Genetic Analysis of Yield and Its Components of Some Egyptian Cotton Crosses (*Gossypium barbadense* L.)

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ABSTRACT

Eight Egyptian cotton genotypes namely G.85, TNB, G.86, Suvin, G.93, C.B.58, G.92 and Pima S_6 were crossed using generation means analysis during 2012 and 2013 summer seasons to produce six generations that evaluated in summer 2014 season at Sakha Agricultural Research Station. The studied material were grown in randomized complete block design with three replications. Means of the six generations, P_1, P_2, F_1, F_2, BC_1 and BC_2 of four cotton crosses recorded for boll weight, seed cotton and lint yields per plant, lint percentage, number of bolls per plant and seed index, were subjected to scaling test and six parameters method to detect epistasis and estimates of genetic varianc components. Results showed that the additive dominance model was adequate to demonstrate the genetic variation and its importance on the inheritance of most studied traits. Non-allelic gene interaction was calculated and operating with the control of genetic variation in most studied traits. The epistatic effects, additive x additive (i) and dominance x dominance (h) were highly significant in most studied traits. Also, the inheritance of all studied traits was controlling by additive and non-additive genetic effects, but dominance gene effects play the major role in controlling the genetic variation of the most studied traits for all the studied crosses. Significant positive heterosis relative to mid-parents was found for all the studied traits in all crosses as well as, positive relative heterosis values above the better parent was found for all the studied traits except lint percentage in the third cross (G93X C.B58. Inbreeding depression estimates were found to positive and highly significant for all the studied traits in all crosses with few exceptions.

Key words: Genetic analysis, Lint yield, Six generations, Egyptian cotton.

INTRODUCTION

In Egypt, cotton is one of the most important economic crops, where it plays a vital role in agricultural and industrial development. In recent years, the total cultivated area began to decline, which requires working to increase the production of unit area overcome the shortage of cotton acrage. The breeders have to develop a new set of varieties with higher production, the true knowledge of the gene action for a various cotton traits is useful in making decisions with regard to appropriate breeding system. It is important to study the genetic diversity of Egyptian cotton varieties, which will be used for the development of new cotton genotypes. Knowledge of genetic diversity and relationships among breeding materials is essential to the plant breeders for improving this crop. Generation mean analysis is a quantitative genetic method be able to estimate additive, dominance and epistatic effects (Mather and Jinks, 1982). Genetic analysis using generation means have been used in cotton breeding to estimate the type of gene action controlling of quantative traits (Dani and Kohel, 1989; El-Disoqi *et al* , 2000; El-Akhedar, 2001; Iqbal and Nadeem, 2003; Ment *et al*., 2004; Esmail, 2007 and Dawwam., 2009), Heterosis breeding is an important genetic tool to facilitate yield enhancement and help enrich many other descriptive quantitative and qualitative traits. In cotton,

significant positive heterosis over-mid-and better parent was detected and found to be significantly positive for seed cotton yield, lint yield and number of bolls per plant, boll weight, lint percentage and, seed index (Jagtap, 1993; Nassar *et al*., 1995; Ismail, 1996; El-Disouqi and Ziena, 2001; El-Helw, 2002; Tuteja and Singh, 2002; Abd El-Barey 2003; Abdel-Hafez *et al*., 2007 and Emine and Oktay, 2010).

The expression of heterosis is influenced by genetic diversity of parents involved in hybridization and the characters under study. Therefore, hybrids between closely related genotypes which have been developed from very narrow germplasm give little or no heterosis and vice versa.

Gene action refers to behaviour or mode of genes expression in a genetic population. Knowledge of nature of gene action helps in the selection of parents for use in the hybridization program and choice appropriate breeding procedure for the genetic improvement various connotative. Hence, in sight into the nature of gene action involved in the expression of various connotative traits is essential to plant breeder for striating a judicious breeding program.

The present study aims to obtain useful information about gene action of some quantitative traits as well as the extent of hybrid vigour and inbreeding depression in four cotton crosses.

MATERIALS AND METHODS

Eight cotton genotypes belonging to *Gossypium barbadense* L. representing wide range of yield and yield components devoted to establish the experimental materials for this investigation. The present study was carried out during the period of 2012, 2013 and 2014 growing seasons, at the Experimental Farm of Sakha Agriculture Research Station, eight varieties were used for this study namely G.85, TNB, G.86, Suvin, G.93, C.B.58, G.92 and Pima S_6. The origin and pedigree of these genotypes are presented in Table (1).

