

GENETIC ESTIMATION OF YIELD AND YIELD COMPONENTS IN COTTON THROUGH TRIPLE TEST CROSS ANALYSIS

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ABSTRACT

The success of plant breeding operations relies heavily on the nature and extent of genetic components of variation. Thus it is imperative to have reliable estimates of such components in order to formulate an efficient breeding strategy. In the present study, ten diverse lines in F_2 generation were crossed to three testers viz., Giza 86(L_1), Australian(L_2) and their F_1 Giza86 X Australian (L_3). The parents (lines and testers) and crosses were evaluated in randomized complete block design. Analysis of variance revealed significant differences among progenies. The deviations (cultivars L_1 + cultivars L_2 – cultivars $2 L_3$) 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 insignificant for all traits. The partitioning of the total epistasis, showed significance of (i) types fixable part of epistasis for all traits except lint percentage, fiber strength and micronaire, while the unfixable epistasis, dominance x dominance and dominance x additive was significant for all traits except lint percentage, fiber strength and micronaire. Additive gene action played the important role for all studied traits except for lint cotton yield, upper half mean, fiber strength and micronaire. While, dominance effects were insignificant for all traits. The degree of dominance revealed that the ratio was less than unit indicated the predominant role of additivity in controlling boll weight, seed and lint cotton yield, seed index and uniformity ratio, whilst this ratio was equal to unity for lint percentage and upper half mean showed the important of both additive and dominance properties of genes, The higher degree of dominance for fiber strength and micronaire showed over-dominance. The results showed that the dominant alleles were dispersed between testers, as hybrids did not show any proof of directional dominance for all characters.

Keywords: Cotton, triple test cross, epistasis.

INTRODUCTION

The success of selection in 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 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. Many investigators reported that additive and dominance gene effects were involved and the relative contribution of each component varied from trait to another (Garg *et al.* 1987,

Kumar and Raveendran 2001, Khedr 2003, Bhatti *et al.* 2006b, El-Akheder 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 86, and Australian as L_1 and L_2 , respectively, were used as tester genotypes. The two genotypes were crossed and the resulting F_1 was used as the third tester designated L_3 . From F_2 population, 10 plants were randomly selected as males and crossed back to the three testers, P_1, P_2 and F_1 , to generate $L_{1i}(P_1 \times F_2)$, $L_{2i}(P_2 \times F_2)$ and $L_{3i}(F_1 \times F_2)$ families. Thus, the experiment consisted of 30 families (3 testers and 10 lines) were obtained for genetic studies. The materials were 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: It estimated as the weight of seed cotton yield and was computed in kentar/Feddan (k/fed).

2. Lint yield: It estimated as the weight of lint cotton yield in kentar/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. Seed index (gm): It determined as the weight of 100 seeds taken randomly from each plot.

5. Boll weight in grams (B.W. gm): The average boll weight in grams of 50 bolls picked at random from each plot

6. Fiber length (upper half mean): It measured by HVI in (mm).

7. Fiber strength (F.S): Measured by HVI in gram / tex

8. Micronaire value (Mic): Fineness was expressed as micronaire reading. The characters were measured with micromat instrument. ASTM D-3818-98.

9. Uniformity ratio (UR%) = 100 (fiber length at 50% SL / fiber length at 2.5% SL)

The analysis of variance was performed following the method described by Singh and Chaudhary (1985) to determine the significance of treatments and to partition it to determine its components.

Test for epistasis

For test of epistasis ten values ($L_{1j} + L_{2j} - 2L_{3j}$, $i = 1$ to 10 with 9 degree of freedom (n) was used to test for overall epistasis. 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 +1) type, additive x dominance and dominance x dominance) for 9 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 9 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 (1985).

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:

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

$$s^2s = (1/4) D$$

$$D = 4(MSs - MSe)/2r$$

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

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

$$s^2s = (1/4) H$$

$$H = 4(MSd - MSe)/2r$$

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. The obtained ten 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 programmed.

