ROLE OF EPISTASIS IN THE INHERITANCE OF CHARACTERS RELATED TO EARLINESS IN COTTON

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ABSTRACT: *Genetic relationships of morphological and physiological components of earliness and seed of cotton yield as well as fiber characters were evaluated following triple test cross analysis. Analysis of variance revealed significant differences between triple test cross families which reflect high amount of genetic variability among parental genotypes. Back crosses to the Russian variety (Kar2) appeared to improve most earliness characters, increase values for relative growth rate of boll and earliness index, and decrease values for boll maturation period and first fruiting node. Results from genetic analysis revealed that epistasis was be an integral part of genetic variation for relative growth rate of boll in the first and second stages, E.I., B.M.P as well as fiber characters. It was further reveled that (I) type additive x additive was the predominant effect for relative growth rate of boll, earliness index, boll maturation period, in the first stage, and Micronaire. Additive x dominance and dominance x dominance were significant for relative growth rate in the first and second stages and fiber length. The dominance components were larger than additive component for most characters resulting in degree of dominance more than one and suggesting some of over dominance gene effects in the genetic control of such characters. The estimates of F (covariance sums differences) values were significant and negative for earliness index, boll maturation period and micronaire indicating, unidirectional dominace genes and the dominance reducers alleles were more frequent. Results from prediction revealed that it could be feasible to predict as early as possible for transgrassive segregants which can surpass parental range for harvest index, root-shoot allomatic and fiber length.*

Genetic correlation revealed that additive and epistatic gene effect controlling most earliness characters were associated with each other. Since these correlation based on additive and additive x additive type of epistasis. Thus it could be easily fixed by selfing and selection between and within families would be effective to improve such characters.

Keywords: Triple test cross, additive, dominance, epistasis, cotton

INTRODUCTION

Earliness of crop maturity is an important objective in most cotton breeding programs, although the development factors that determine it are not completely understood. Early maturity is the end result of several growth

and physiological processes or components which are interrelated, and which presumably can be manipulated separately in the breeding process. The efficiency with these manipulations can be affected depends considerably on what we understand about the inheritance and interrelationships among the determinants of earliness.

Development of early mature and high yield cotton could be achieved by combining the genes of both traits. Therefore, cotton breeders are interested in incorporating new source of variation to enlage genetic variabilities in such quantitative traits (El-Mansy, 2005).

A review indicates considerable variation in how earliness is defined, and an unclear picture of how various components are inherited and related to each other. Also, it is apparent that no single criterion provides an adequate, functional as indicator of earliness, and that effective alteration of maturity can best be achieved by selecting for more than one component of earliness (Godoy and Palomo, 1999).

Several parameters have been used as indicators of earliness including relative growth rate of boll. The different patterns of growth might reveal the different expressivity of certain genes during various stages of development (Xia and Tang, 1995), boll maturation period and production rate index (Godoy and Palmo, 1999) which are controlled by additive genetic variance. (Xie *et al.,* 1996) noticed genotypic differences in the time of boll setting and the peak boll period showing ten days earlier than the control cultivar. Node number of first fruiting branch is one morphological characters that can be used as indicator for earliness of maturity (Azhar *et al.*, 2007).

The use of statistical method which could help cotton breeder for assessing and quantifying the genetic variation for earliness and yield characters is important. Triple test cross (TTC) is more widely applicable for studying populations of various kinds and has the least assumptions. In addition, to allowing an unambiguous detection of epistasis and unbiased estimation of additive and dominance genetic components could be useful (Keausy and Jinks (1968), Kearsy and Pooni (1996) and Zhu and Zhang (2007).

Jinks and Pooni (1976) reported that, if estimates of additive dominance and epistatic genetic variability are available we can assess the relative advantages and disadvantages of hybrids versus inbreeds and we can also predict the probabilities of obtaining inbreeds which are superior to the hybrids or to original inbreeds.

In the present investigation TTC technique was used to detect the epistasis, in addition to estimate the presence of additive and non-additive components of variation controlling earliness and other characters, and making predictions for the studied characters to help breeder for identifying the favorable combinations to improve the efficiency of selection and to determine the promising genotypes which may produce transgressive segregates in early generation.