In 2012 season, the eight genotypes were sown and four crosses were made to produce F_1 crosses: cross No. 1 (G.85 x TNB), Cross No. 2 (G.86 x Suvin), Cross No. 3 (G.93 x C.B.58) and Cross No. 4 (G.92 x Pima S_6). In 2013 season, crossing was made between F_1 hybrids of each cross and its two respective parents to produce the first (F_1 x P_1) and second (F_1 x P_2) backcross (BC_1 and BC_2). At the same time, crossing was made among the parents of each cross to produce F_1 seeds again, as well as some F_1 hybrids were selfed to produce the F_2 generation. In 2014 season, the six basic generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of each of the four crosses were sown in a randomized complete block design with three replications. Each replicate consisted of 2 rows each of the parents and F_1's, 5 rows of each back-cross and 10 rows for the F_2 populations. Rows were 4 m long and 70 cm apart and 40 cm between plants and all genotypes were thinned at one plant per hill. The recommended cultural practices were adopted all over the growing seasons. Data were recorded an individual plant basis as follows: boll weight (BW), seed cotton yield per plant (SCY/P), lint cotton yield per plant (LCY/P), lint percentage (L%), number of bolls per plant (No.B/P) and seed index (SI).

Statistical and genetic analysis:

Data of the six basic generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for each cross were statistically analyzed using (RCBD). The scaling testes (A,B, and C) were calculated for each trait to determine the adequacy of the additive-dominance model or the presence of non-allelic gene interaction according to Mather and Jinks (1982) as follows:

$$A = 2\overline{BC_1} - \overline{P_1} - \overline{F_1}$$
$$B = 2\overline{BC_2} - \overline{P_2} - \overline{F_1}$$
$$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2}$$

The three tests (scales) A, B and C should be zero within the limits of their standard errors. Significance of any of these scales is taken to indicate the presence of non-allelic interaction. The significant from zero were tested by using t-test as follows:

$$\text{Calculated} \pm t = \frac{\text{Effect}}{\sqrt{\text{Variance of effects}}}$$

The variance means for these estimates are obtained as follows:

$$VA = 4V(\overline{BC_1}) + V(\overline{P_1}) + V(\overline{F_1})$$
$$VB = 4V(\overline{BC_2}) + V(\overline{P_2}) + V(\overline{F_1})$$
$$VC = 16V(\overline{F_2}) + 4V(\overline{F_1}) + V(\overline{P_1}) + V(\overline{P_2})$$

Where: VA, VB, VC are the variances of different effects and VP_1, VP_2, VF_1, VF_2, VBC_1 and VBC_2 are the variances of mean for the different population of each cross.

Estimates of gene effects:

The means of the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2 generations) in each cross were used to estimate the six parameters type of gene action for each cross according to.

Jinks and Jones (1958) and Gamble (1962). Means of the six population of each cross were used to estimate the six parameters of gene effects as follows:

$$m = \overline{F_2} = \frac{1}{2}\overline{P_1} + \frac{1}{2}\overline{P_1} + 4\overline{F_2} - 2\overline{BC_1}$$

$$d = \overline{BC_1} - \overline{BC_2}$$

$$h = \overline{F_1} + 2\overline{BC_1} + 2\overline{BC_2} - 4\overline{F_2} - \frac{1}{2}\overline{P_1} - \frac{1}{2}\overline{P_2}$$

Table 1: The entry name, pedigree and origin of eight genotypes.

Genotypes	Species	Pedigree	Origin
G.85	*G. barbadense*	G.67 x C.B.58	Egypt
TNB	*G. barbadense*	Unknown	USA
G.86	*G. barbadense*	G.85 x G.81	Egypt
Suvin	*G. barbadense*	Unknown	India
G.93	*G. barbadense*	G.77 x Pima S_6	Egypt
C.B.58	*G. barbadense*	Unknown	USA
G.92	*G. barbadense*	G.84 x G.74 x G.68	Egypt
Pima S_6	*G. barbadense*	Unknown	USA

$$i = 2\overline{BC_1} + 2\overline{BC_2} - 4\overline{F_2}$$

$$j = \frac{1}{2}\overline{P_2} + \overline{BC_1} - \frac{1}{2}\overline{P_1} - \overline{BC_2}$$

$$L = \overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{BC_1} - 4\overline{BC_2}$$