RESULTS AND DISCUSSION

The analysis of variance for different studied traits are presented in Table (2). Data revealed highly significant mean squares due to genotypes

(hybrids, lines and tester) for all characters indicated considerable genetic variations existed in the genotypes and these variability could be transmitted through generation. Thus, the breeder could be exploited variability through breeding programme. Mean squares of p_1 vs p_2 and p_1+p_2 vs f_1 were highly significant for boll weight, seed cotton yield, lint percentage and uniformity ratio reflected the existence of variation between tester (L_1 and L_2) results into expression of high mean performance of their $f_1(L_3)$ which revealed by significant mean squares due to p_1+p_2 vs f_1 since the difference for these traits. They precise estimates of additive and dominance variance as reported by Kearsey and Jinks (1968).

Lines vs. testers were highly significant for boll weight, seed and lint cotton yield and lint percentage was significant only in uniformity ratio. Hybrids vs. parents were also highly significant for all characters except seed cotton yield, seed index and upper half mean. These results were in agreement with those obtained by EL-Akheder and El-Lawendey (2006), and Soliman *et al.*, (2008).

Division of total epistasis into I and j+I types of epistasis indicated the presence of i+j types of epistasis for all traits (Table 3). The I type epistasis was found to be much larger in magnitude than j+I type of epistasis indicating the predominant role of I type non-allelic interaction in the inheritance of these traits. The results showed that I and j+I types of epistasis were in complete harmony with those obtained by Saleem *et al.*, (2005b) and Muhamad *et al.* (2009). The existence of non-allelic interactions for economic character might have important role in inheritance in plant breeding. The I type of epistasis represents fixable while j+I types show non-fixable portion of genetic variations (Mather, (1949). The results have indicated the presence of I and j+I types of epistasis for most of characters, therefore in this condition recurrent selection technique is suggested:

The epistatic deviations of individual lines are shown in (Table 4). The data indicated that the epistatic deviations were exhibited by L_1 for all studied characters except lint cotton yield, upper half mean and uniformity ratio, L_2 for boll weight, seed cotton yield, lint percentage, seed index, upper half mean, micronaire and uniformity ratio. L_3 for most characters except lint cotton yield, lint percentage and micronaire. L_4 for seed cotton yield, seed index, upper half mean, fiber strength, micronaire and uniformity ratio. L_5 for all characters except lint cotton yield and micronaire. L_6 for all characters except boll weight, lint cotton yield and upper half mean. L_7 for boll weight, seed cotton yield, upper half mean and fiber strength. L_8 for all characters except lint cotton yield. L_9 for seed cotton yield, lint percentage, seed index, fiber strength and micronaire. L_{10} for all characters except lint cotton yield, seed index and micronaire. It is evident that all these lines displayed a significant positive role towards the total non-allelic interaction.

The present study also indicated the importance of additive and dominance genetic component for the character studied (Table 5). The mean square for sum and differences provided direct test of the significance of additive (significant of sum) and dominance components (significant of differences).

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The mean squares for sums and differences characters were highly significant and significant for all traits except for lint cotton yield and upper half mean. The estimates of additive (D) and dominance (H) components in the present study were presented in Table (5). Accordingly, the component D was significant for boll weight, seed cotton yield, lint percentage, seed index and uniformity ratio, H component was insignificant for all traits. These traits exhibited total epistasis, Table (3) the knowledge of genetic architecture was important for success of any plant breeding program. The ratio ($\sqrt{H/D}$) was less than unity indicated the predominant role of additivity in controlling boll weight, seed and lint cotton yield, seed index and uniformity ratio, Whilst this ratio was equal to unity for lint percentage and upper half mean showed the important of both additive and dominance properties of genes. The higher degree of dominance ($\sqrt{H/D} > 1$) for fiber strength and micronaire showed over-dominance this was in harmony with the results obtained by Garg *et al.* (1987), El-Akheder and EL-Lawendey (2006), Bhatti *et al.* (2006a) and Soliman *et al.*, (2008).

