

EPISTASIS AND GENETIC CORRELATION IN COTTON USING F₂ TRIPLE TEST CROSS

A.A.A El-Akheder and Y.M.EL-Mansy

Cotton Research institute, Agricultural Research Center, Egypt.

ABSTRACT

*Assessment and quantifying the components of genetic variance, epistasis and additive, together with dominance genetic correlation using 30 families of cotton (*Gossypium barbadense*) was done in F₂ triple test cross analysis derived from Giza 45 x Karshenky₂. Results revealed that overall epistasis were important role in the inheritance of all traits, except for boll weight. Partitioning of epistasis into its components, (i) type of epistasis, additive × additive and (i+j) types of epistasis, additive × dominance and dominance × dominance were significant for most traits with predominant of (i) type, additive × additive. Additive gene effects were significant and played a major role for all characters, while dominance gene effects were significant for some characters.*

The estimates of F value (direction of dominance) were not significant for all characters irrespective of their sign indicated ambidirectional dominant genes among parents. Genetic correlations revealed additive and epistasis gene effect controlling most traits were associated with each other. Thus selection based on such type may indicate that the direct selection would be effective for improving such characters.

Key words: *Cotton, Triple test cross, Gene effects, Correlation.*

INTRODUCTION

Choice of the most efficient breeding methodology mainly depends upon the type of gene action controlling the genetic variation. Therefore unambiguous tests of the genetic components help the breeder for rightful decision making about the most effective breeding method to be applied. Several genetic procedures are available to study the nature and magnitude of genetic variation. But, the triple test cross (TTC) breeding programme, a multiple mating scheme proposed by Kearsy and Jinks (1968), is theoretically the best design for detecting the presence of non-allelic interaction and estimating the additive, dominance components of variation for quantitative traits. This design is so versatile that it can be applied to any population regardless of its gene linkage and genotype

frequencies or its degree of inbreeding (Pooni *et al* 1994). Moreover, this analysis can also be used to investigate inbred lines as well as the F₂ generation.

The orthogonally of triple test cross families (Jinks and Perkins 1970) make correlation computed from them to be more reliable. Garg *et al* (1987), Kumar and Raveendran (2001) and Khedr (2003) applied F₂ triple test cross analysis in cotton and revealed the importance of epistatic gene effects in controlling most characters. Dhillon (1978) and Cruz (1981) reported epistasis to be an important component of variation for yield and other agronomic characters.

In the light of the advantages of TTC analysis, the present investigation was, therefore designated to use triple test cross analysis as an efficient method to test for epistasis and estimate additive and dominance genetic components as well as compute genetic correlation among different characters to help breeders to identify the favorable combination of characters to improve the efficiency of selection.

MATERIALS AND METHODS

Materials

The F₂ triple test cross used involved crossing random 10 F₂ individual plants of a cross Giza 45 × Karshenky₂ (Kar₂) with Giza 45, Karshenky₂ and their first fertile generation, F₁ (Giza 45 × Karshenky₂). The two cotton parents involved in the present study were extremes with respect to earliness (Karshenky₂) and high fiber quality (Giza 45). Yields of 30 families were cross-classified into L_{1i} (F₂ × P₁), L_{2i} (F₂ × P₂) and L_{3i} (F₂ × F₁) groups, where i varied from 1 to 10, thus the thirty families were developed and sown

A completely randomized block design with three replications was used. Ridge length was 4m and 70 cm apart. Plant to plant spacing was 30 cm. Data were recorded on position of the first fruiting node. Days to first flower, Lint yield/plant (g), Boll weight (g), Lint %, Seed index (g), Lint index (g) and halo Length (mm). The investigation was carried out at the farm of Sakha Agricultural Research Station, during three seasons of, 2003, 2004 and 2005.

Biometrical analyses

The triple test cross families were subjected firstly to the congenital one way analysis of variance for (L₁, L₂ and L₃) and (L₁

and L_2) sets of families each character separately to detect significance between T.T.C families .

The orthogonal comparisons $[\bar{L}_1i + \bar{L}_2i - 2\bar{L}_3i]$, $[\bar{L}_1i + \bar{L}_2i + \bar{L}_3i]$ (sums) and $[\bar{L}_1i - \bar{L}_2i]$ (differences) provided tests and estimates of the epistasis, additive and dominance components of genetic variation, respectively (Kearsey and Jinks 1968 and Jinks and Perkins 1970).

The degree of dominance was calculated as $\sqrt{D/A}$ the direction of dominance (F value) was computed from the covariance of sums / differences which equal to $(-1/8 F)$ where F is the association dispersion of dominant alleles in the parental lines. The correlation coefficient (r) of sums/ differences was used to test the significance of F value (Jinks and Perkins 1970).

