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Generation Mean Analysis for Yield, its Components and Quality Characteristics in Four Crosses of Egyptian Cotton (*Gossypium barbadense* L.)

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ABSTRACT

The objective of the present investigation was to estimate genetic variance components and type of gene action controlling yield, its components and quality characteristics of some cotton crosses, by means of the six populations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) of the four cotton crosses. Results revealed that the estimated mean effects (m) were highly significant for all traits in all crosses, indicated that these traits were quantitatively inherited. Additive and dominant gene effects were highly significant for No. of bolls/plant, boll weight in the fourth cross, 2.5% span length in the second cross, fiber fineness in the first and fourth crosses, with larger of dominance effects in magnitude than additive ones. Dominance, additive \times dominance and dominance \times dominance were at least significant for No. of bolls/plant in the first cross, seed and lint cotton yields in the first and second crosses, boll weight in the fourth cross, 2.5% span length and fiber fineness in the first cross and fiber strength in the second cross, indicated that these traits were greatly affected by dominance and their non-allelic interactions. Narrow-sense heritability and genetic advance were low in most cases due to the opposite directions of dominance and dominance \times dominance effects resulted in lower overall dominance variance. It could be concluded that heterosis over mid and better parent were highly significant in all crosses for No. of bolls/plant, seed and lint cotton yields/plant with low inbreeding depression.

Key words: Generation mean analysis, six populations, heterosis, heritability, genetic advance

INTRODUCTION

Cotton (*Gossypium barbadense* L.) is one of the most important fiber crops all over the world. In Egypt, its importance is derived from being one of the main sources of foreign currency as well as the principle raw material for the national textile industry and one of the important sources of edible oil (El-Saeidy *et al.*, 2003). The total cultivate began to decline in the last decade, which requires working to increase the production of unit area to compensate the shortfall in the cultivated area. Knowledge of genetic diversity and relationships among breeding materials is essential to the plant breeders for improving the crop (Abd El-Haleem *et al.*, 2010).

Gamble (1962) reported that epistatic gene effects are present in sufficient magnitude in quantitative traits which may alter the breeders account for the breeding method which must be followed. If the additive genetic variance is of major importance, the intra-population selection will be considered as the most effective procedure for gathering the favorable genetic constitutions. If dominance variance especially over-dominant is predominant, then the hybrid program for

commercial purpose may be the appropriate choice. Therefore, the estimation of gene action and the inheritance of the traits especially seed yield is an interesting procedure for the breeders in order to formulate the most efficient breeding method to bring about the maximum improvement of the attribute in question. Both additive and non-additive genetic effects control seed cotton yield (Kalsy and Garg, 1988; Tyagi, 1988; Deshpande and Baig, 2003). However, McCarty *et al.* (2004) reported additive×additive epistatic effects for the inheritance of seed cotton yield and Basbag *et al.* (2008) reported heterotic effects in some cotton crosses. Pathak (1975) used six populations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) of five upland cotton (*Gossypium hirsutum* L.) crosses to evaluate genetic effects for fiber traits.

Improvement in textile processing has led to increased emphasis on breeding cotton for improved fiber properties. Fiber fineness determines the texture of cotton fiber. Cotton fiber may be classified as soft and silky or coarse and harsh.

Cotton breeding program based on the genetic information of traits needs to be improved (Rahman and Mahk, 2008). Therefore, the present study aimed to obtain useful information about gene action of yield and quality characters as well as the extent of hybrid vigour, heritability and genetic advance in the four cotton crosses.

MATERIALS AND METHODS

The experiments reported herein were carried out during 2007, 2008 and 2009 seasons. The four initial crosses Giza 45×Pima S₇, Giza 88×Pima S₇, Giza 90×Suvin and Giza 88×Suvin which designated in the text as first, second, third and fourth cross, respectively. Pedigree, origin and characteristics of the parental varieties are shown in Table 1.

The crosses were developed in 2007 season at the Faculty of Agriculture farm, Tanta University. In 2008 season, F_1 plants were selfed and backcrossed to each parent to obtain the F_2 , BC_1 and BC_2 for each cross. In parallel, the hybrid seeds were obtained by crossing each two parents of each cross as F_1 seeds.

The six populations; P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of each cross were sown at the experimental farm, Faculty of Agriculture, Tanta University during 2009 season as follows: two ridges for each parent and F_1 's, seven ridges for BC's and twelve ridges for the F_2 plants. Two, seven and twelve ridge plots were used to reduce intergenotypic competition between generations and to sample adequately the genetic variability within generations.