MATERIALS AND METHODS

For the present genetic investigation the material was developed following the procedure of triple test cross given by Ketata *et al.* (1976). For this purpose, two diverse cotton genotypes, Giza 75 (L_1) and Karshenky 2 (L_2) of (*Gossypium barbadense* L.) differing in earliness and yield characters were crossed to produce F_1 (L_3) and used as a male lines. Nine true breeding genotypes i.e. Giza 87, Giza 70, Giza 85, Giza 77, Giza 89, Giza 80, Pima S6, Suvin and Australy were cross-classified into L1, L2 and L3 groups. Thus the 27 single crosses were developed and sown using randomized complete block design with three replications at Sakha Agric. Res. St. Farm during 2009 season. The plants were spaced 70 cm between rows and 30 cm between plants. On five random plants data were recorded on relative growth rate (RG.R) of boll weight at three development intervals, 10-20, 20-30 and 30-40 days after anthesis production rate index (P.R.I), Earliness index (EI), harvested index (HI) first fruiting node (F.F.N), boll maturation period (BMP), root-shoot allomatry (R.S.A.), seed cotton yield /plant (SCY/P) lint index (L_1), micronaire reading and fiber length (FL).

The means of T.T.C. crosses for each character were computed and therefore nine values in each cross were obtained (9 L_{1i}, 9L_{2i} and L_{3i}) computation of T.T.C. analysis was done on family means basis. Before proceeding to analysis, the families were subjected to the analysis of variance for L_{1i}, L_{2i} and L_{3i}, L_{1i} and L_{3i} sets of families. The within families analysis for (L_{1i}, L_{2i} and L_3i) were used to test the significant of epistasis ($\overline{L}_{1i} + \overline{L}_{2i} - 2\overline{L}_{3i}$) and additive ($\overline{L}_{1i} + \overline{L}_{2i} + 2\overline{L}_{3i}$) effects. The within families terms (L_{1i} and L_{2i}) were adequate for testing the significance of dominance ($\overline{L}_{1i} - L_{2i}$) effects (Kearsy and Jinks 1968 and Singh and Chaudhary, 1999). Additive and dominance components of the genetic variance in the presence of epistasis were computed according to (Jinks and Perkins, 1970). Also, the F value was computed from the covariance of sums/differences which equal to ($-^1/_8$ F), where F is the association dispersion of dominance alleles in the parental lines (Jinks and Perkins, 1970).

The means of T.T.C families (9 values) for each comparison for each character were used to compute epistasis, additive and dominance genetic correlation, respectively. The information obtained from TTC analysis provide a method to predict the likely proportion of recombinant lines that could be extracted (Jinks and Pooni, 1976). Data processing was performed using Excel and Minitab Computer Programme.

RESULTS AND DISCUSSION

The mean squares of the analysis of variance in Table (1) revealed significant and highly significant differences between TTC families for all characters studied indicating that L_{1i}, L_{2i} and L_{3i}) were significantly different

from each other and assured the variability between parental genotypes. Likewise, the results indicated that L_1, L_2 and L_3 families were significantly from each other in most characters especially earliness characters confirming the presence of high amount of genetic variability which could be assessed by means of triple test cross analysis.

The mean values of backcrosses L_{1i}, L_{2i} and L_{3i} exhibited significant differences for most characters studied (Table 2). Generally mean values of back crosses to the Russian variety Karshinky 2 (L_2) showed decreased values for R.G..R of boll weight at the first stage as well as earliness index, but showed decrease in rest characters. Also showed reduce in boll maturation period. On the reverse trend, backcrosses to Giza 86 (L_1) showed decrease values for R.G.R in the first stage and earliness index which appeared expressed in late maturation but gave high yield potential. In this regard Abo-Arab *et al.* (1998) and Khedr (2002).

However, values of backcross to F_1's (L_3) tended to be approximately to those L_1 for earliness characters and (L_2) for other characters. These results might reflect the conspicuous genetic constitution of the introduced variety Karshenky 2 which might posses many potentials to improve early maturation characters (Khedr, 2002 and El-Mansy, 2005).