The direction of dominance ($r_{s,d}$) 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). It could be concluded that additive gene action played the important role for all studied traits except for lint cotton yield, upper half mean, fiber strength and micronaire. While, dominance effects were insignificant for all traits.

REFERENCES

- ASTM, (1998). (Designation D.4605 – 98 and 3818- 98) Vol. 07. No 1 Easton, MD, USA.
- Bhatti, M.A.; F.M. Azhar and A.W. Alvi (2006a). Triple test cross analysis of seed cotton yield and its components. *Int. J. Agri. Biol.* 8 (6): 820 – 823.
- Bhatti, M.A.; F.M. Azhar and A.W. Alvi (2006b). Estimation of additive, dominance and epistatic components of genetic variation in fiber quality characters of upland cotton grown in salinized conditions. *Int. J. Agric Bio.* 8, (6): 824- 827.
- El-Akheder, A.A.A. and M. M. EL-Lawendey (2006). Inheritance of quantitative characters through triple test cross in cotton. *J. agric. Res. Tanta Univ.*, 32 (1): 63-75.
- Garg, H.R., T.H. Singh and G.S. Chahal (1987). Genetical analysis through triple test cross in F_2 population of upland cotton. *Indian J. Agric. Sci.* 57 (10): 701 – 704.
- Kearsey M.J. and J.L Jinks. (1968). A general method for estimation of additive, dominance and epistatic variation for material traits 1 Theory. *Heredity*, 23:403-409.

- Kearsey M.J.; M.D. Hayward; F.D. Devery and M.M Eissa (1987). Genetical analysis of production characters in lolium. 1. Triple test cross analysis of spaced plant performance. Theor. Appl. Gent. 75: 66- 75.
- Khedr, A. H.(2003). Genetical studies on cotton. Ph.D. thesies, Fac. Agric. Zagazig univ. Egypt.
- Kumar, P.R. and T.S. Raveendran (2001). Genetic evaluation of yield and yield components in upland cotton through triple test cross analysis. Indian J. Agric. Sci., 71: 62– 64
- Maher, K. (1949). Biometrical genetics. 1st ed. Methuem, London.
- Muhammad, Y.S.,J.I Mirza; and M.A. Haq (2009) . Triple cross analysis of some physiomorphological traits basmatic rice Pak. J. Bot., 41 (5): 2411-2418.
- Sandhu, B.S. and J.R.P. Singh (1989). Detection of genetic effects using triple test cross analysis in desi cotton. Res Puniab. Agric. Univ., 26 (1): 10-13.
- Saleem, M.Y., B.M. Atta,A.A. Cheema,Z. Mukhtar and M.A. Haq.(2005b). detection of epistasis and estimation of additive and dominance components of genetic variation using triple test cross analysis(*Oryza satva*L.) Cademo de pequisa Ser Bio., Santa Cruz do Sul., 17:37-50.
- Singh, R.K. and B.D. Chaudhary (1985). Biometrical Method in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi.
- Soliman, Y.A.M.; Y.M. El-Mansy and M.A.M. Allam (2008). Triple test cross analysis of some economic characters in cotton *G. barbadense*. Egypt J. of Appl. Sci., 23 (4A): 125-137.