Each ridge of one side comprised of 20 hills spaced at 20 cm apart and 60 cm wide. Hills were thinned later leaving one plant per each hill. All cultural practices were followed for the ordinary cotton fields in the area.

Data were recorded on an individual guarded plant of the six populations for each cross where 20, 20, 25, 200, 120 and 120 plants were chosen from P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of each cross, respectively, to collect the following traits:

- No. of bolls/plant
- Boll weight in grams
- Seed cotton yield (g)/plant
- Lint cotton yield (g)/plant
- Lint percentage which calculated as lint cotton yield/seed cotton yield×100
- Seed index
- 2.5% span length
- Fiber fineness
- Fiber strength

Table 1: Pedigree, origin and main characteristics of the parental varieties

Genotypes	Pedigree	Origin	Characteristics
Giza 45	Giza 7×Giza 28	Egypt	An extra long staple, extra fineness, strong lint and late maturity
Giza 88	Giza 77×Giza 45	Egypt	An extra long staple, it is characterized by fiber quality and high yielding
Giza.90	Giza 83×Dendera	Egypt	The newest long staple variety for Upper Egypt. It is characterized by high lint percentage and high yield
Pima S ₇	(6614-91-9-3)×(6907-513-509-501)	USA	Long staple, heat tolerance, short plant height, early maturity
Suvin	Sujata×Vincent	India	A new long staple. It is characterized by earliness, heavy boll weight, high yield and short stature

Statistical and genetic analysis: To determine the presence or absence of non- allelic interactions, scaling test as outlined by Mather (1949) was used. The quantities A, B, C and D and their variances have been calculated to test adequacy of the additive-dominance model in each case. Where:

$$A = 2\overline{BC}_1 - \overline{P}_1 - \overline{F}_1$$

$$B = 2\overline{BC}_2 - \overline{P}_2 - \overline{F}_2$$

$$C = 4\overline{F}_2 - 2\overline{F}_1 - \overline{P}_1 - \overline{P}_2$$

$$D = 2\overline{F}_2 - \overline{BC}_1 - \overline{BC}_2$$

And

$$V(A) = 4V(\overline{BC}_1) + V(\overline{P}_1) + V(\overline{F}_1)$$

$$A(B) = 4V(\overline{BC}_2) + V(\overline{P}_2) + V(\overline{F}_1)$$

$$A(C) = 16V(\overline{F}_2) + 4V(\overline{F}_1) + V(\overline{P}_1) + V(\overline{P}_2)$$

$$A[d] = 4V(\overline{F}_2) + V(\overline{BC}_1) + V(\overline{BC}_2)$$

The standard error of A, B, C and D is worked out by taking square root of respectively variances. The t-values are calculated by dividing the effects of A, B, C and D by the respectively standard error. The calculated t-values were compared with tabulated value of t at 5% levels of probability in each test, the degrees of freedom (df) is sum of (df) of various generation involved. The significance of A and B scales indicate the presence of all types of non-allelic gene interactions. The significance of C scale suggests (dd) types of epistasis. The significance of D scale reveals (aa) gene interactions, significance of C and D scale indicates (aa) and (dd) type of gene interactions (Singh and Narayanan, 1993).

Genetic analysis of generation means to give estimates of the types of gene effects were obtained using the relationships given by Gamble (1962).

Jinks and Jones (1958) however, used following formulae to estimate m, a and d components in the absence of non-allelic interactions:

$$m = \frac{1}{2}\overline{P}_1 + \frac{1}{2}\overline{P}_2 + 4\overline{F}_1 - 2\overline{BC}_1 - 2\overline{BC}_2$$

$$d = \frac{1}{2}\bar{P}_1 - \frac{1}{2}\bar{P}_2$$

$$h = 6\bar{BC}_1 + 6\bar{BC}_2 - 8\bar{F}_2 - \bar{F}_1 - \frac{3}{2}\bar{P}_1 - \frac{3}{2}\bar{P}_2$$

where, Their variances have been computed using following formulae:

$$V_m = \frac{1}{4}V\bar{P}_1 + \frac{1}{4}V\bar{P}_2 + 16V\bar{F}_1 + 4V\bar{BC}_1 + 4V\bar{BC}_2$$

$$V_d = \frac{1}{4}V\bar{P}_1 + \frac{1}{4}V\bar{P}_2$$

And

$$V_h = 36V\bar{BC}_1 + 36V\bar{BC}_2 + 64V\bar{F}_2 + V\bar{F}_1 + \frac{9}{4}V\bar{P}_1 + \frac{9}{4}V\bar{P}_2$$