Generally, backcrosses to Karshinky 2 (L_1) appeared to improve most of earliness characters than those of other parental (L_2). Such result might confirm the early maturation characteristics of the introduced Russian variety which might be useful for improving earliness in Egyptian cotton.

The magnitude of epistasis deviations were generally variable among the nine lines. Most of epistasis deviations values were significantly, positive or negative, different from zero. The positive epistasis deviation values were prevalent for most characters which reflected the great contribution of the parental testers. Moreover, negative epistasis deviation were predominant for earliness characters, RGR at the first and third stages, F.FN and B.M.P which reverse greater contribution of F_1 (Table 3).

Mean squares due to epistasis, additive and dominance effects (Table 4) revealed highly significant over all epistasis for R.G.R. at the first and second stage, EI, T.Dw 100 and fiber characters, while it was not significant for other characters. Further partitioning of epistasis revealed that additive x additive (i) type of epistasis was significant for RGR at the first stage, EI, B.M.P, and mcironaire value. Rest of the epistatic components (I + J) type, additive x dominance and dominance x dominance were significant for RGR at the first and second stage and fiber length. In this connection Abo-Arab *et al.* (1998) reported that epistatic effects played a role in RGR of boll at the first interval of boll development while Khedr (2002) and El-Mansy (2005) detected epistatic effects for RGR in all stages of boll development and most earliness characters as well as yield characters. On the other side, Soliman *et al.* (2008) found no significant overall epistasis or any component part (I) type or (I + J) type for any yield and fiber characters.

Table 1

Table 2

Table 3

Table 4

Though the estimates of additive and dominance components will be biased, as a result of epistasis. Ignoring such effects lead to lose information about epistasis, but, additive and dominance components would be biased. Thus, the breeder should take epistasis into account in producing genetic models.

The mean squares due to sums (additive) and differences (dominance) revealed highly significant for F.F.N, allomatic coefficient, L.I and fiber characters (Table 4). While, RGR in the first stage was controlled by additive coupled with epistatic gene effects. On the other side EI and BMP were controlled by dominance and additive x additive gene effects. Similar results were obtained by El-Akheder and El-Mansy 2006, Azhar *et al.,* 2007, Soliman *et al.,* 2008 and Kumar *et al.,* 2009).

As regards to the relative magnitude of additive (A) and dominance (D) components, D values were higher than those of A for most characters resulting in $\sqrt{\dfrac{D}{A}}$ values more than unity (Table 5) and suggesting some sort of over dominance gene effects in the genetic control of these characters, which is in agreement with Reddy *et al.* (1999); Khedr (2002), El-Mansy (2005) and Bhatti *et al.* (2006) was found.

The covariance of sums and differences (F) values (Table 5) significant and negative for EI, BMP and micronaire values revealing that the dominance was unidirectional among parents and the dominant reducing alleles was more frequent, for rest characters the correlation coefficients were insignificant revealing that umbidirectional dominance genes.

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

Triple test cross design may be considered as a useful source for information about prediction of new recombinant lines. These information will allow predictions of the proportion of inbreeds which could be as good as or superior to better parents (Pooni and Jinks, 1979) and (Eissa, 1994b). Prediction results (Table 6) revealed that it could be feasible to predict transgrassive segregants as early as possible which out perform parental range for H.I, T.DW, Allomatic R/S and fiber length. For the remaining characters the range of inbreeds likely exceeded parental range was relatively low. The obtained low proportion as a result of the prevalence of non-additive gene effects for most characters. Some investigators isolated high proportion of recombinant segregates for different cotton yield Attriubtes (Awaad and Hassan, 1996 and El-Mansy, 2005).

Table 5

Table 6

Partioning the total genetic correlation to its components of epistasis, additive and dominance genetic correlations. Table 7 revealed significant additive and epistatic genetic correlation between genes controlled RGR in the first stage with each of PRI and seed cotton yield/plant. While, increasing additive and epistatic genes controlling PRI were correlated with those increasing ones for seed cotton yield/plant which is correlated with lint index.

Additive gene effects controlled R.G.R1 were correlated significantly with those controlled EI, HI and F.F.N. Decreasing the period of boll maturation correlated with RGR of the second stage. This was true, since this stage was the final period for fiber development and start of wall thickness. In the same trend increasing growth period of boll in the third stage led to increasing wall thickness and resulting in increasing micronaire value. RGR of the third stage negatively, correlated epistatic genes with micronaire value. Since these correlation are based on additive and additive x additive type of epistasis it could be easily fixed by selfing and selection between and within families would be effective in improving these characters exhibited such associations.

