

DETECTION OF EPISTASIS, ADDITIVE AND DOMINANCE AS GENETIC COMPONENTS FOR SOME COTTON GENOTYPES

EL-HOSEINY, H. A, M.H. M. ORABI, AZIZA M. SULTAN AND T.A. EL-FEKI

Cotton Research Institute, ARC, Giza, Egypt.

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Abstract

This study aimed to determine whether epistasis played a significant role in genetic system for selected traits among several cotton cultivars and to evaluate the importance of additive vs dominance gene effects for traits not influenced by epistasis. The two cultivars referred to as tester L1 and L2 and their F1 (L3) were crossed to each of seven other cultivars. The deviations (cultivars L1 + cultivars L2 – cultivars 2 L3) were analyzed to provide a test of epistasis. Additive- dominance model was fitted to the data for these traits not influenced by gene interaction. The results indicated that total epistasis was significant for lint percentage and upper half mean. The partitioning of the total epistasis, showed insignificance of (i) types fixable part of epistasis for all studied traits while the unfixable epistasis, dominance x dominance and dominance x additive was significant only for lint percentage. Additive gene action played the important role for all studied traits except for boll weight. While, dominance effects were insignificant for all traits except for lint percentage. The results indicated difficulty in obtaining clear picture about genetic system of lint percentage and upper half mean. The degree of dominance revealed the predominant nature of additive genetic components.

Also the results showed that the dominant alleles were dispersed between testers, as hybrids did not show any proof of directional dominance for all characters

INTRODUCTION

The success in the selection of plant breeding program largely depends upon the nature and magnitude of gene action present in the material being handled by breeder. However, the estimation of these components becomes significantly biased in the presence of epistasis, which leads to erroneous estimation of genetic parameters and expected genetic gain under selection. So triple test cross analysis provides unambiguous test for the presence of epistasis regardless of gene frequencies, degree of breeding and linkage of relationships.

Bhatti *et al.*, (2006A) revealed that epistasis component played important role in the genetic control for all traits. Also, many investigators reported that additive and dominance gene effects were involved and the relative contribution of each component varied from traits to another (Garg *et al.* 1987, Kumar and Raveendran 2001, Khedr 2003, Bhatti *et al.* 2006B, ElAkheder and EL-lawendey 2006 and Soliman

et al., 2008). They indicated that the partitioning of the total epistasis showed significance of (i) type, additive x additive, of epistasis for boll weight and uniformity ratio only. Additive gene effects were significant for most traits, while the dominance effects were highly significant for uniformity ratio.

The present investigation was undertaken to detect the presence of epistasis and to estimate the additive and dominance components of genetic variation of same quantitative traits in cotton

MATERIALS AND METHODS

Two cotton genotypes, Giza 70, and Pima S₆ as L₁ and L₂, respectively, were used as tester genotypes. They represented the two extreme high and low genotypes for most of the characters and had diverse geographic origin. The two genotypes were crossed and the resulting F₁ was used as the third tester designated L₃. Seven true cotton breeding genotypes i.e. Australian, G.92, (G.77 X Pima S₆), (G.75 X Sea), (10229 x G.86), (G.89 X G.86), (G.89 X Pima S₆), were crossed as females with each of the three testers (L₁, L₂ and L₃) in the entire triple test cross combinations. The experiment thus consisted of 9 inbred lines (two testers and seven female lines), 15 single crosses and seven three-way crosses. The material was planted in a randomized complete block design with three replications at Sakha Agricultural Research Station farm during the 2011 season. The data were recorded from the harvested plot for the following traits.

1. **Seed cotton yield**, estimated as the weight of seed cotton yield and was computed in kantar/Feddan (k/fed).
2. **Lint yield**, estimated as the weight of lint cotton yield in kantar/Feddan (k/fed)
3. **lint percentage**: Ratio of lint cotton yield to seed cotton yield sample expressed as percentage using the formula

$$L\% = \frac{\text{weight of lint in sample}}{\text{weight of seed cotton in the same sample}} \times 100$$

4. **Boll weight in grams (B.W. gm)**: The average boll weight in grams of 50 bolls picked at random from each plot.
5. **Fiber length (upper half mean)**: measured by HVI in (mm).
6. **Fiber strength (F.S)**: Measured by HVI in gram / tex units
7. **Micronaire value (Mic)**: Fineness was expressed as micronaire instrument reading. The characters were measured with micromat instrument. ASTM D-3818-98

The analysis of variance was performed following the method described by Singh and Chaudhary (1999) to determine the significance of treatments and to partition it to determine its components.