The means of TTC families, 10 values, for each comparison for each character were used to compute epistasis, additive and dominance genetic correlation, respectively (Kearsey *et al* 1987). All these computations were performed using Minitab Computer Programme.

RESULTS AND DISCUSSION

Mean squares of the analysis of variance (Table 1) revealed significant differences between T.T.C families in all the studied characters, indicating that L_{1i} , L_{2i} and L_{3i} T.T.C families were significantly different from each other, providing evidence for adequate amount of genetic variability and assured the variability between the parents.

The results of applying the test for epistasis in our data, namely, which based on the comparison on $[\bar{L}_1i + \bar{L}_2i - 2\bar{L}_3i]$ are given in Table (2). Results provide evidence for significant overall epistasis for all studied character in T.T.C, except for boll weight, agreeing with Garg *et al* (1987). Further partitioning of epistasis to its component parts revealed (i) type of epistasis (additive \times additive) was significant for most characters and accounted for the great part of overall epistatic effects. The prevalence of additive \times additive gene effects may suggest that selection in early segregating generations would be effective for improving these characters. Khedr (2003) and El-Mansy (2005) revealed importance of additive \times additive type of epistasis in the genetic control for earliness and yield characters.

Table 1. Analysis of variance and mean squares among T.T.C families for eight characters.

S.O.V	d.f	M.S							
		Pos. of first fruiting node	Days to first flower	Lint yield/plant (g)	Boll weight (g)	Lint percentage	Seed index (g)	Lint index (g)	Halo length (mm)
Between T.T.C families	29	2.25**	17.40*	112.40*	0.273*	16.049*	2.015**	1.081*	7.430**
B. L ₁	9	1.89**	6.11**	125.24**	0.455**	13.091**	3.871**	0.988**	3.292**
B. L ₂	9	1.81**	5.21**	143.71**	0.308**	15.997**	1.187**	1.147**	3.110**
B. L ₃	9	0.62**	6.71**	58.60**	0.098*	21.481**	0.785*	0.992**	4.394**
Residual	2	9.93**	157.10**	36.0**	0.086**	5.155**	2.921*	1.604**	59.506**
Within T.T.C families	60	0.11	0.455	4.006	0.034	0.317	0.377	0.036	0.259
B. L ₁ , L ₂ families	19	2.53**	21.59**	118.75**	0.370**	14.095**	1.269**	1.131**	9.199**
Within families	40	0.11	0.385	4.33	0.015	0.259	0.431	0.031	0.292

* and ** significant at 0.05 and 0.01 levels of probability, respectively

Table 2. Mean squares for epistatic deviation [$L1i + L2i - 2L3i$] for eight studied characters in triple test cross.

S.O.V	d.f	M.S							
		Pos. of first fruiting node	Days to first flower	Lint yield/plant (g)	Boll weight (g)	Lint percentage	Seed index (g)	Lint index (g)	Halo length (mm)
(i) type	1	4.744**	11.199**	202.28**	0.0021	2.7120**	1.652*	1.240**	0.778
(i + j) type	9	0.1910	0.3367	39.739**	0.0594	8.0057**	0.773*	0.462**	1.262**
Over all/epistasis	10	0.6463**	1.4230**	55.993**	0.0537	7.4763**	0.861*	0.540**	1.214**
Within families	60	0.1090	0.455	4.006	0.0304	0.3168	0.377	0.0361	0.2592

* and ** significant at 0.05 and 0.01 levels of probability, respectively

On the other side the non-fixable type of epistasis ($i \times j$ type) additive \times dominance and dominance \times dominance were also significant for most characters, except for position of the first fruiting node and days to first flower which were controlled mainly by additive type. The greater magnitude of ($i + J$) type of epistasis for some characters suggested that epistasis was mainly due to non-fixable type. These results were in agreement with finding of Basu (1997). Since ($i+j$) type are not fixable by selection, therefore population improvement through recurrent selection might give a good response.

Epistasis played an important role in governing most of the studied characters and resulted in biased estimates for the genetic variance. Thus, the breeder should take epistasis into account in producing genetic models for studying quantitatively inherited characters. Wherever ignoring such effect one would not only loose information about epistasis, but, also the estimates of additive and dominance components would be biased.

The mean squares for detecting and estimating from orthogonal comparisons, $[\bar{L}1i + \bar{L}2i - 2\bar{L}3i]$ and $[\bar{L}1i - \bar{L}2i]$ between the means of the L_{1i} , L_{2i} and L_{3i} families are presented in Table (3) and the estimates of additive (A) and dominance (D) derived from them are presented in Table (4). The data revealed significant mean squares for both tests in most studied characters, providing evidence for the presence of additive and dominance gene effect in the genetic control of the studied characters. The additive component was larger in magnitude than the dominance one for different characters. These results reflected less dominance ratio than unity and explaining that the additive component was the predominant type in the inheritance of all the studied characters.