Regarding to dominance genetic correlation (Table 7) revealed significant dominance gene correlation controlled RGR-I with those of PRI and HI. Also, between PRI and SCY/P.

Results of genetic correlations, generally, revealed the presence of significant additive, dominance and epistatic genetic correlations. These genetic correlations might due to a common genetic control, pleiotropy or linkage. Thus, improving efficiency of indirect selection could be applied. Xia and Tang (1995) reported that boll development was correlated with increasing in dry matter accumulation in the boll.

Table 7

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دورالتفاعل الغير أليلى "التفوق" فى وراثة الصفات المرتبطة بالتبكير فى القطن

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الملخص العربى

أجرى هـذا البحـث بغـرض دراسـة العلاقـة الوراثيـة بـين بعـض المكونـات المورفولوجيـة والفسيولوجية للتبكير ومحصول القطن الزهر وصفات التيلة باستخدام تحليل التلقيح الاختيارى الثلاثى. تـم دراسـة صـفات معـدل النمـو النسبى للـوزة عنـد ٣ مراحـل وهـى ١٠-٢٠ يـوم ، ٢٠-٣٠ يوم ، ٣٠-٤٠ يوم من التلقيح ، معامل التبكير ، دليل الحصاد ، ارتفاع أول عقدة ثمرية ، فترة نمو اللوزة كصفات تبكير ، محصول القطن الزهر ، معامل الشعر كصفات محصول ، قيمة الميكرونير ، طول التيلة.

أظهرت النتائج وجود اختلافات معنوية بين كل الصفات المدروسـة مما يدل علـى وجود كمية كبيرة من الاختلافات الوراثية كما أوضحت أن التهجين الرجعى للصنف الروسى كارشنكى٢ أظهر تحسين لمعظم صفات التبكير.

أوضحت نتائج التحليل الوراثى أن التفوق كان جزءا مكمـلا للتباين الوراثى لصفات معدل نمو اللوزة فـى المرحلـة الأولى والثانيـة ومعامل التبكير وفترة نمـو اللوزة وصفات التيلة كما أظهرت نتائج تجزئة التفوق الكلى أن النوع (المضيف × المضيف) كان الأكثر أهمية فى وراثة معدل نمو اللوزة فـى المرحلـة الأولى ، معامل التبكير وفترة نمـو اللوزة ، قراءة الميكرونير بينمـا النـوع (المضيف × السيادى) و (السيادى × السيادى) كان عالى المعنوية لصفات معدل نمو اللوزة فـى المرحلة الأولى والثانية وطول التيلة.

كان المكون السيادى مـن التبـاين الوراثى الأكبر والأكثـر أهميـة لمعظم الصفات المدروسـة وينعكس ذلك فى درجـة السيادة حيث كانت أكبر مـن الواحد الصحيح مما يعكس دور السيادة الفائقة فى وراثة هذه الصفات.

أوضحت تقديرا قيم (F) أن السيادة كانت موجهة فى إتجاه أحد الأبوين لصفات معامل التبكير وفترة نمو اللوزة وقراءة الميكرونير حيث كان معامل الإرتباط معنوى بينما كانت غير موجهة "التوزيع المتشتت للجينات السائدة بين كلا الأبوين" لباقى الصفات.

كما أظهرت نتائج التنبؤ إنه يمكن عمليا التنبؤ المبكر للنباتات التى بها إنعزالات فائقة وفاقت حدود الأباء لبعض الصفات والتى بها التباين المضيف عالى.

أظهرت نتائج الإرتباط الوراثى إلى وجود إرتباط وراثى بين الجينات المضيفة وجينات التفاعل الغير أليلى "التفوق" لمعظم صفات التبكير وحيث أن الطراز المضيف × المضيف هو الأكثر أهمية فى وراثة هذه الصفات مع وجود الفعل الجينى المضيف.