Test for epistasis

For test of epistasis seven values ($L_{1j} + L_{2j} - 2L_{3j}$, $i = 1$ to 7 with 7 degree of freedom (n) was used to test for overall epistasis (Jinks and Virk, 1977). The total epistasis was partitioned into two components i.e. (i) type measure mainly the epistasis due to additive by additive type for 1 degree of freedom and (J +I) type, additive x dominance and dominance x dominance) for 6 degrees of freedom (n-1).

Estimation of additive variance component (D)

The mean square due to sums of ($L_{1j} + L_{2j}$) and differences ($L_{1j} - L_{2j}$) for 6 degrees of freedom were used to detect additive and dominance gene effects. From the analysis of variance in Table (1), the estimation of additive D and dominance H were obtained according to Singh and Chaudhary (1999).

Table 1. The analysis of variance for sums (additive) and differences, dominance. Sums

Source	d.f	M.S.	E. (M.S.)
Replications	$r-1$	MSr	
Genotype sum ($L_{1j} + L_{2j}$)	$n-1$	MSs	$s^2e + 2rs^2s$
Error	$(n-1)(r-1)$	Mse	s^2

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

$$s^2s = (MSs - MSe)/2r$$

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

Differences

Source	d.f	M.S.	E. (M.S.)
Replications	$r-1$	MSr	
Genotype sum ($L_{1j} - L_{2j}$)	$n-1$	MSs	$s^2e + 2rs^2s$
Error	$(n-1)(r-1)$	Mse	s^2

$$s^2d = (MSd - MSe)/2r$$

$$s^2s = (1/4) H \quad H = 4(MSd - MSe)/2r$$

Where: r = Replication; n = Genotypes,

The direction of dominance by the correlation coefficient of sums/differences was used to test the significance of F value (Jinks *et al.*, 1969). The obtained seven values for each of, $L_{1j} + L_{2j} - 2L_{3j}$, $L_{1j} + L_{2j}$ and $L_{1j} - L_{2j}$. in every character was used to compute epistasis, additive and dominance genetic correlations according to

Kearsey *et al.* (1987). All these computations were performed using Excel and Minitab computer programme.

RESULTS AND DISCUSSION

Highly significant differences in genotypes (hybrids, lines and tester) were noted for all the traits except for difference of testers for boll weight, upper half mean and micronaire reading. Indicating the presence of considerable variability among genotypes (Table 2). The significant mean squares of P_1 vs P_2 and $P_1 + P_2$ vs F_1 for seed and lint cotton yield and lint percentage showed the existence of variation between testers (L_1 and L_2). marked differences between L_1 and L_2 results into expression of high mean performance of their F_1 (L_3) were revealed by significant mean squares due to $P_1 + P_2$ vs F_1 . Since the two tester represented highly significant differences for these traits. they would provide precise estimates of additive and dominance variance as-reported by Kearsey and Jinks (1968).

Lines vs. testers were highly significant for all traits. Hybrids vs. parent were also highly significant for all characters except upper half mean, fiber strength and micronaire reading. These results were in agreement with those obtained by EL-Akheder and El-Lawendey (2006), and Soliman *et al.*, (2008).

Table 2. Analysis of variance for the studied traits in cotton.

Source	d.f	Boll weight	seed cotton yield k/f	Lint cotton yield k/f	Lint %	Upper half mean	Fiber strength	Micronair
Replications	2	0.045	1.76	2.78	0.35	0.89	0.04	0.12
Genotypes	30	0.106**	18.01*	33.17*	6.29*	2.57**	0.64**	0.19**
Hybrids (H)	20	0.099**	14.65*	24.28*	3.32*	2.72**	0.47	0.13**
Parent (P)	9	0.103*	25.28*	52.79*	13.20*	2.51*	1.07**	0.33**
Line (L)	6	0.096*	11.85*	34.49*	16.90*	3.48*	0.66	0.48**
Tester (T)	2	0.069	50.24*	89.63*	7.62*	0.22	1.03*	0.04
$P_1 + P_2$ vs F_1	1	0.019	47.16*	87.49*	7.61*	0.30	1.45*	0.06
P_1 vs P_2	1	0.113	37.59*	62.61*	5.09*	0.04	0.14	0.00
L vs T	1	8.693**	29.08*	35.79*	805.57*	689.08**	93.19**	13.18**
H vs P	1	0.264*	19.81*	34.50*	3.55*	0.02	0.13	0.05
Error	60	0.040	4.50	6.36	0.21	1.14	0.30	0.04
Total	133	0.043	6.12	10.39	1.52	1.11	0.28	0.06