- $SE(m) = (Vm)^{\frac{1}{2}}$, $SE[d] = (Vd)^{\frac{1}{2}}$ and $SE[h] = (Vh)^{\frac{1}{2}}$
- $t(m) = m/SE(m)$, $t[d] = d/SE[d]$ and $t[h] = h/SE[h]$

Broad+sense heritability (H^2) for F_2^- generation was estimated based on the equation:

$$H_2 = \frac{V_g}{V_g + V_e} \times 100$$

The genetic variance (V_g) and environmental (V_e) were estimated according to Mansur *et al.* (1993) as follows:

$$V_g = V_{F_2} - V_e$$

$$V_e = n_e^{-1}(n_{P_1}V_{P_1} + n_{P_2}V_{P_2} + n_{F_1}V_{F_1})$$

where, $n_e = n_{P_1} + n_{P_2} + n_{F_1}$ and n_{P_1} , n_{P_2} and n_{F_1} are the number of plants of P_1 , P_2 and F_1 generations in each cross, respectively.

Narrow-sense heritability (h^2) for F_2^- generation was estimated as proposed by Warner (1952). Where:

$$h^2 = \frac{VF_2(VBC_1 + VBC_2)}{VF_2} \times 100$$

The Phenotypic (PCV%) and Genotypic (GCV%) coefficient of variation were estimated as formulae developed by Burton (1952).

The expected genetic advance from selection (G_a) was calculated as the formulae proposed by Johnson *et al.* (1955), using the selection differential (k) equal 2.06 for 5% selection intensity and heritability in narrow sense.

The predicted genetic advance where the expected genetic gain upon selection was expressed as percentage of F_2 mean ($G_a\%$) was calculated following Miller *et al.* (1958).

The amount of heterosis was expressed as the percentage deviation of F_1 mean performance from mid-parent and better parent. Inbreeding depression was calculated as the difference between the F_1 and F_2 means as a percentage of F_1 . The "t" test was used to determine the significance of these deviations where the standard error (SE) was calculated as follows:

$$\text{SE for mid parental heterosis } (\bar{F}_1 - \overline{\text{MP}}) = (\overline{\text{VF}}_1 + \frac{1}{4}\overline{\text{VP}}_1 + \frac{1}{4}\overline{\text{VP}}_2)^{\frac{1}{2}}$$

$$\text{SE for better parental heterosis } (\bar{F}_1 - \overline{\text{BP}}) = (\overline{\text{VF}}_1 + \overline{\text{VBP}})^{\frac{1}{2}}$$

$$\text{SE for inbreeding depression } (\bar{F}_1 - \bar{F}_2) = (\overline{\text{VF}}_1 + \overline{\text{VF}}_2)^{\frac{1}{2}}$$

where, the t is the deviation/SE at the corresponding degrees of freedom.

RESULTS AND DISCUSSION

The data presented in Table 2 revealed the mean performance of the six generations and variance of mean advanced from the four crosses of cotton for the traits in view. These data used to calculate the salling test and six parameters as Gamble procedure. At least one of the scales was significant in the four crosses for all studied traits, except lint percentage in the second and third crosses boll weight in the first and second crosses seed index in the first cross; 2.5% span length, fiber fineness and fiber strength in the third and fourth crosses, where all scales were not significant. However, the significance of any one of the scale reveals the presence of non- allelic interaction as pointed out in Table 3. Hence, for non expected traits additive- dominance model was not sufficient to explain most the genetic variation for the expression of these traits. This show that epistatic effects were contributed to the inheritance of these traits in the crosses pointed out and this might suggest that, the inheritance of these traits is complex and polygenic (Warnock *et al.*, 1998). On the other side, the insignificant of all scales for the excepted traits mentioned, indicating a simple additive-dominance model was adequate for estimating the genetic components of variance of these traits. This indicates that, selection could be practiced effectively in F_2 generation for improving theses traits. However, additive gene effects were highly significant in all cases, except lint percentage in the second cross and fiber strength in the fourth cross, indicating that the additive genes were more important than dominant ones in controlling the inheritance of these traits.

The estimated mean effects (m), which reflects the contribution due to over-all mean plus the locus effects and interaction of the fixed loci was found to be highly significant for all studied traits in all crosses, indicted that these traits were quantitatively inherited. From the obtained results (Table 3), it could be detected that, additive [d] and dominant [h] gene effects were highly significant for number of bolls/plant and boll weight in the cross IV, 2.5% span length in the cross II, fiber fineness in the cross I and IV, indicating that both additive and dominance were important for the inheritance of these traits.

