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GENERATION MEANS ANALYSIS FOR SOME QUANTITATIVE CHARACTERS IN COTTON

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ABSTRACT: ***The present work aimed mainly at analysis of gene effects using means of the six populations, P_1, P_2, F_1, F_2, BC_1 and BC_2 for ten characters in two crosses namely cross I (Giza 96 x 10229) and cross II (Giza 89 x 10229). The experiment was grown in a randomized complete blocks design with four replications at Sakha Agricultural Research Station, Kafr El-Shiekh, Egypt. The mean values F_1 population was better than the respective parents, F_2, BC_1 and BC_2 populations for most of the traits studied for the two crosses. Highly significant and positive (desirable) heterosis relative to mid- and better-parents for most traits studied was found in the two crosses. On the other hand, the heterosis relative to mid- and better-parent was highly significant and negative (useful) for micronaire reading of the two crosses. Inbreeding depression was highly significant and positive for all traits studied in the two crosses, except number of bolls/plant in the two crosses and micronaire reading in cross II (Giza 89 x 10229) which exhibited highly significant and negative inbreeding depression. The values of phenotypic coefficient of variation (PCV) were higher than the values of genotypic coefficient of variation (GCV) for all the traits studied of the two crosses. Six parameters gene effects exhibited that the dominance gene effect, were higher than additive gene effects for all traits studied in the two crosses, indicating predominant role of dominant component of gene action in inheritance of these traits. High heritability in broad-sense estimates (>50%) were detected for all the traits studied at the two crosses except seed cotton yield/plant at cross II (Giza 89 x 10229) and boll weight of cross I (Giza 96 x 10229). The heritability in narrow-sense estimates ranged from 3.29% to 35.70% for boll weight and uniformity index of cross I (Giza 96 x 10229), respectively. The expected genetic advance (Δg%) under 10% selection of the individual plants in the F_2 generation ranged from 10.37% to 92.28% for uniformity index of cross II (Giza 89 x 10229) and lint cotton yield/plant of cross I (Giza 96 x 10229), respectively.***

Key words: ***Cotton, Gossypium barbadense, Heterosis, Inbreeding depression, Heritability, Expected genetic advance.***

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 acreage. 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 which is able to estimate additive, dominance and epistatic effects. Abd-El-

Haleem *et al.,* (2010) reported that additive and dominant gene effects were highly significant for number of bolls/plant, boll weight, 2.5% span length and fiber fineness in the most crosses. Dominance, additive x dominance and dominance x dominance were significant for number of bolls/plant, seed and lint cotton yields, boll weight, 2.5% span length, fiber fineness and fiber strength in most studied crosses. Both additive and dominance type of genetic effects were significant for all the studied traits except monopodia. The additive x additive (i) and dominance x dominance (l) gene interactions were significant for all the studied traits. El-Seoudy *et al*., (2014) found that heterosis values over the mid- and the better-parent varied between positive or negative significant and highly significant for most of the studied traits. Dominance estimates were higher than the additive estimates for all the studied traits, indicating more importance for dominance gene effects in the inheritance of these traits. Estimates of heritability in both broad and narrow-senses for yield and its components were high for all the studied traits under investigation. Deore *et al*., (2014). Additive, dominance gene effects and epistatic gene interactions additive × additive, additive × dominance and dominance × dominance also played an important role in the inheritance of all the studied fiber traits in one or other cross. AL-Hibbiny *et al*., (2015) found that highly significant positive (desirable) relative to mid and better-parents for most studied traits in the two crosses, while had highly significant heterosis negative (useful) relative to mid- and better-parent for fiber fineness of the cross II. The highest values of phenotypic (PCV) and genotypic (GCV) coefficient of variations were obtained for number of bolls/plant, lint cotton yield/plant and fiber fineness traits in the cross I and boll weight trait in the cross II. The results indicated that the PCV had high values than GCV in all traits in the two crosses. AL-Hibbiny *et al*., (2019) showed that the inbreeding depression for most crosses were significant and negative for most the studied traits, but the other crosses showed significant and positive inbreeding depression. The results indicated that the non-additive genetic variance was larger than the additive genetic variance in F_1 and F_2 crosses with respect to all the studied traits, except No. of bolls/plant (F_1 and F_2 crosses), seed and lint cotton yield in F_2 crosses. Mabrouk *et al.,* (2018) cleared that the following crosses Giza 70 x Giza 86, Giza 70 x Australy 13 and Australy 13 x Pima S_4 demonstrated best heterosis relative to mid- and better-parent for some studied yield traits, while the crosses Giza 70 x Giza 92 and Giza 70 x Giza 86 indicated best heterosis relative to mid-parent for uniformity ratio. The results pointed out that the non-additive genetic variances were larger than the additive genetic variance with respect to all the studied traits except, lint percentage, fiber length and fiber strength characters. The results, also revealed that broad-sense heritability (h^2_b%) estimates were larger than the corresponding values of narrow-sense heritability (h^2_n%) of all studied traits, except fiber length.