*,** significantly different at the 0.05 and 0.01 levels of probability, respectively

The analysis of variance for the detection of epistasis. (Table 3) revealed the presence of epistasis gene action for lint percentage and upper half mean. This indicated that one would not have obtained a clear picture about the genetic system for lint percentage and upper half mean if a procedure had been used assuming no epistasis. While, the other studied traits showed no epistasis. This finding indicated that one would have obtained a clear picture about the genetic systems for these traits. These results were in partial harmony partially with those obtained by Garge *et al.* (1987) who found no significant overall epistasis or any components parts (1) or (L1j) type for any traits in Bc₁ generation

Table 3. Analysis of variance for the test of epistasis for the studied traits in cotton.

Source	d.f	Boll weight	seed cotton yield k/f	Lint cotton yield k/f	Lint %	Upper half mean	Fiber strength	Micronair
Total epistasis	7	1.23	62.2	100.34	6.71*	31.90*	4.09	0.29
i type epistasis	1	0.08	48.4	126.99	26.93	126.79	6.74	0.35
j +l type epistasis	6	1.15	62.2	95.89	3.34*	16.08	3.65	0.28
Total epistasis + replicates	14	1.27	46.3	65.35	1.80	10.68	1.77	0.21
i type epistasis + blocks	2	0.04	12.1	31.75	6.73	31.70	1.69	0.09
j +l type epistasis + blocks	12	1.23	52.0	70.95	0.98	7.18	1.79	0.23

*, ** significantly different at the 0.05 and 0.01 levels of probability, respectively

Further partitioning of the epistasis (Table 3) revealed the absence of (i) types of epistasis which represent fixable interaction for all traits. While unfixable epistasis (j + i) represent (additive x dominance, dominance x additive, respectively) were significant for lint percentage only. This result was in agreement with those obtained by Soliman *et al.* (2008) who revealed significance of I type fixable for boll weight and uniformity ratio only. The epistatic deviations of individual lines are shown in Table (4). The data indicated that the epistatic deviations were exhibited by Australian for boll weight, Giza 92 for lint percentage and upper half mean, (Giza 77 x Pima S₆) for upper half mean , lines (10229 x Giza 86) for lint cotton yield and lint percentage. (Giza 89 x Giza 86) for lint percentage and line of (Giza 89 x Pima S₆) for lint percentage. It is evident that most lines exhibited epistatic deviation for lint percentage.

Table 4. Epistatic deviations of individual cotton genotypes

Genotypes	Boll weight	seed cotton yield k/f	Lint cotton yield k/f	Lint %	Upper half mean	Fiber strength	Micronair
Australian	-0.42*	4.35	5.32	-0.05	-1.77	-1.40	0.17
G.92	-0.13	1.98	3.28	1.92**	-3.83*	1.43	-0.17
G.77 X Pima S ₆	-0.29	4.15	5.02	0.52	-6.93*	1.67	0.33
G.75 X Sea	0.16	-2.69	-3.43	-0.34	-1.73	0.50	0.17
10229 x G.86	-0.17	8.84	11.95*	1.96**	-0.63	0.47	0.63*
G.89 X G.86	0.22	-3.90	-3.74	1.80**	-2.27	1.50	0.03
G.89 X Pima S ₆	0.18	-2.10	-1.18	2.13**	-0.03	-0.20	-0.27

*= significantly at the 0.05 level.

The present study also indicated the importance of additive and dominance genetic component for the character studied (Table 5). The absence of epistasis, the analysis of variance for sum and differences provided direct test of the significance of additive (significant of sum) and dominance components (significant of differences). The sums item were highly significant for all traits except for boll weight. The differences in items were insignificant for all traits except for lint percentage which exhibited significant differences. The estimates of additive (D) and dominance (H) components in the present study were presented in Table (5). Accordingly, the component D was significant in all traits except for boll weight, H component was insignificant for all traits except for lint percentage and upper half mean. These traits exhibited total epistasis, Table (3) the knowledge of genetic architecture was important for success of any plant breeding programe.

Table 5. Mean squares due to sums (L1i + L2i) and difference (L1i – L2i) estimates of additive (D), dominance (H), and degree of dominance $\sqrt{H/D}$ and direction of dominance (r s,d) for studied traits in cotton.

