Lint cotton yield/plant	Lint percentage	Seed index
D	0.119	11427.717	1639.852	12.924	0.917
H	0.158	8202.585	1240.385	14.460	0.508
$(H/D)^{0.5}$	1.151	0.847	0.870	1.058	0.745
F	-0.204	-14671.799	-1871.336	-22.899	-0.751
r (sums/differences)	-0.501	-0.482	-0.410	-0.565	-0.299
Items \ Traits	Lint index	Fiber length	Micronaire reading	Fiber strength	Uniformity index
D	0.959	4.012	0.338	0.255	2.646
H	1.822	3.257	0.273	0.579	1.761
$(H/D)^{0.5}$	1.378	0.901	0.899	1.507	0.816
F	-2.332	2.979	-0.656	0.702	2.126
r (sums/differences)	-0.560	0.310	-0.714	0.388	0.352

* and ** are the significance at 0.05 and 0.01 level of probability, respectively.

3.6 Genetic correlation

The kind of relationships, which may occur among traits is an important tool for selection in breeding programs. Partitioning the total genetic variation to its components; additive (rD), dominance (rH) and epistasis (ri) is illustrated in Table (7). Obtained results provided

evidence for positive and significant correlation between additive gene effects (rD) controlling between boll weight and seed index, seed cotton yield/plant and lint cotton yield/plant and lint percentage and lint index, while negative and significant additive genotypic correlation was registered between lint percentage and fiber length.

Table (7): Genotypic correlation between epistasis (i), additive (D) and dominance (H) for all the studied traits in the cotton cross Giza 94 × Australy.

Traits		Seed cotton yield/plant	Lint cotton yield/plant	Lint percentage	Seed index	Lint index	Fiber length	Micronaire reading	Fiber strength	Uniformity index
Boll weight	r _i	0.250	0.239	-0.045	0.527**	0.497*	0.200	-0.126	0.136	0.141
	r _D	0.140	0.124	-0.084	0.636**	0.246	0.057	-0.130	0.075	-0.066
	r _H	0.363	0.407*	0.353	0.456*	0.450*	-0.346	0.069	-0.060	-0.188
Seed cotton yield/plant	r _i		0.985**	0.010	0.230	0.336	-0.004	-0.003	-0.028	0.102
	r _D		0.985**	-0.033	0.323	0.173	-0.106	0.189	-0.029	-0.092
	r _H		0.979**	0.088	0.209	0.189	0.165	0.293	-0.023	0.061
Lint cotton yield/plant	r _i			0.177	0.175	0.369	-0.077	-0.064	-0.067	0.043
	r _D			0.129	0.287	0.314	-0.168	0.200	0.007	-0.078
	r _H			0.274	0.251	0.365	0.118	0.317	-0.099	-0.022
Lint percentage	r _i				-0.368	0.210	-0.374	-0.368	-0.169	-0.391
	r _D				-0.298	0.809**	-0.443*	0.084	0.094	-0.029
	r _H				0.209	0.934**	-0.187	0.156	-0.370	-0.320
Seed index	r _i					0.458*	0.404*	0.098	0.226	0.446*
	r _D					0.280	0.208	0.030	0.054	-0.133
	r _H					0.493*	-0.502*	0.137	-0.012	-0.108
Lint index	r _i						-0.022	0.110	0.292	-0.127
	r _D						-0.253	0.098	0.121	-0.016
	r _H						-0.308	0.168	-0.398*	-0.340
Fiber length	r _i							-0.140	0.568**	0.575**
	r _D							-0.067	0.213	0.325
	r _H							-0.217	0.048	0.568**
Micronaire reading	r _i								0.117	-0.191
	r _D								-0.074	-0.172
	r _H								0.228	-0.214
Fiber strength	r _i									0.050
	r _D									0.273
	r _H									0.262

Concerning the dominance genotypic correlations (r_H), the results showed positive and significant correlation between boll weight with lint cotton yield/plant, seed index and lint index, seed cotton yield/plant with lint cotton yield/plant, lint percentage with lint index and fiber length with uniformity index, on the other hand negative and significant genotypic correlation was detected between seed index and fiber length and lint index with fiber strength. Regarding epistasis genotypic correlation (r_i) the results indicated positive and significant correlation between boll weight with seed index and lint index, seed cotton yield/plant with lint cotton yield/plant, seed index with lint index, fiber length and uniformity index and fiber length with

fiber strength and uniformity index. The previous results of genotypic correlation showed that some of the studied traits were positively associated with each other confirmed that selection for anyone will improve the other traits. As well as some of them were positively associated with yield traits, so, the cotton breeder can increase yield productivity by using indirect selection for yield components.

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