The direction of dominance as indicated by (F) value (Table 4) showed that F value was non-significant, revealing that dominance was umbidierectional. It is interesting to mention that F and H values have positive sign for lint index and lint cotton yield /plant. Thus the decreasing alleles were more frequent in the genetic constitution of two characters. Similar results were obtained by Garg *et al* (1987), Khedr (2003) and El-Mansy (2005).

Table 3. Analysis of variance for sums (additive) and differences (dominance) for eight studied characters in triple test cross.

S.O.V	d.f	Pos. of first fruiting node	Days to first flower	Lint yield/plant (g)	Boll weight (g)	Lint percentage	Seed index (g)	Lint index (g)	Halo length (mm)
Sums	9	0.930**	4.595**	57.743**	0.182**	11.554**	0.955*	0.671**	2.265**
Within families	60	0.109	0.455	4.006	0.0304	0.317	0.377	0.0361	0.2592
Differences.	9	0.1673	0.286	22.850**	0.074**	1.322**	0.60	0.183**	0.671*
Within families	40	0.10	0.385	4.326	0.0145	0.259	0.731	0.0308	0.292

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

Table 4. Estimates of additive (A) and dominance (D) components as well as F value for eight studied characters

Components	Pos. of first fruiting node	Days to first flower	Lint yield/plant (g)	Boll weight (g)	Lint percentage	Seed index (g)	Lint index (g)	Halo length (mm)
A	0.730	3.6808	47.766	0.135	9.989	0.514	0.564	1.7828
D	0.076	-0.1329	24.699	0.079	1.417	0.225	0.202	0.5047
$\sqrt{D/A}$	0.324	-0.1900	0.719	0.766	0.377	0.662	0.599	0.5321
F	-1.925	-1.5896	76.842	-0.729	-7.082	-6.246	2.098	-15.1816

* and ** significant at 0.05 and 0.01 levels of probability, respectively

Partitioning the total genetic correlation to its components of epistasis, additive and dominance were computed for different traits (Table 5) provided evidence for negative and significant genetic correlation between epistasis gene effects controlling first fruiting node and boll weight as well as halo length. Also significant positive epistasis correlation values between lint cotton yield/plant with days to first flower and lint percentage. The latest traits were correlated with lint index.

Table 5. Estimates of additive (RA) dominance (RD) and epistasis (RE) correlation coefficients among eight studied characters.

Correlation	Days to first flower	Boll weight (g)	Lint yield/plant (g)	Lint percentage	Seed index (g)	Lint index (g)	Halo length (mm)
Position of first fruiting node							
RA	0.686*	-0.649*	-0.488	-0.218	-0.350	-0.559	0.160
RD	-0.355	-0.604	0.019	0.464	0.199	-0.015	0.376
RE	-0.254	-0.765*	-0.396	0.301	-0.342	0.116	-0.667*
Days to first Flower							
RA		-0.366	-0.629*	-0.163	-0.251	-0.355	-0.324
RD		0.496	0.086	0.177	0.032	0.125	-0.433
RE		0.144	0.726*	0.418	0.048	0.377	0.024
Boll weight							
RA			0.465	0.324	0.058	0.420	0.190
RD			0.439	-0.174	0.192	0.013	-0.267
RE			0.586	0.130	0.319	0.187	0.561
Lint cotton yield							
RA				0.153	0.678*	0.593	0.177
RD				0.285	0.098	0.310	-0.180
RE				0.636*	0.014	0.556	-0.078
Lint percentage							
RA					-0.316	0.701*	-0.099
RD					-0.066	0.316	-0.100
RE					0.054	0.920*	-0.379
Seed index							
RA						0.433	-0.203
RD						0.511	-0.070
RE						0.387	0.560
Lint index							
RA							-0.194
RD							-0.194
RE							-
							0.128

* and ** significant at 0.05 and 0.01 levels of probability, respectively

Increasing additive genes controlling first fruiting node would be correlated with decreasing ones of boll weight, the same trend between lint cotton yield/plant and days to first flower. However, significantly positive additive correlation was obtained

between lint yield and seed index, and between lint percent and lint index.

Results obtained from the analysis of genetic correlation, generally revealed that additive and epistasis gene effects controlling most traits were associated with each other. Such genetic correlation may be due to a common genetic control, pleiotropy or linkage. Thus improving efficiency of indirect selection could be applied to improve such characters. Present findings agreed with the findings of Smith and Coyle (1997), Abo Arab (1999) and EL-Akheldar and El-Lawendey (2006).