It could be observed that dominance effects are several times larger than additive one and this might indicate that dominance gene effects play the major role in controlling the genetic variation of most studied traits. These results are in the same trend with those reported by

Table 2: Analysis of the six generations advanced from four crosses of cotton for yield, its components and some technological characteristics

Traits	Statistic	Cross I (Giza 45×Pima S ₇)						Cross II (Giza 88×Pima S ₇)					
		F ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂	F ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
No. of bolls/plant	\bar{X}	26.080	39.290	42.000	42.38	43.890	43.530	32.990	39.550	43.090	42.670	41.920	42.010
	S _x ²	0.575	1.022	0.075	1.991	0.908	0.959	0.400	0.449	0.325	1.061	0.445	0.475
Seed cotton yield/plant (g)	\bar{X}	74.230	115.360	131.200	130.010	131.440	132.370	97.830	115.670	130.260	127.790	127.440	129.590
	S _x ²	0.435	0.697	0.868	2.282	1.180	0.624	1.371	0.300	1.985	1.511	0.870	0.518
Lint cotton yield/plant (g)	\bar{X}	25.050	43.550	49.920	51.140	50.340	52.540	36.740	43.420	50.300	47.710	47.960	48.980
	S _x ²	0.035	0.000	0.110	2.319	1.252	0.834	0.046	0.084	0.135	0.362	0.121	0.180
Lint percentage (%)	\bar{X}	33.750	37.560	38.050	38.990	37.860	39.600	37.560	37.540	38.620	37.340	37.640	37.790
	S _x ²	0.023	0.013	0.027	0.201	0.116	0.081	0.100	0.016	0.044	0.189	0.156	0.031
Boll weight (g)	\bar{X}	2.850	2.940	3.130	3.070	3.000	3.050	2.970	2.980	3.080	3.000	3.040	3.090
	S _x ²	0.005	0.003	0.002	0.005	0.002	0.003	0.003	0.003	0.004	0.006	0.003	0.003
Seed index	\bar{X}	10.050	9.690	10.330	10.480	10.510	10.130	10.540	9.690	10.360	10.310	10.510	10.000
	S _x ²	0.005	0.005	0.008	0.009	0.002	0.007	0.014	0.007	0.005	0.036	0.023	0.012
2.5% span length (cm)	\bar{X}	35.340	33.530	30.270	34.810	35.410	35.310	34.630	33.530	33.290	33.510	33.460	32.970
	S _x ²	0.002	0.001	0.002	0.109	0.035	0.050	0.015	0.002	0.003	0.022	0.013	0.001
Fiber fineness	\bar{X}	3.310	4.330	3.800	3.790	3.650	3.540	3.820	4.330	3.690	3.660	3.900	3.580
	S _x ²	0.001	0.001	0.001	0.002	0.001	0.001	0.006	0.000	0.003	0.013	0.004	0.008
Fiber strength	\bar{X}	11.900	8.550	11.860	11.430	11.670	10.500	10.540	8.520	10.530	10.500	10.480	10.430
	S _x ²	0.014	0.016	0.008	0.039	0.007	0.028	0.001	0.001	0.006	0.009	0.004	0.002

Table 2: Continue

Traits	Statistic	Cross I (Giza 45×Pima S ₇)						Cross II (Giza 88×Pima S ₇)					
		P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
No. of bolls/plant	\bar{X}	43.120	38.690	45.100	42.170	42.520	42.720	33.680	38.690	46.440	46.080	47.090	50.860
	S _x ²	0.068	0.078	0.191	0.164	0.040	0.121	0.018	0.109	0.192	0.265	0.130	0.309
Seed cotton yield/plant (g)	\bar{X}	130.520	96.790	134.680	133.280	130.280	126.920	97.830	96.820	142.870	141.080	135.330	137.010
	S _x ²	1.121	0.762	1.150	4.461	2.427	1.340	0.271	0.619	0.760	1.649	0.988	0.576
Lint cotton yield/plant (g)	\bar{X}	48.790	34.410	52.080	49.980	49.330	47.040	36.500	34.410	54.980	53.660	51.210	50.490
	S _x ²	0.530	0.292	0.375	0.560	0.442	0.046	0.019	0.094	0.157	0.265	0.148	0.039
Lint percentage (%)	\bar{X}	37.380	35.550	38.670	37.500	37.860	37.070	37.310	35.550	38.480	38.040	37.840	36.850
	S _x ²	0.039	0.072	0.063	0.081	0.012	0.059	0.019	0.022	0.038	0.034	0.004	0.024
Boll weight (g)	\bar{X}	3.030	2.500	2.990	3.160	3.070	2.970	2.910	2.500	3.080	3.060	2.880	2.700
	S _x ²	0.002	0.001	0.003	0.005	0.002	0.003	0.000	0.000	0.001	0.004	0.002	0.001
Seed index	\bar{X}	9.750	9.040	10.130	10.070	9.950	10.090	10.540	9.040	10.590	10.220	10.270	10.180
	S _x ²	0.008	0.004	0.005	0.011	0.004	0.005	0.002	0.004	0.015	0.017	0.007	0.009
2.5% span length (cm)	\bar{X}	36.620	31.240	36.740	36.010	35.610	35.520	37.530	35.420	38.140	37.340	37.980	37.070
	S _x ²	0.005	0.012	0.011	0.024	0.009	0.010	0.013	0.025	0.009	0.096	0.017	0.065
Fiber fineness	\bar{X}	2.750	2.450	3.080	3.100	2.980	2.900	2.190	2.350	2.460	2.480	2.360	2.320
	S _x ²	0.001	0.000	0.003	0.010	0.002	0.004	0.000	0.001	0.001	0.002	0.001	0.000
Fiber strength	\bar{X}	10.410	9.690	10.280	10.180	10.080	10.140	9.590	9.500	10.130	10.070	9.950	10.090
	S _x ²	0.001	0.001	0.012	0.010	0.004	0.004	0.001	0.001	0.003	0.003	0.015	0.002