بالتالى فإن المربى يمكنه تثبيت هذه الصفات بسهولة عن طريق التلقيح الذاتى والإنتخاب بين المعاملات واختيار أحسن النباتات داخل العائلات المنتخبة لتحسين مثل هذه الصفات.

Table (1): The analysis of variance of triple test cross families for the traits studied.

S.O.V.	d.P	RgR1	RgR2	RgR3	PRI	EI	HI	FFN	B.M.W.	Mic	SCY/P	F.L	Li	Allo
BetweenT.T.C.families	26	0.03345**	0.02067**	0.0152**	0.2888**	369.6**	68.3*	3.126**	13.9900**	0.5319**	302.5**	4.776**	1.472**	0.00116**
Between L$_1$	8	0.02339**	0.02424**	0.0078*	0.1893*	135.7**	113.40**	0.651*	4.480**	0.4190**	160.500*	3.636**	0.5631**	0.0015**
L$_2$	8	0.01818	0.02225**	0.00818*	0.2042**	15.800	59.400	1.463**	0.583	0.1742**	185.300**	5.893**	0.5173**	0.0005**
L$_3$	8	0.03003**	0.01659**	0.01321**	0.099	22.5	44.27	1.024**	1.83	0.0870	58.90	5.479**	0.396*	0.0011**
Residual	2	0.1484**	0.01641**	0.06011**	1.4841**	4109.500**	19.825	28.0900**	154.2315**	4.1937**	2114.45**	2.0575*	13.2347**	0.0027**
Within T.T.C. families	52	0.00451	0.00507	0.0030	0.0716	15.2	28.8	0.173	1.23	0.0443	61.8	0.438	0.130	0.00011
Between L$_1$, L$_2$	17	0.03440**	0.02259**	0.0152**	0.3950**	497.2**	83.5*	4.266**	19.133**	0.7369**	434.900**	4.513**	2.0649**	0.0013**
Within families	34	0.00447	0.00627	0.00330	0.0568	15.6	37.5	0.212	0.901	0.0356	52.300	0.353	0.0707	0.0001

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

Table (2):   Mean values of tripe test cross families for the traits studied.

T.TC fami	10-20	20-30	30-40	PRI	EI	HI	F.F.N	BMP	Mic	SCY	F.L	LI	Allo
L$_1$	0.95	0.76	0.39	2.60	44.6	48.22	8.01	48.26	4.46	73.14	34.51	6.54	0.547
L$_2$	1.09	0.72	0.30	2.08	67.38	46.59	5.98	43.67	3.70	54.63	34.01	5.14	0.526
L$_3$	1.07	0.71	0.35	2.33	48.81	46.95	7.17	47.11	3.90	63.63	33.96	5.82	0.535
L.S.D.	0.110	0.116	0.090	0.439	6.398	8.807	0.683	1.820	0.345	12.902	1.086	0.592	0.017

Table (3):   Individual epistasis deviation for each male in T.T.C. for the traits studied.

Characters T.T.C. families	RGR 10-20	RGR 20-30	RGR 30-40	PRI	EI	HI	F.F.N	BMP	Mic	SCY	F.L	LI	Allo
1	-0.333	0.173	-0.463	0.0467	-0.15	6.9	-11.867	0.4	-1	-0.167	-4.433	-2.733	0.034
2	-0.3	-0.533	0.303	-0.033	-1.027	8.533	-9.333	0.2	-2.667	0.733	-32.533	2.2	-0.016
3	-0.233	-0.14	-0.213	0.247	-0.777	11.233	7.333	-0.733	-0.667	0	-14.733	2.133	0.013
4	0.3	-0.05	0.067	-0.073	0.247	17.867	5.5	-0.933	-3.667	0.733	5.267	-1.067	-0.043
5	0.467	0.023	0.237	-0.18	0.657	15.033	6.067	0.6	-2.667	0.967	18.267	2.567	0.005
6	-0.233	-0.37	0.043	-0.107	-0.283	10.067	-1.1	-1.533	-2	0.333	3.267	-0.533	0.022
7	0.1	0.03	0.273	0	0.617	13.567	5.233	-0.533	-2.667	0.567	10.8	1.2	0.032
8	0.833	-0.07	0.127	-0.13	0.517	18.667	-5.767	-0.667	-1.667	0.433	10.233	3.633	-0.026
9	-0.2	0.04	0.213	0.083	0.307	27.433	12.1	0	-3.667	-0.3	8.5	0.667	-0.011

Table (4): Analysis of variance and mean squares for test of epistasis, sums (additive), $L_{1i} + L_{2i} + L_{3i}$ and difference ($L_{1i} - L_{2i}$), dominance for the traits studied characters of triple test cross.