Since the fixable type of epistasis additive \times additive was of great magnitude, thus direct selection on such type may be effective in improving such characters.

REFERENCES

- Abo-Arab, A.R. (1999).** Using biparental mating system for encouraging desirable recombinations in cotton. *Menofiya, J. Agric. Res.* 24(6):1999-2014.
- Basu, A.K. (1997).** Progress of breeding barbadense cotton in India. *J. Ind. Soc. Cotton. Improve.* 18:95-102
- Cruz, O. Dela (1981).** Genetical analysis of frego Bract and some quantitative characters in upland cotton M.Sc. Thesis Punjab. Agric. Univ. Ludhiana.
- Dhillan, S.S. (1978).** Biometrical analysis to predict the breeding potential in a cross of upland cotton. Ph. D. Thesis, Punjab Agric. Univ. Ludhiana.
- El-Akheldar, A.A.A. and M.A.M.EL-Lawendey (2006).** Inheritance of quantitative characters through triple test cross in cotton (*Gossypium barbadense* L.) *J. Agric. Res. Tanta Univ.* 32(1): 63-75.
- El-Mansy, Y.M. (2005).** Using genetic components for predicting new recombination in some cotton crosses. Ph.D. Thesis, Fac. Agric. Mansoura Univ. Egypt.
- Garg, H.R., T.H. Singh and G.S. Chahal (1987).** Genetical analysis through triple-test cross in the F_2 population of upland cotton. *Indian. J. of Agric. Sci.* 57(10): 701-704.
- Jinks, J.L. and J.M. Perkins (1970).** A general method for detection of additive, dominance and epistatic components of variation 111- F_2 and backcross populations. *Heredity*, 25: 419-429.
- Kearsey, M.J. and J.L. Jinks (1968).** A general method of detecting additive, dominance and epistasis variation for a material trait. I. Theory. *Heredity*, 23, 403-409.

- Khedr, A.I. (2003).** Genetical studies on cotton. Ph.D. Thesis, 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. Ind. J. Agric. Sci. 71(1) 62-64.
- Pooni, H. S., I. S. H. Kumar and G.S. Khush (1994).** A general method of detecting additive, dominance and epistatic variation for metrical traits Heredity 72:563-569.
- Smith, C.W. and G.G Coyle (1997).** Association of fiber quality parameters and within boll yield components in upland cotton. Crop Sci. 37:1775-1779.

التفاعل الغير اليلى والارتباط الوراثى فى القطن باستخدام التلقيح الرجعى الثلاثى للجيل الثانى

عادل عبدالعظيم ابواليزيد الاخضر ، ياسر محمد السيد المنسى

معهد بحوث القطن - مركز البحوث الزراعية

اجرى هذا البحث بغرض اختبار التفاعل الغير اليلى وتجزئة مكونات التباين الوراثى وكذلك حساب الارتباط بين جينات التفاعل الغير اليلى والجينات المضيفة والسائدة باستخدام التلقيح الرجعى الثلاثى للجيل الثانى حيث تم الحصول على ٣٠ عائلة من عائلات التهجين الرجعى الثلاثى للجيل الثانى من الهجين جيزه ٤٥ × كارشنسكى ٢. وظهرت النتائج ان التفاعل الغير اليلى *Epistasis* يلعب دورا هاما فى وراثه كل الصفات ماعدا صفة وزن اللوزة. كما ان الطراز المضيف × المضيف والمضيف × السيدى ، والسيدى × السيدى كانت معنوية لمعظم الصفات مع سيادة الطراز المضيف × المضيف واهميته .

كان التباين الوراثى المضيف معنويا لكل الصفات المدروسة وكان المكون الاعظم لجميع الصفات بينما كان التباين الوراثى السيدى معنويا لبعض الصفات وكان اقل فى الاهمية. اظهرت درجة السيادة سيادة جزئية اقل من ١ الصحيح مما يؤكد دور التباين الوراثى المضيف فى التحكم الوراثى لكل الصفات. اوضحت تقديرات قيم *F* غير معنوية لكل الصفات المدروسة وذلك بغض النظر عن الاشارة والتي تدل على ان السيادة غير موحية لهذا الصفات.

تشير نتائج الارتباط الى وجود ارتباط بين الجينات المضيفة لبعض الصفات وكذلك من حيث جينات التفاعل الغير اليلى وبما ان الطراز الاكثر اهمية من هذا التفاعل هو المضيف × المضيف بالتالى فان المربي يمكنه تحسين هذه الصفات عن طريق الانتخاب .

المجلة المصرية لتربية النبات ١٠ (١): ٣٧٧ - ٣٨٥ (٢٠٠٦)