Table 3: Estimates of scaling test and type of gene action of four cotton for nine traits

Traits	Cross	Scaling test										
		A	B	C	D	m±SE	[d]±SE	[h]±SE	[i]±SE	[j]±SE	[l]±SE	
No. of bolls/plant	I	19.708**	5.768**	20.150**	-2.663	42.378±1.411**	0.363±1.366	14.635±6.308**	5.325±6.270	6.970±1.505**	-30.80±2.47**	
	II	7.755**	1.373	11.963**	1.418	42.673±1.030**	-0.087±0.959	3.986±4.603	-2.835±4.545	3.191±1.064**	-6.36±3.48	
	III	-3.175**	1.643	-3.348**	-0.908	42.165±0.405**	-0.193±0.402	6.011±1.829**	1.815±1.807	-2.409±0.445**	-0.28±1.57	
	IV	14.063**	16.590**	19.093**	-5.780**	46.083±0.514**	-3.770±0.663**	21.816±2.493**	11.560±2.448**	-1.264±0.687	-42.21±3.48**	
Seed cotton yield/plant (gm)	I	57.438**	18.185**	68.028**	-3.798	130.005±1.511**	-0.938±1.343	44.004±6.699**	7.595±6.612	19.626±1.445**	-83.03±7.75**	
	II	26.780**	13.250**	37.135**	-1.447	127.790±1.229**	-2.158±1.178	26.408±5.668**	2.895±5.452	6.765±1.344	-42.93±7.48**	
	III	-4.638	22.373**	36.440**	9.353*	133.275±2.112**	3.363±1.941**	2.315±8.867	-18.705±9.298**	-13.505±2.118**	0.97±11.75	
	IV	29.960**	34.325**	83.940**	9.828	141.080±1.284**	-1.678±1.251	25.895±5.799**	-19.655±5.713**	-2.183±1.337	-44.63±7.44**	
Lint cotton yield/plant (gm)	I	25.715**	11.610**	36.100**	-0.613	51.135±1.523**	-2.198±1.444	16.850±6.750*	1.225±6.742	7.053±1.447	-38.55±8.42**	
	II	8.873**	4.235**	10.093**	-1.508	47.713±0.601**	-1.023±0.549	13.241±2.676**	3.015±2.644	2.319±0.577**	-16.12±3.36**	
	III	-2.213	7.593**	12.555**	3.588*	49.978±0.748**	2.287±0.698**	3.308±3.120	-7.175±3.303**	-4.903±0.833**	1.79±4.37	
	IV	10.935**	11.585**	33.775**	5.628	53.660±0.515**	0.718±0.432	8.268±2.275**	-11.255±2.234*	-0.325±0.464	-11.26±4.47*	
Lint percentage (%)	I	3.923**	3.598**	8.555**	0.518	38.990±0.448**	-1.743±0.444**	1.363±2.010	-1.035±2.001	0.162±0.454	-6.48±2.55*	
	II	-0.905	-0.575	-2.965	-0.743	41.17±1.216**	0.013±0.170	2.562±3.081	-	-	-	
	III	-0.325	-0.070	-0.250	0.072	41.27±1.147**	0.915±0.167**	1.525±3.085	-	-	-	
	IV	-0.110	-0.320	2.335**	1.383*	38.038±0.184**	0.987±0.195**	-0.713±0.862	-2.765±0.833**	0.105±0.220	3.19±1.09**	
Boll weight (gm)	I	0.018	0.025	0.255	0.106	3.315±0.219**	-0.045±0.004**	-0.185±0.735	-	-	-	
	II	0.093	0.223	0.055	-0.130	2.781±0.081**	0.022±0.002**	0.913±0.622	-	-	-	
	III	0.115	0.455**	1.145**	0.288	3.163±0.071**	0.092±0.068	-0.352±0.328	-0.575±0.314	-0.170±0.074*	0.005±0.41	
	IV	-0.233**	-0.190*	0.688**	0.555	3.063±0.061**	0.180±0.056**	-0.736±0.272**	-1.110±0.270**	-0.021±0.056	1.53±0.340**	