Source	d.f	Boll weight	seed cotton yield k/f	Lint cotton yield k/f	Lint %	Upper half mean	Fiber strength	Micronair
Sums	6	2.889*	34.55**	69.96**	12.55**	2.42**	1.39*	0.41**
Sums x Replicates	12	0.920	5.96	8.48	0.52	0.55	0.34	0.03
Differences	6	0.457	6.75	9.53	2.43*	0.83	0.68	0.09
Differences x replication	12	0.450	11.50	16.37	0.44	0.64	0.34	0.04
D		0.270*	19.064**	40.987**	8.016**	1.244* *	0.698**	0.248**
H		0.026	-3.170	-4.558	1.326*	0.126	0.226	0.028
$\sqrt{H/D}$		0.309	0.00	0.00	0.407	0.318	0.569	0.334
r s,d		-0.078	-0.464	-0.411	0.183	0.414	0.059	-0.373

*, ** significantly different at the 0.05 and 0.01 levels of probability, respectively

The results of the present study revealed the presence of epistasis for two traits vis. Lint present and upper half mean. This indicates that one would not have obtained clear picture about system of these traits while, another traits one would have obtained clear picture about of genetic system. The absence of significant I type of epistasis for all traits, however indicated that (i) type of epstasis is relatively a minor component of epstasis.

The degree of dominance further revealed the predominant nature of additive genetic component for all the traits. These results revealed that the higher magnitude of additive genetic component compared with dominance component. this was in harmony with the results by Garg *et al.* (1987), El-Akheder and EL-Lawendey (2006) and Soliman *et al.*,(2008). The direction of dominance (rs,d) was insignificant and negative which showed that the dominant alleles were dispersed between testers, therefore they did not show any proof of directional dominance for these traits. Thus, in decreasing alleles were more frequent in the genetic constitution of studied cotton genotypes (Sandhu and Singh 1989 and Soliman *et al.* (2008).

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تحديد التفوق والتباين المضيف والسيادى كمكونات للتباين الوراثى لبعض الطرز الوراثية للقطن

حسن أمين الحسيني ، مصطفى حسنى محمد عرابى، عزيزة محمد سلطان ، طلعت احمد محمود الفقى

معهد بحوث القطن - مركز البحوث الزراعية

استخدم فى هذا البحث الابوين ج 70، بيما س6 وكذلك الجيل الاول (F1) الناتج منهما كأباء اختبارية تم تهجينها مع سبعة سلالات كامهات وهى استرالى ، ج 92 ، ، (ج 75 × سى)، (10229 × ج 86)، (ج 89 × ج 86) ، (ج 89 × بيما س6).
تم تقييم الطرز الوراثية الاباء + 21 هجين فى تجربة قطاعات كاملة عشوائية ذات ثلاث مكررات بمحطة البحوث الزراعية بسخا موسم 2011 بهدف اختبار وكشف التفاعل الغير الاليلى وتجزئته الى مكوناته وكذلك مكونات التباينات الوراثية المضيفة والسيادية ومدى مناسبة المادة الوراثية لنموذج additive-dominance وكانت اهم النتائج المتحصل عليها:

- 1- وجود اختلافات معنوية بين التراكيب الوراثية والهجن لكل الصفات المدروسة.
- 2- اظهر اختبار التفاعل غير الاليلى وجود تفاعل كلى غير اليلى فى صفتي نسبة التصافى وصفة طول التيلة (طول الشعيرات عند الربيع الاعلى)
- 3- كانت التباينات غير الاليلية فى جميع الصفات غير معنوية لكل الصفات ما عد المكون (سيادى × سيادى ، سيادى × اضافى) حيث كان معنوى فى صفة تصافى الحليج.
- 4- كان التفاعل الفردى غير الاليلى للاصناف معنوا فى صفة تصافى الحليج ماعد استرالى ، ج 92 ، (ج 75 × سى) كما اظهر الاسترالى تفاعل فردى غير اليلى لصفة وزن اللوزة وكذلك ج 92 ، (ج 77 × بيما س6) فى صفة طول التيلة (طول الشعيرات عند الربيع الاعلى).
- 5- كان التأثير الاضافى معنوى فى جميع الصفات المدروسة ماعدا صفة وزن اللوزة.
- 6- كان التأثير السيادةى غير معنوى لجميع الصفات المدروسة ما عدا صفة تصافى الحليج.
- 7- اظهرت كل الصفات سيادة جزئية.
- 8- كانت قيم الارتباط غير معنوية مما يدل على تشتت توزيع السيادة بين الاباء.