Where, the parameters m, d, h, i, j. and L refer to mean effects, additive, dominance, additive x additive, additive x dominance, dominance x dominance gene effects, respectively, whenever the phenotypic variance for each character was partitioned into additive (D), dominance (H) and environmental (E) variances using Mather and Jinks (1982) as follows:

$$E = \frac{1}{3}(V_{\overline{P_1}} + V_{\overline{P_2}} + V_{\overline{F_1}})$$

$$D = 4V_{\overline{F_2}} - 2(V_{\overline{BC_1}} + V_{\overline{BC_2}})$$

$$H = 4(V_{\overline{F_2}} - \frac{1}{2}V_D - V_E)$$

The t test was performed as follows:

$$\pm T = \frac{\text{Effect}}{\sqrt{\text{Variance of effect}}}$$

Heterosis:

Estimates of heterosis (%) were calculated as the percent deviation of F_1 mean performance over that of either mid parents (MP) or better parent as follows:

Heterosis from the mid-parents:

$$H(\overline{MP})\% = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

Heterosis deviation $= \overline{F_1} - \overline{MP}$

Variance of heterosis deviation=

$$V\overline{F}1 + \frac{1}{4}(\overline{VP_1} + \overline{VP_2})$$

The t- test was used to determine the significance of heterosis

$$\text{Calculated } t = \frac{\text{Deviation}}{\sqrt{\text{Variance of deviation}}}$$

Heterosis over the better parent:

$$H(\overline{BP})\% = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

Heterosis deviation $= \overline{F_1} - \overline{BP}$

Variance of heterosis deviation $= V\overline{F_1} + V\overline{BP}$

The t-test was used to determine the significance of heterosis:

$$\text{Calculated } t = \frac{\text{Deviation}}{\sqrt{\text{Variance of deviation}}}$$

Inbreeding depression: its values were measured from the following equations:

$$ID = \frac{F_1 - F_2}{F_1} \times 100$$

Variance of inbreeding depression (VID) =

$$V\overline{F_1} + V\overline{F_2}$$

$$JID = \frac{F_1 - F_2}{\sqrt{VID}}$$

Estimation of phenotypic and genotypic coefficient of variability:

Phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) calculated according to Singh and Chaudhary (1977) as follows:

$$PCV = \frac{\sqrt{V\overline{F_2}}}{\overline{F_2}}$$

$$GCV = \frac{\sqrt{V\overline{F_2} - V\overline{E}}}{\overline{F_2}}$$

RESULTS AND DISCUSSION

The mean values and standard errors of the six generations in each cross for the studid traits were calculated and presented in Table (2). The results cleared that the mean values of F_1's were higher than either the eight parents and these results cleared that over dominance respectively towards the respective parents for all the studied traits except number of balls / plant in the third cross . With except L% in the third cross where the F, value was lower than P_2 but this value was higher than mid-parents values and these results indicated that there was a partial dominance.

Also, the F_1 values were higher than F_2's values for all the studied traits in the four studied crosses except L% and No. B/P in the third cross.

For BC_1 and BC_2 mean performances, the results indicated that the values were superior than P_1 or P_2 for most of studied traits for all studied crosses. Similar results were obtained by El-Disouqi and Zeina (2001), Abdel-Hafez et al. (2007), Esmail (2007), El-Beially and Mohamed (2008), Nidagundi et al. (2012) and Sarwar et al. (2012).

Testing for non-allelic interactions (A, B and C) together with the six parameters model and type of epistasis are calculated and given in table (3).

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Table 2: Mean performance and standard error of parents, F1, F2, and backcross generations in four cotton crosses for all studied traits .