Table 3: Countinue

		Six parameters as gamble procedure									
		Scaling test									
Traits	Cross	A	B	C	D	m±SE	[d]±SE	[h]±SE	[i]±SE	[j]±SE	[l]±SE
Seed index	I	0.640**	0.240	1.520**	0.320	10.475±0.097**	0.380±0.095**	-0.180±0.444	-0.640±0.433	0.200±0.108	-0.24±0.58
	II	0.118	-0.040	0.317	0.120	10.52±0.473**	0.426±0.07**	-0.158±1.895	-	-	-
	III	0.033	1.020**	1.228**	0.087	10.065±0.104**	-0.138±0.093	0.559±0.463	-0.175±0.454	-0.494±0.108**	-0.88±0.58
	IV	-0.595**	0.735**	0.135	-0.002	10.223±0.129**	0.082±0.123	0.807±0.586	0.005±0.572	-0.665±0.128**	-0.15±0.76
2.5% Span length (cm)	I	5.220**	6.828**	9.818**	-1.115	34.805±0.330**	0.100±0.292	-1.936±1.445	2.230±1.444	-0.804±0.294**	-1.4.28±1.76**
	II	-1.003**	-0.883**	-0.715	0.585*	33.505±0.147**	0.490±0.117**	-1.963±0.639**	-1.170±0.634	-0.060±0.134	3.055**±0.77
	III	-2.140	3.060	2.700	0.890	38.63±0.255**	2.69±0.065**	-0.116±1.513	-	-	-
	IV	0.182	0.583	0.145	-0.310	39.0±0.687**	1.055±0.097**	3.685±3.03	-	-	-
Fiber fineness	I	0.190**	-1.038**	-0.072	0.388**	3.790±0.039**	0.107±0.038**	-0.796±0.178**	-0.775±0.174**	0.614±0.041**	1.623±0.23**
	II	0.288	-0.853**	-0.880**	-0.158	3.663±0.113**	0.318±0.109**	-0.065±0.506	0.315±0.502	0.570±0.115**	0.250±0.64
	III	0.128	0.268	1.053	0.328	3.103±0.054**	0.833±0.079**	-0.175±0.279	-	-	-
	IV	0.077	-0.178	0.450	0.275	2.725±0.169**	-0.085±0.013**	-0.985±0.430*	-	-	-
Fiber strength	I	-0.415*	0.600	1.545**	0.680	11.425±0.198**	1.170**±0.185	0.272±0.885	-1.360±0.876	-0.508±0.205*	1.175±1.11
	II	-0.115	1.803**	1.868**	0.090	10.495±0.094**	0.050±0.082	0.819±0.419*	-0.180±0.410	-0.959±0.085**	-1.508±0.52**
	III	-0.533	0.318	0.073	0.144	10.700±0.257**	0.360±0.012**	-0.562±0.952	-	-	-
	IV	0.185	0.547	0.907	0.087	9.985±0.229**	0.045±0.024	0.995±0.547	-	-	-

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

Abd El-Haleem *et al.* (2010) and Karademir and Gencer (2010). However, the three quality characters i.e., 2.5% span length, fiber fineness and fiber strength could be excepted from the latest conclusion, where additive gene effects were highly significant in most crosses and larger in magnitude than dominant ones, which reflect the great importance of additive genes in the inheritance of these traits.

Jagtap (1986) stated that when additive effects are larger than non-additive ones, it is suggested that selection in early segregating generations would be effects, while if the non-additive portion are larger than additive one, the improvement of the characters need intensive selection through later generation. These conclusion are in the same line with those found by Dhillon and Singh (1980), Singh *et al.* (1983), Lin and Zhao (1988), Mert *et al.* (2003), Murtaza (2005) and Esmail (2007).