S.O.V	dF	RGR 10-20	RGR 20-30	RGR 30-40	PRI	EI	HI	F.F.N	B.M.W.	Mic	S.C.Y	F.L	Li	Allo
Overall epistasis	9	0.0178**	0.0204**	0.0051	0.1109	80.6763**	20.6305	0.1869	2.0905	0.1018*	72.6235	1.4799**	0.051	0.00021
(i) type	1	0.0298*	0.0128	0.0011	0.00043	619.2033**	2.4702	0.3793	15.8189**	0.4033**	0.7951	2.4100*	0.0059	0.000002
I + J type	8	0.0163**	0.0211**	0.0560	0.1247	13.1604	22.9005	0.1629	0.3445	0.0641	81.6020	1.3617**	0.0056	0.00023
Within families(L_{1i},L_{2i}, L_{3i})	52	0.0045	0.0050	0.0030	0.0716	15.200	28.800	0.173	1.230	0.0443	61.800	0.438	0.130	0.00011
Between sums	8	0.0131**	0.0052	0.0037	0.0843	24.6963	33.0903	0.8429**	1.6152	0.1631**	82.5688	3.3345**	0.4415**	0.00053**
Within families	52	0.0045	0.0050	0.0030	0.0716	15.200	28.800	0.173	1.230	0.0443	61.800	0.438	0.130	0.0011
Between difference	8	0.0061	0.0063	0.0058	0.0641	120.2458**	28.3174	0.8454**	4.4516**	0.1394**	75.7744	0.9879*	0.3901**	0.00048**
Within families	34	0.0045	0.00623	0.0034	0.0568	15.600	37.500	0.212	0.901	0.0356	52.300	0.353	0.0707	0.00010

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

Table (5): Estimates of additive (A), dominance (D) genetic components, degree of dominance $\left(\sqrt{\dfrac{D}{A}}\right)$ and covariance between sums and differences (F) in triple test cross for the traits studied.

Parameters	RGR 10-20	RGR 20-30	RGR 30-40	PRI	EI	HI	F.F.N	B.M.P	Mic	S.C.Y	F.L	LI	Allo
A	0.0076	0.002	0.006	0.0112	8.4412	3.8136	0.5960	0.3424	.1056	21.127	.5747	0.2769	0.0005
D	0.0021	0.00003	0.0032	0.0097	139.529	-12.2435	0.8445	4.7341	0.1384	31.2992	0.8465	0.4258	0.0005
$\sqrt{\dfrac{D}{A}}$	0.53	0.39	2.3	0.93	4.07	-1.79	1.19	3.72	1.14	3.19	0.57	1.24	1.00
F	-0.0448	-0.0248	-0.0288	-0.1200	-361.314*	-224.4512	3.0552	-14.0248*	-0.8992*	-19.8488	0.74	-0.252	-0.0033
r	0.390	0.225	0.429	0.172	0.732*	0.377	-0.487	0.799*	0.701*	0.033	-0.021	0.129	0.037

* Significant for 5% level of probability.

Table (6): Predicting the range of new recombinants expected to fall outside their parental range for the traits studied characters in triple test cross.