Generations	Cross1	Cross2	Cross3	Cross4	Cross1	Cross2	Cross3	Cross4
	Boll weiht (B.W.)				Seed cotton yield per plant (SCY/P)			
P1	3.07 ± 0.02	3.51 ± 0.01	3.37 ± 0.03	2.99 ± 0.01	74.15 ± 1.80	107.12 ± 0.34	82.75 ± 1.17	64.57 ± 1.09
P2	3.27 ± 0.01	3.35 ± 0.01	3.38 ± 0.03	3.29 ± 0.02	68.49 ± 1.18	83.4 0 ± 1.21	57.21 ± 1.13	64.06 ± 2.63
F1	3.71 ± 0.02	3.95 ± 0.02	3.67 ± 0.02	3.85 ± 0.02	111.92 ± 1.43	147.7 ± 0.55	113.45 ± 0.81	109.13 ± 0.61
F2	3.44 ± 0.03	3.22 ± 0.04	3.52 ± 0.04	3.45 ± 0.04	85.29 ± 2.27	85.34 ± 2.92	64.79 ± 1.79	71.78 ± 2.59
BC1	3.69 ± 0.07	3.55 ± 0.09	3.58 ± 0.08	3.60 ± 0.07	96.89 ± 3.42	86.25 ± 4.05	83.63 ± 4.55	66.39 ± 3.27
BC2	2.25 ± 0.08	3.59 ± 0.08	3.51 ± 0.06	3.30 ± 0.09	62.56 ± 3.20	74.43 ± 3.35	79.80 ± 3.23	52.79 ± 1.62
	Lint cotton yield per plant (LCY/P)				Lint percentage (L%)(%			
P1	26.95 ± 0.67	39.72 ± 0.17	31.28 ± 0.44	22.87 ± 0.37	36.34 ± 0.15	37.08 ± 0.12	37.81 ± 0.10	35.44 ± 0.08
P2	24.37 ± 0.43	29.55 ± 0.43	20.25 ± 0.49	23.11 ± 0.97	35.58 ± 0.06	35.43 ± 0.07	35.39 ± 0.47	36.05 ± 0.14
F1	42.67 ± 0.57	57.95 ± 0.32	42.85 ± 0.38	42.34 ± 0.20	38.13 ± 0.15	39.23 ± 0.10	37.76 ± 0.14	38.51 ± 0.12
F2	32.04 ± 0.88	32.50 ± 1.09	24.86 ± 0.70	26.29 ± 0.96	37.53 ± 0.19	38.33 ± 0.26	38.27 ± 0.17	36.69 ± 0.21
BC1	36.13 ± 1.32	33.22 ± 1.57	31.40 ± 1.74	66.39 ± 3.27	37.30 ± 0.33	38.53 ± 0.22	37.52 ± 0.30	37.07 ± 0.32
BC2	22.87 ± 1.18	28.20 ± 1.33	29.97 ± 1.23	19.25 ± 0.57	36.60 ± 0.44	37.87 ± 0.32	37.54 ± 0.28	36.50 ± 0.25
	Number of bolls per plant (No.B/P)				Seed index (S.I)			
P1	24.09 ± 0.65	30.55 ± 0.10	24.52 ± 0.39	21.53 ± 0.35	8.41 ± 0.07	9.47 ± 0.04	8.48 ± 0.06	8.73 ± 0.17
P2	20.94 ± 0.37	24.91 ± 0.37	16.93 ± 0.38	19.48 ± 0.79	9.20 ± 0.14	8.52 ± 0.05	8.38 ± 0.13	8.99 ± 0.05
F1	30.18 ± 0.43	37.39 ± 0.17	17.30 ± 0.33	28.39 ± 0.23	10.0 ± 1 0.01	9.76 ± 0.04	10.13 ± 0.05	10.15 ± 0.02
F2	24.98 ± 0.69	26.24 ± 0.83	18.37 ± 0.46	20.73 ± 0.69	8.19 ± 0.11	8.26 ± 0.12	8.30 ± 0.09	8.19 ± 0.10
BC1	26.41 ± 1.07	24.21 ± 0.82	23.52 ± 1.37	18.54 ± 0.94	9.24 ± 0.25	8.02 ± 0.13	8.14 ± 0.27	8.74 ± 0.28
BC2	19,33 ± 0.98	21.04 ± 1.18	22.87 ± 1.05	16.08 ± 0.69	8.79 ± 0.24	9.77 ± .0.14	8.69 ± 0.21	8.06 ± 0.10

Cross 1: G.85 x TNB , Cross2 : G.86 x Suven , Cross3: G.93 x C.B.58 and Cross 4 : G.92 x Pima S6

Table 3: The scaling test and estimates of additive, dominance and interaction parameters in four cotton crosses for all studied traits.