With regard to the negative values observed in most cases either with main effects; [d] and [h] or the non-allelic interactions; [i], [j] and [l], these might indicate that, the alleles responsible for less values traits were over dominant over the alleles controlling high value. However, it could be detected that the effects of additive and dominant genes were in the opposite direction, where its signs were not similar. This was true for all traits in all crosses, except No. of bolls/plant in the first cross, seed cotton yield/plant in the third cross, lint cotton yield/plant in the third and fourth crosses, seed index and 2.5% span length in the fourth cross and fiber strength in the first, second and fourth crosses.

In all crosses for all studied traits, it could be observed that the signs of dominance [h] and dominance \times dominance [l] gene effects were opposite, except seed and lint cotton yield in the cross III; 2.5% span length and fiber strength in the cross I, suggesting duplicated type of non-allelic interaction in these traits.

Since none of the sings of [h] were similar to the [i] type of epistasis, it was concluded that no complementary type of interaction was present in the genetic control of the studied traits. However, dominance [h], additive \times dominance [j] and dominance \times dominance [l] which referred as non-additive genetic variance were at least significant for number of bolls/plant in the cross I, seed and lint cotton yields in the crosses I and II, boll weight in the cross IV, 2.5% span length and fiber fineness in the cross I and fiber strength in the cross II. This would indicate that, these traits were greatly affected by dominance as main effect and their non-allelic interactions as epistatic effects. These results are in good agreement with those reported by Bhardwaj and Kapoor (1998), Esmail *et al.* (1999), El-Disouqi and Ziena (2001), Abdul-Hafeez *et al.* (2007), Esmail (2007), El-Beially and Mohamed (2008) and Abd El-Haleem *et al.* (2010). However, when epistatic effects were significant for a trait, the possibility of obtaining desirable segregates through inter-mating in early segregations by breaking undesirable hnkage could be available or it is suggested to adopt recurrent selection for handling the above crosses for rapid improvement. Abo El-Zahab and Amein (2000), Dong *et al.* (2006), El-Beially and Mohamed (2008) and Hendawy *et al.* (2009) came to the same conclusion.

Heterosis over mid-parent and better parent, inbreeding depression, heritability in broad and narrow-senses, genetic advance, phenotypic and genotypic coefficient of variations are presented in Table 4. Highly significant heterosis over mid-parent and better parent was observed in all crosses for number of bolls/plant, seed and lint cotton yields/plant with low inbreeding depression.

Table 4: The genotypic and phenotypic analysis of four cotton crosses for nine traits

Traits	Cross	Heterosis (%)				Heritability (%)		Genetic advance			
		\overline{MP}	\overline{BP}	P	ID(%)	H ²	h ²	G _a	G _a (%)	PCV(%)	GCV(%)
No. of bolls/plant	I	24.48**	6.87**	1.41	-0.90	73.87	6.19	0.179	0.424	3.33	2.86
	II	18.80**	8.95**	2.08	0.97	63.62	13.28	0.282	0.660	2.41	1.93
	III	10.27**	4.59**	1.89	6.52**	27.96	1.58	0.013	0.031	0.96	0.11
	IV	28.35**	20.04**	4.09	0.75	57.29	9.41	0.099	0.216	0.76	0.33
Seed cotton yield/plant	I	38.41**	13.74**	4.61	0.91	70.19	20.92	0.651	0.500	1.16	1.12
	II	22.03**	12.61**	2.63	1.89	15.46	8.08	0.204	0.160	0.96	0.18
	III	18.49**	3.18	1.25	1.04	77.09	15.56	0.060	0.045	1.58	1.39
	IV	46.81**	46.05**	90.20	1.25	65.68	5.15	0.136	0.096	0.73	0.71
Lint cotton yield	I	45.58**	14.65**	3.70	-2.42	97.72	18.01	0.565	1.105	2.98	2.94
	II	25.53**	15.87**	3.06	5.15**	74.56	16.78	0.208	0.436	1.26	1.09
	III	25.22**	6.76**	1.46	4.05*	29.07	12.85	0.198	0.396	1.50	0.81
	IV	55.06**	50.64**	18.77	2.38*	64.19	14.55	0.154	0.288	0.96	0.77
Lint percentage	I	7.29**	1.33	1.36	-2.47*	89.35	1.84	0.017	0.044	3.64	1.09
	II	2.87*	2.82*	72.00	3.31**	71.96	1.16	0.010	0.028	1.16	0.98
	III	6.07**	3.48**	2.25	3.03**	28.30	12.60	0.074	0.197	0.76	0.41
	IV	5.64**	3.14**	2.33	1.17	20.35	17.70	0.067	0.176	0.52	0.22
Boll weight	I	7.77**	6.12**	5.00	1.60	41.51	7.55	0.011	0.368	2.37	1.52
	II	2.72	2.03	4.00	0.66	48.39	6.45	0.010	0.348	2.62	1.82
	III	7.97**	-1.32	0.85	-6.04*	60.00	8.00	0.012	0.368	2.23	1.73
	IV	13.70**	5.86**	1.85	0.32	85.26	18.42	0.023	0.764	2.05	1.86
Seed index	I	4.66**	2.78*	2.55	-1.45	36.17	3.19	0.006	0.061	0.93	0.56
	II	2.42*	-1.70	0.58	0.38	76.66	4.72	0.018	0.179	1.84	1.61
	III	7.83**	3.90**	2.05	0.59	46.73	19.63	0.042	0.415	1.03	0.70
	IV	8.23**	0.57	1.08	3.49*	55.09	9.58	0.025	0.249	1.26	0.94
2.5% span length	I	-12.11**	14.35**	-4.63	-15.00**	98.50	21.58	0.147	0.421	0.95	0.94
	II	-2.34*	-3.90**	-1.45	-0.66	71.43	36.86	0.112	0.315	0.44	0.37
	III	8.28**	0.33	1.04	1.98*	78.19	21.81	0.070	0.194	0.43	0.38
	IV	4.59**	1.65	1.59	2.10*	84.37	14.79	0.094	0.252	0.84	0.76
Fiber fineness	I	-0.65	14.50**	-0.05	0.00	50.00	6.67	0.005	0.140	1.02	0.72
	II	-9.33**	-3.40	-1.52	0.81	76.56	7.81	0.018	0.497	3.09	2.70
	III	19.38**	26.23**	3.22	-0.65	87.87	37.37	0.076	0.451	3.20	3.00
	IV	8.17**	4.25*	2.17	-0.82	62.50	25.00	0.023	0.931	1.81	1.43
Fiber strength	I	15.95**	-0.42	0.97	3.63*	68.78	12.94	0.053	0.463	1.74	1.44
	II	10.45**	0.09	0.99	0.028	63.64	23.86	0.046	0.439	0.89	0.71
	III	2.29*	-1.25	0.64	0.97	51.53	24.48	0.049	0.482	0.97	0.69
	IV	6.13**	5.63**	13.00	0.69	43.94	16.13	0.018	0.178	0.55	0.37