The present work was carried out to study the heterosis, inbreeding depression, phenotypic and genotypic coefficients of variability, gene effects, heritability and genetic advance for yield, its components and fiber properties in the two crosses (Giza 96 x 10229) and (Giza 89 x 10229).

MATERIALS AND METHODS

Genetic material and field procedure

The genetic materials used in the present investigation included three

cotton varieties belong to (*Gossypium barbadense* L.). Two of them are Egyptian cotton varieties; Giza 96 and Giza 89. The other one is Australian strain (10229). The experiments investigation was carried out at Sakha Agricultural Research Station at Kafr El-Shiekh Governorate, Egypt during the three successive seasons from 2017 to 2019.

In 2017 season, the parental cultivars were crossed to produce F1 hybrid seeds for two crosses (Giza 96 x 10229) and (Giza 89 x 10229). In 2018, each of F_1 was backcrossed to both parents to produce BC1 and BC2 generations. The parents were also crossed for more hybrid seeds. The F_1 was selfed to obtain F_2 seeds. In 2019 year, the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for each of the two crosses were evaluated separately in a randomized complete blocks design with four replications. Each replicate consisted of 24 rows, 10 rows for F_2, 5 rows for BC_1 and BC_2 crosses (segregating generations), and 3 rows for each non-segregating generations P_1, P_2 and F_1. Each row was 4 meters long and 0.60 m width and comprised 10 hills. Hills were spaced at 40 cm apart and thinned to one plant per hill. Agricultural practices were done as research recommended.

The data on an individual plant basis of the six populations were recorded for the following traits:

- **Number of bolls/plant (NB/P)**
- **Lint cotton yield/plant (LCY/P.g)**
- **Boll weight (BW.g)**
- **Upper half means (UHM).**
- **Fiber strength (FS).**
- **Seed cotton yield/plant (SCY/P.g)**
- **Lint percentage (L%)**
- **Seed index (SI g)**
- **Micronaire reading (MIC).**
- **Uniformity index (UI).**

All fiber properties were measured in the laboratory of the Cotton Technology Research Department, Cotton Research Institute at Giza.

Statistical and genetic procedures

Heterosis and inbreeding depression (%) were estimated according to Miller *et al.,* (1958). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated using the formula suggested by Dudley and Moll (1969). The analysis was proceeded to estimate the various gene effects using the six parameter genetic models of Jinks and Jones (1958) and Hayman (1958). The scaling tests (A, B and C) were calculated for each trait to detect the adequacy of the additive dominance model or the presence of non-allelic gene interaction according to Mather and Jinks (1982). Genetic advance ΔG (10% selection intensity) and genetic advance as a percentage of F_2 mean (ΔG%) were estimated as given by Allard (1960).

RESULTS AND DISCUSSION

Mean performances

The mean values and standard errors of the six generations in each cross for all the traits studied were calculated and presented in Table (1). The results for all traits indicated that the performance of P_1 (Giza 96) was better than P_2 (10229) for all studied traits, except lint percentage and micronaire reading traits of the cross I (Giza 96 x 10229), also the P_1 (Giza 89) was better than P_2 (10229) for all traits studied, except lint percentage, micronaire reading, fiber strength and uniformity index traits of the cross II (Giza 89 x 10229). The F_1 population was better than the respective parents, F_2, BC_1 and BC_2 populations for most the traits studied of the two crosses. Also, the relation between F_2 and F_1 revealed that there is different behavior, where the F_1 was better than F_2 all the traits studied

Table 1. Means and standard errors of the six populations (P_1, P_2, F_1, BC_1, BC_2 and F_2) for all traits studied in Cross I (Giza 96 x 10229) and Cross II (Giza 89 x 10229).