Scaling test and Parameters	Cross1	Cross2	Cross3	Cross4	Cross1	Cross2	Cross3	Cross4	Cross1	Cross2	Cross3	Cross4
	Boll weight (B.W.)				Seed cotton yield per plant (SCY/P)				Lint cotton yield per plant (LCY/P)			
A	0.607**	-0.359*	0.014	0,362*	7.71	-82.24**	-28.94**	-40.92**	2.65	-31.22**	-11.32**	67.56**
B	-0.484**	-0.113	-0.127	-0.461*	-55.28**	-82.25**	-11.05	-67.60**	-21.30**	-31.09**	-3.16	-26.94**
C	0.024	-1.859**	-0.197	-0.187	-25.33**	-144.57**	-107.67**	-59.74**	-8.49**	-55.20**	-37.80**	-25.49**
d	0.446**	-0.045	0.069	0.266*	34.32**	11.82*	3.82	13.59**	13.26**	5.02*	1.43	47.13**
h	0.637**	1.910**	0.467*	0.792**	18.36	32.44**	111.16**	-3.97	6.85	16.19**	40.39**	85.46**
i	0.099	1.387**	0.084	0.088	-22.24	-20.01	67.96**	-48.78**	-10.16*	-7.13	23.31**	66.11**
j	0.545**	-0.123	0.071	0.412**	31.50**	-0.04	-8.95	13.34**	11.98**	-0.07	-4.08*	47.25**
L	-0.222	-0.914*	0.028	0.009	69.81	184.58**	-27.70	157.30***	28.82**	69.45**	-8.82	-106.72**
	Lint percentage (L%)				Number of bolls per plant (No.B/P)				Seed index (S.I)			
A	0.128	0.746	-0.524	-0.110	-1.45	-19.51**	-7.63**	-12.84**	0.063	-3.18**	-2.33**	-1.404*
B	-0.505	1.076	1.929**	-1.860**	-12.46**	20.21**	-1.36	-15.72**	-1.633**	1.26**	-1.14**	-3.02**
C	1.941*	2.320**	4.343**	-2.330**	-5.46*	-25.27**	-28.30**	-14.89**	-4.877**	-4.45**	-3.93**	-5.27**
d	0.699	0.659	-0.022	0.567	7.08**	3.17*	0.655	2.46*	0.453	-1.75**	-0.54	0.68*
h	-0.151	2.475*	-1.779	3.429*	-0.79	-4.80	28.75**	-5.78	4.511**	3.30**	2.16**	2.13**
i	-2.318	-0.497	-2.988**	0.365	-8.45*	-14.46**	19.30**	-13.67**	3.307**	2.53*	0.46	0.85
j	0.316	-0.164	-1.227**	0.873*	5.50**	0.348	-3.14*	1.43	0.848*	-2.22**	-0.59*	0.81**
L	2.696	-1.327	1.532	1.602	22.37**	54.18**	-10.31	42.23**	-1.737	-0.61	3.01**	3.57**

Cross 1 : G.85 x TNB , Cross2 : G.86 x Suven , Cross3: G.93 x C.B.58 and Cross 4 : G.92 x Pima S6

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

The results revealed the presence of nonallilic interaction for all the studied traits in all crosses, it is worthy to mention that at least one of the A, B and C tests was significant for the studied traits, except boll weight in the third cross. These results may be taken as an evidence for the failure of simple genetic model to a certain the genetic variation for these traits in the crosses bonding cross. Therefore, the six parameters model was applied in order to assess the genetic interaction types controlling the genetic variation. Similar results were obtained by Iqbal and Nadeem (2003), Ment *et al*. (2004), Abdel-Hafez *et al*. (2007), El-Beially and Mohamed (2008), and Dawwam (2009).

From the Table (3), the results cleared that both additive (d) and dominance (h) parameters were significant or highly significant in the tested crosses for some studied traits indicating that both additive and non- additive effects were important in the inheritance of most studied traits. The same findings were also reported by El-Disouqi and Ziena (2001), Abdel-Hafez *et al*. (2007), and El-Beially and Mohamed (2008).