***Significant at 0.05 and 0.01 levels of probability, respectively, \overline{MP} : Heterosis over mid-parent, \overline{BP} : Better parent, P: Potence ratio, ID: Inbreeding depression, H₂: Heritability in broad, h₂: Narrow-senses, PCV: Phenotypic coefficient of variance, GCV: Genotypic coefficient of variance

Over-dominance (p<+1) is not only the case of heterotic effects but also the non-allelic interactions might be mainly caused this heterosis for these traits. Significant heterotic effects relative mid-parent and better parent were detected in all crosses for lint percentage, boll weight and seed index, except the cross II for boll weight, where the two values were not significant, the cross I for

lint percentage and cross VI for seed index, where the values over better parent were positive but insignificant. However, the heterotic effects in most cases pointed out were attributed to over dominance, where potency ratio exceeded the unity ($p < +1$). The low values of inbreeding depressions reflects the low reduction in the mean of F_2^- generation due to the direct effect of homozygosity, this low reduction might be attributed to the low sensitivity of the present materials to the inbreeding processes. Abdalla (2007) reported that cotton has a relatively low inbreeding depression.

Narrow-sense heritability estimates were generally lower than the corresponding broad sense heritabilities, indicating the presence of non-additive gene action. The low h^2 estimates which ranged from 1.16-36.86%, suggested that the inheritance is complex. From six generations of four crosses, environmental, additive and dominance variances were estimated to calculate heritability and genetic advance. In most cases, narrow-sense heritability and genetic advance were very low due to the opposite direction of additive and dominance variances. Moreover, the opposite directions of dominance and dominance \times dominance effects results in lower overall dominance variance (Table 3). The genetic gains as a parameter for selection efficiency are related to genetic variability and selection intensity. Low genetic gains which an expected results due to the low values of h^2 and genotypic (GCV%) and phenotypic (PCV%) coefficient of variability, indicated that phenotypic effect is mainly controlled by environmental variation. Therefore, for selection of the best genotype, it should concentrate mainly on yield components more than yield itself.

CONCLUSIONS

From this investigation it could be concluded that (1) dominance gene effects play the major role in controlling the genetic variance of yield and most of its components, while additive genes were the predominant for quality characters (2) heterosis over mid and better parent were highly significant in all crosses for No. of bolls/plant, seed and lint cotton yields/plant with low inbreeding depression and (3) narrow-sense heritability and genetic advance were very low due to the opposite direction of additive and dominance variances.

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