التقدير الوراثي للمحصول ومكوناته في القطن المصري من خلال التلقيح الرجعي الثلاثي

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استخدم في هذا البحث الابوين صنفين القطن جيزة 86، استرالي وكذلك الجيل الاول (F_1) الناتج منهما كآباء اختبارية تم تهجينها مع عشرة سلالات كامهات من نباتات الجيل الثاني وتم اختيارها عشوائيا وهي ($L_1, L_2, L_3, L_4, L_5, L_6, L_7, L_8, L_9, L_{10}$) تم تقييم الطرز الوراثية الآباء + 30 هجين في تجربة في تصميم القطاعات الكاملة العشوائية ذات ثلاث مكررات بمحطة البحوث الزراعية بسخا موسم 2011 بهدف اختبار وكشف التفاعل الغير الاليلي 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 الاليلي وجود تفاعل كلى غير اليلي في كل الصفات تحت الدراسة.
- 3- كانت التباينات غير الاليلية معنوية لكل الصفات بالنسبة للمكون (مضيف x مضيف) عدا صفة متانة التيلة اما بالنسبة للمكون (سيادى x سيادى ، سيادى x اضافى) حيث كان معنوى في الصفات التالية تصافى الحليج ووزن 100 بذرة، طول التيلة، متانة التيلة، الميكرونير، نسبة الانتظام.

- ٤- كان التفاعل الفردى غير الالىلى للسلاطات معنوى فى كل الصفات ماعدا السلاطات (L₂, L₄, L₆, L₈) لمتوسط وزن اللوزة , كل السلاطات غير معنوية لصفة محصول القطن الشعير و السلاطات (L₃, L₄, L₅) لصفة تصافى الحليج والسلاطات (L₇, L₁₀) لصفة وزن ١٠٠ ابذرة و السلاطات (L₁, L₆, L₉) لصفة طول التيلة (طول الشعيرات عند الربيع الاعلى). السلالة (L₂) لصفة متانة التيلة و السلاطات (L₃, L₅, L₇, L₁₀) لصفة النعومة (الميكرونيير) وكذلك السلاطات (L₁, L₇, L₉) لصفة الانتظام .
- ٥- كان التأثير الاضافى معنوى فى جميع الصفات المدروسة ماعدا صفات محصول القطن الشعير , طول التيلة , متانة التيلة والنعومة (الميكرونيير).
- ٦- كان التأثير السىادى غير معنوى لجميع الصفات المدروسة.
- ٧- اظهرت معظم الصفات سيادة جزئية ولكن بعض الصفات اظهرت انعدام السيادة لصفتى . تصافى الحليج, طول التيلة وكانت درجة السيادة اكبر من ١ الصحيح لصفتى المتانة والنعومة (الميكرونيير)
- ٨- كانت قيم الارتباط غير معنوية مما يدل على تشتت توزيع السيادة بين الابعاء . نستخلص من النتائج ان التفاعل الالىلى المضيف كان لة دور كبير فى توريث الصفات عدا صفة محصول القطن الشعير, طول التيلة, متانة التيلة والميكرونيير اما التأثير السىادى لم يكن معنوى لكا الصفات

قام بتحكيم البحث

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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 %	Seed index	Upper half mean	Fiber strength	Micronair	Uniformity ratio
Replications	2	0.017	0.004	0.030	0.568**	0.064	0.128	0.431	0.033	0.005
Genotypes	42	0.176**	4.58**	7.607**	9.391**	10296**	0.660**	0.652**	2288.2**	0.435**
Hybrids (H)	29	0.178**	5.13**	8.093**	4.944**	10639**	0.631**	0.683**	1594.3**	0.412**
Parent (P)	12	0.174**	3.62**	7.046**	19.419**	0.490**	0.746**	0.515**	423.87**	0.498**
Line (L)	9	0.079**	3.04**	4.115**	7.960**	0.374**	0.826**	0.616**	528.36**	0.391**
Tester (T)	2	0.121**	0.99**	0.002**	26.798**	1.041**	0.754**	0.148	165.55**	1.068**
P ₁ +P ₂ vs F ₁	1	0.024**	1.09**	0.001	29.183**	0.282	0.350	0.220	0.042	1.450**
P ₁ vs P ₂	1	0.209**	0.53**	0.003	14.685**	1.707	1.042**	0.002	0.107	0.202
L vs T	1	1.142**	14.13**	47.517**	107.795**	0.425	0.012	0.342	0.059	0.318*
H vs P	1	0.152**	0.06	0.254**	18.017**	1.012	0.494	1.382**	44781.6**	0.346*
Error	84	0.020	0.03	4296.8	0.451	0.123	0.114	0.185	0.033	0.064
Total	184	0.050	1.06	1963.3	2.356	0.352	0.204	0.238	522.317	0.129