Parameters / Characters	[m]	[d]	[A]	Range of inbreeds	Probability	Proportion of inbreeds falling outside parental range %
RGR 1 stage	1.07	-0.14	0.0076	1.24-0.90	1.606	5.4799
RGR 2 stage	0.71	0.04	0.0002	0.74-0.68	2.828	2.477
RGR 3 stage	0.35	0.09	0.0006	0.40-0.30	3.674	0.0121
P.R.I	2.33	0.52	0.112	2.54-2.12	4.914	0.004
EI	48.81	-22.78	8.4412	54.62-43.00	7.841	0.0001
HI	46.95	1.63	3.8136	50.86-43.04	0.835	20.3270
F.F.N	7.17	2.03	0.5960	8.71-5.63	2.629	4.3965
B.M.P	47.11	4.59	0.3424	48.28-45.94	7.844	0.000
S.Cy/P	63.63	18.51	21.127	72.82-54.44	4.027	0.0024
LI	5.82	1.40	0.2769	6.87-+4.77	2.661	3.9070
MNic	3.90	0.76	0.1056	4.55-3.25	2.339	9.9031
F.L	33.96	0.20	2.5747	37.17-30.75	0.125	45.2240
Allomatric	0.535	0.20	0.0005	0.580-0.490	1.118	11.9000

Table (7): Estimates of epistasis (RE), additive (RA) and dominance (RD) genetic correlation coefficients among characters studied.

		RGR			P.RI	EJ	HI	F.F.N	B.M.P	S.CY/P	LI	Mic	F.L	R-S Allo
		10-20	20-30	30-40										
RGR2 20-30	RE	-0.356												
	RA	0.264												
	RD	0.159												
RGR3 30-40	E	0.122	-0.478											
	A	0.074	-0.519											
	D	0.195	-0.716*											
PRI	E	0.686*	0.304	-0.489										
	A	0.826*	0.046	0.456										
	D	0.774*	0.207	0.233										
EI	E	0.347	0.443	-0.049	0.575									
	A	0.792*	0.484	-0.021	0.581									
	D	0.554	-0.191	0.359	0.555									
HI	E	0.274	0.334	0.241	0.374	0.660*								
	A	0.684*	0.703*	-0.076	0.504	0.822*								
	D	0.910*	0.132	0.265	0.883*	0.501								
F.F.N	E	0.327	0.017	-0.014	0.078	-0.016	-0.169							
	A	-0.755*	-0.138	-0.250	-0.817*	-0.526	-0.674*							
	D	0.145	0.006	-0.138	0.232	-0.124	0.037							
B.M.P	E	0.018	-0.718*	0.377	-0.399	-0.696*	-0.459	-0.063						
	A	-0.155	-0.564	0.684*	0.291	-0.468	-0.421	0.040						
	D	-0.582	-0.409	0.256	-0.081	-0.038	-0.460	0.297						
S.Cy/P	E	0.698*	0.187	-0.452	0.946*	0.545	0.463	-0.084	-0.301					
	A	0.826*	0.033	0.413	0.989*	0.595	0.488	-0.775*	0.298					
	D	-0.480	0.458	0.110	0.835*	0.274	0.538	0.213	0.215					
LI	E	0.267	0.359	-0.617	0.704*	0.396	0.100	-0.057	-0.170	0.698*				
	A	0.324	0.342	0.430	0.422	0.332	0.681*	-0.664*	-0.088	0.341				
	D	0.393	0.215	-0.277	-0.180	-0.064	0.143	0.152	-0.786*	-0.480				
Mic	E	-0.327	0.589	-0.709*	0.203	-0.169	-0.051	0.019	-0.344	0.106	0.529			
	A	0.453	0.324	0.354	0.682*	0.352	0.550	-0.425	0.356	0.666*	0.519			
	D	-0.388	-0.340	-0.132	-0.196	0.343	-0.414	-0.009	0.571	-0.111	-0.473			
F.L	E	-0.286	0.586	-0.136	0.080	0.240	0.178	0.083	0.023	0.001	0.514	0.379		
	A	-0.547	-0.063	-0.045	-0.390	-0.420	-0.593	-0.714*	0.204	-0.327	-0.530	-0.022		
	D	0.510	0.499	-0.801*	-0.027	-0.326	-0.018		-0.266	-0.008	0.510	-0.067		
R.S allo	E	0.209	-0.411	0.283	-0.083	-0.538	-0.127	0.097	0.544	0.023	-0.484	-0.329	-0.294	
	A	0.183	-0.119	0.693*	0.447	0.058	-0.095	-0.165	0.335	-0.356	0.223	0.088	0.104	
	D	-0.391	0.452	-0.527	0.053	-0.714*	-0.320	0.124	0.331	0.346	-0.391	-0.067	0.434	

* Significant at 0.05 level of probability