The results also indicated that the dominance parameters (h) showed the largest in magnitude in most crosses for most of studied traits, indicating that dominance gene effects play the major role in controlling the genetic variation of the most studied traits. These results are in line with those reported by Iqbal and Nadeem (2003), Ment *et al*. (2004), and Emeni and Oktay (2010). With regard to the negative value of (h) observed for some studied traits indicated that the alleles responsible for less value of traits were over dominant over the alleles controlling high value as well as, the absence of significant (h) components would imply no dominance genetic differences or presence of ambidirectional dominance between the two parents and the dominant effects seemed to be not important in the genetic control of these crosses. The epistatic effects additive x additive (i) and dominance x dominance (L) were very important in the inheritance of these studied traits. These results were in agreement with Kalsy and Gorg (1988); Nassar *et al*. (1995), El-Disoqui and Ziena (2001), Abdel Hafez *et al*. (2007);

Esmail(2007); El-Beially and Mohamed (2008). The signs of (h) and (L) were opposite in all studied traits for most crosses suggesting duplicate type of non-allelic interaction in these traits. Kalsy and Gorg (1988) and Sarwar *et al*. (2012) found preponderance of non-additive gene action in the inheritance of cotton yield per plant and majority of its components. Jagtap (1993) stated that when additive effect of larger than the non-additive, it is suggested that selection in early segregation generations would be effective, while if the non-additive portion are larger than additive, the improvement of the characters need intensive

selection through later generation, when epistatic effects were significant for traits, the possibility of obtaining desirable segregates through intermating in early segregations by breaking undesirable linkage as it is suggested to adopt recurrent selection for handling the above crosses for rapid improvement. El-Disouqi and Zeina (2001), Abdel Hafez *et al*. (2007), Esmail (2007),El-Beially and Mohamed (2008), Nidagundi *et al*. (2012) and Sarwar *et al*. (2012) reported the same conclusion.

The (j) parameter additive x dominance was significant and highly significant positive or negative, indicating that dominance was towards direction of increasing and decreasing respectively for studied traits. However, Ramalingam and Sivasamy (2002), Iqbal and Nadeem (2003), and Nidagundi *et al*. (2012) stated that the preponderance of additive x dominance epistatic effect (highest magnitude) for the trait suggesting delayed selection and intermating the segregates followed by recurrent selection for improvement of these traits.

Heterosis relative to mid-parents, above the better parent, inbreeding depression % and phenotypic(PCV) and genotypic (GCV) coefficients of variability calculated and are presented in Table (4). Heterosis relative to mid-parents was positive and significant or highly significant for all the studied traits with all studied crosses and the same results also cleared that for the heterosis above the better parent for all the studied traits with except lint percentage for the third cross and these results indicating the importance of hybrid vigor for these traits. These results were opposite with Hendawy *et al*. (1994) El-Disouqi and Zeina (2001), Abdel-Hafez *et al*. (2007), and Emine and Oktay (2010).

Positive inbreeding depression values were obtained for all studied traits in all studied crosses with the except lint percent (L%) in the third cross. This finding indicated the accumulation of additive gene effects which in turn increased the mean expression of these traits, whereas, inbreeding depression was negative for lint percentage in the third cross suggesting that genes were not completely segregated and mainly due to non-fixable type. These results also cleared the presence of overdominance lint percentage which may be due to repulsion linkage of genes controlled these trait.

Estimates of phenotypic and genotypic coefficient of variability (PCV and GCV) values were presented in Table 4. The phenotypic coefficient (PCV) of variability values were higher than GCV for all studied traits in the four crosses and these results cleared that these traits are more sensitive to the environmental conditions. These results are in agreement and in line with those reported by El-Disouqi and Zeina (2001), Abdel-Hafez *et al*. (2007), Esmail (2007), and El-Beially and Mohamed (2008).

Table 4: Heterosis, inbreeding depression % and phenotypic (PCV) and genotypic (GCV) coefficient variability in four cotton crosses for all studied traits.