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

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 %	Seed index	Upper half mean	Fiber strength	Micronaire	Uniformity ratio
Total epistasis	10	0.935**	69.097**	114.51**	39.38**	3.37**	4.478**	5.09**	1.061**	3.993**
i type epistasis	1	5.932**	643.3**	1058.3**	24.18**	10.44**	19.04**	0.19	1.045*	13.872**
i+l type epistasis	9	0.380	5.294	9.644**	41.07**	2.59*	2.86*	5.63**	1.062**	2.896**
Total epistasis + replicates	2	1.483	160.8	264.6	6.045	2.61	4.760	0.05	0.261	3.468
i type epistasis + blocks	18	0.123	0.239	0.413	2.375	0.87	0.669	0.79	0.212	0.582
i+l type epistasis + blocks	20	0.259	16.298	26.830	2.742	1.04	1.078	0.72	0.217	0.871

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

Table 4. Epistatic deviations of individual cotton genotypes

Source	Boll weight	seed cotton yield k/f	Lint cotton yield k/f	Lint %	Seed index	Upper half mean	Fiber strength	Micronair	Uniformity ratio
L1	-0.098**	-5.30**	-6.115	1.620**	1.367**	0.3667	-2.17**	-0.800**	-0.267
L2	-0.22	-5.09**	-5.91	1.764*	0.567*	1.300**	0.03	0.700**	0.800**
L3	-0.5**	-7.50**	-9.345	-0.296	1.967**	1.1333**	-1.00**	-0.200	0.500*
L4	-0.1	-4.41**	-5.635	-0.917	1.533**	1.6667**	-0.33**	0.767**	1.533*8
L5	-0.3*	-3.72**	-5.17	-2.760**	0.9**	0.9333**	2.80**	-0.033	-0.467*
L6	-0.17	-5.13**	-6.82	-1.999**	1.167**	-1.0333**	-0.77**	0.600**	1.833**
L7	-1.0**	-4.30**	-5.255	0.328	-0.367	1.9000**	-0.73**	0.233	0.167
L8	-0.49**	-4.93**	-7.835	-6.935*8	-1.100**	-0.4000	1.30**	1.033**	2.433**
L9	-0.03	-2.67**	-4.475	-50583**	0.833**	1.8000**	-0.47	-0.533**	-0.333
L10	-0.8**	-3.27**	-2.835	5799*	-0.133	1.800**	0.53**	0.100	0.600**

*= significantly at the 0.05 level.

Table 5. Mean squares due to sums ($L_{1i} + L_{2i}$) and difference ($L_{1i} - L_{2i}$) 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 %	Seed index	Upper half mean	Fiber strength	Micronair	
Sums	9	0567**	2.451**	3.481	6.818**	5.409**	1.176	0.4813	0.111	0.798**
Sums x Replicates	18	0.042	0.057	0.138	0.7632	0.2111	0.3451	0.3402	0.062	0.199
Differences	9	0.097	10555	2.043	8.761	2.6561	1.5114	0.908	0.247	0.531
Differences x replication	18	0.120**	0.026**	0.071	0.973**	0.098**	0.4126	0.282	0.043	0.187*
D		0.349**	1.5960**	2.228	4.036**	3.465**	0.554	0.024	0.033**	0.025**
H		0.055	1.020	1.314	5.192	1.707	0.733	0.104	0.136	0.014
$\sqrt{H/D}$		0.397	0.799	0.768	1.134	0.702	1.11	2.11	2.048	0.757
r s,d		-0.334	0.155	0.200	0.553	-0.233	0.058	-0.342	0.400	0.076

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