Traits	Cross No.	Heterosis		Inbreeding depression	Phenotypic Coefficient Variability (PCV)	Genotypic Coefficient Variability (GCV)
		M.P	B.P			
Boll weight	Cross 1	16.96**	13.41**	7.089**	12.58	12.39
	Cross 2	15.26**	12.67**	18.38**	15.54	15.48
	Cross3	11.32**	11.24**	6.39**	13.93	13.47
	Cross 4	22.37**	16.97**	10.36**	14.31	14.15
Seed cotton yield per plant	Cross 1	56.93**	50.94**	23.79**	37.59	36.77
	Cross 2	55.05**	37.89**	42.22**	48.43	48.25
	Cross3	62.13**	37.10**	42.89**	39.15	38.46
	Cross 4	69.68**	69.01**	34.22**	51.01	49.91
Lint cotton yield per plant	Cross 1	66.31**	58.35**	24.91**	38.75	37.93
	Cross 2	67.31**	45.89**	43.93**	47.52	47.30
	Cross3	66.28**	36.97**	41.99**	40.03	39.24
	Cross 4	84.17**	·83.24**	37.90**	51.64	50.58
Lint percentage	Cross 1	6.03**	4.91**	1.59*	7.20	7.03
	Cross 2	8.20**	5.79**	2.31**	9.56	9.49
	Cross3	3.17**	-0.122	-1.34**	6.17	5.14
	Cross 4	8.57**	7.64**	5.45**	8.07	7.95
Number of bolls per plant	Cross 1	34.05**	25.27**	17.23**	38.94	37.90
	Cross 2	34.85**	22.39**	29.82**	44.67	44.47
	Cross3	45.55**	23.03**	39.09**	35.79	34.66
	Cross 4	38.42**	31.82**	26.99**	47.12	45.77
Seed index	Cross 1	13.67**	8.79**	18.19**	19.58	19.21
	Cross 2	8.49**	3.09**	15.32**	21.12	20.96
	Cross3	20.17**	19.84**	18.08**	15.61	14.91
	Cross 4	14.48**	12.81**	19.30**	16.61	15.57

Cross 1 : G.85 x TNB, Cross2 : G.86 x Suven , Cross3: G.93 x C.B.58 and Cross 4 : G.92 x Pima S6

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

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الملخص العربى

التحليل الوراثى للمحصول ومكوناته فى بعض هجن القطن المصرى

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استخدم في هذه الدراسة ثمانية أصناف من القطن تابعة جميعها للقطن المصرى. وتم التهجين فيما بينهـا فـى موسمى ٢٠١٢، ٢٠١٣ للحصول على التراكيب الوراثية الآتية لبذور الجيل الأول والجيل الثانى بالإضافة للهجـن الرجعية الأول والثانى (F₁, F₂, BC₁, BC₂) الناتجة من الآباء الثمانية وذلك في محطة البحوث الزراعية بسخا وفـى موسم ٢٠١٤ تم تقييم هذه التراكيب الوراثية من الهجن الأربع بالإضافة للآباء الداخلة في كل هجـين فـى تجربـة قطاعات كاملة العشوائية في ثلاث مكرارت. وأجريت جميع العمليات المتبعة فى إنتاج محصول القطـن كمـا هـو موصى بها وتم الخف على نبات واحد وقد تم أخذ البيانات على الصفات التالية: متوسـط وزن اللـوزة، متوسـط محصول القطن الزهر للنبات، متوسط محصول القطن الشعر للنبات، تصافى الحليج، متوسط عدد اللوز المتفتح على النبات بالإضافة إلى صفة معامل البذرة.

واتضح من النتائج المتحصل عليها أن كل من التأثير الجيني المضيف وغير المضيف يـؤثران فـي تـوارث صفات الصفات المدروسة إلى جانب أن قيم التأثير السيادى(الغير مضيف) كانت أكبر من قيم التأثير الجينى الاضافى لمعظم الصفات الموجودة تحت الدراسة أظهرت أيضا النتائج وجود تفاعل غير أليلى بين الجينات وهذا يتضح من معنوية قيم (scaling test A, B, C) إلى جانب تأثير تفوقى ناتج من التفاعل الاضافى × الاضافى إلى جانب التفاعل السيادى × السيادى والذى ظهر في الكثير من الصفات تحت الدراسة في كل الهجن المدروسة. أظهرت النتائج أيضا أن قـيم قوة الهجين على أساس متوسط الآباء وأفضل الآباء كانت موجبة ومعنوية لكل الصفات تحت الدراسة لكـل الهجـن المدروسة ماعدا صفة تصافى الحليج فى الهجين الثالث (G93XC.B 58). وأظهرت النتائج أيضا أن قيم معامل التربية الداخلية أو الانخفاض الناتج عن التربية الداخلية كانت موجبة ومعنوية لكل الصفات تحت الدراسة تقريبا مما يعنـى أن متوسط الجيل الاول كان أعلى من الجيل الثانى لكل الصفات. وتوضح النتائج أنه يمكن الحصول على تراكيـب وراثية جيدة وإجراء تحسين متوقع لهذه الهجن عن طريق برامج الانتخاب أو الانتخاب المتكرر.