Traits	crosses	P_1	P_2	F_1	BC_1	BC_2	F_2
Number of bolls/plant	I	42.57±0.52	39.35±0.60	46.04±0.50	46.72±0.29	47.04±0.86	47.03±0.89
	II	41.14±1.41	39.35±0.60	42.20±0.58	44.84±0.84	44.77±1.14	44.55±1.47
Seed cotton yield/plant (g)	I	149.13±0.13	108.13±0.25	163.98±1.28	160.58±0.24	163.38±1.68	161.43±1.91
	II	158.38±3.85	108.13±0.25	162.38±1.35	156.81±1.72	159.55±1.91	162.11±2.65
Lint cotton yield/plant (g)	I	56.44±0.15	43.80±0.21	67.49±0.82	65.96±0.59	67.70±0.54	66.21±0.92
	II	63.23±1.02	43.80±0.21	67.38±0.46	63.55±0.76	64.70±0.93	66.78±1.25
Lint percentage	I	37.85±0.10	40.51±0.16	41.16±0.41	41.08±0.33	41.44±0.13	41.02±0.37
	II	39.95±0.33	40.51±0.16	41.50±0.20	40.53±0.25	40.55±0.23	41.20±0.35
Boll weight (g)	I	3.51±0.04	2.75±0.05	3.56±0.03	3.44±0.02	3.48±0.05	3.43±0.03
	II	3.86±0.07	2.75±0.05	3.85±0.06	3.50±0.06	3.57±0.06	3.63±0.08
Seed index (g)	I	10.43±0.05	9.23±0.07	10.63±0.09	10.43±0.05	10.53±0.09	10.38±0.11
	II	11.78±0.08	9.23±0.07	11.90±0.11	11.58±0.08	11.48±0.09	11.63±0.13
Micronaire reading	I	4.13±0.02	3.78±0.05	3.78±0.05	3.73±0.03	3.83±0.06	3.60±0.07
	II	4.33±0.12	3.78±0.05	3.75±0.03	3.93±0.05	3.85±0.09	3.95±3.95
Upper half means	I	37.20±0.18	32.65±0.30	37.35±0.20	35.28±0.33	35.11±0.08	35.78±0.38
	II	34.78±0.20	32.65±0.30	34.93±0.13	32.95±0.30	32.45±0.30	33.35±0.46
Fiber strength	I	11.68±0.09	10.35±0.03	11.85±0.13	11.50±0.13	11.63±0.05	11.60±0.15
	II	9.33±0.15	10.35±0.03	10.45±0.06	10.18±0.09	10.28±0.09	10.03±0.13
Uniformity index	I	87.95±0.21	86.45±0.29	88.45±0.43	87.00±0.29	87.18±0.32	88.30±0.55
	II	86.35±0.18	86.45±0.29	86.80±0.39	86.15±0.36	86.10±0.09	86.58±0.38

except number of bolls/plant in the two crosses and micronaire reading in the cross II (Giza 89 x 10229). The mean values of the segregating generations compared with their parents was higher than the higher parent for most traits studied in the two studied crosses, indicating appreciable amount of genetic variability for these characters in the corresponding crosses. Generally, the relationship among non-segregating and segregating generations would be more accurate when illustrating the genetic parameters.

Heterosis and inbreeding depression

Heterosis as percentage over mid- and better-parents and inbreeding depression values are presented in Table (2). The results noticed highly significant and positive (desirable) heterosis relative to mid-parent for number of bolls/plant, seed cotton yield/plant, lint cotton yield/plant, boll weight, seed index and fiber strength in the two crosses and lint percentage at cross I (Giza 96 x 10229), while highly significant and negative (desirable) for micronaire reading in the two crosses. On the other hand, the heterosis relative to better-parent was highly significant and positive (desirable) for (seed index in the two crosses), (lint cotton yield/plant, lint percentage, boll weight, micronaire reading and fiber strength at cross I Giza 96 x 10229) and (number of bolls/plant and seed cotton yield/plant at cross II Giza 89 x 10229), but highly significant and negative (desirable) for micronaire reading at cross II Giza 89 x 10229. Significant heterobeltiosis in cotton is attributed to the major combined effects of additive × dominance and dominance × dominance gene effects. Absence of significant heterosis in other cases could be due to the internal cancellation of heterosis components.

Concerning the inbreeding depression in F_2 relative to F_1 (Table 2), the results exhibited highly significant and positive inbreeding depression for all traits studied in the two crosses, except number of bolls/plant in the two crosses and micronaire reading in cross II (Giza 89 x 10229) which exhibited highly significant and negative inbreeding depression. The coincidence of sign and magnitude of heterosis and inbreeding depression was detected for most traits in the two crosses. This is logic and expected since the expression of heterosis in F_1 will be followed by a considerable reduction in F_2 due to homozygosity. (El-Hashash 2004). Abd-El-Haleem *et al*., (2010) reported that, highly significant and positive heterosis relative to mid- and better-parents were found for number of bolls/plant, boll weight, seed cotton yield/plant, lint cotton yield/plant and lint percentage traits in most studied crosses. They added that the inbreeding depression estimates were found to be significant or highly significant and positive for number of bolls/plant, boll weight, seed cotton yield/plant, lint cotton yield/plant and lint percentage traits in all studied crosses. AL-Hibbiny *et al* (2015) found that inbreeding depression was highly significant and positive for all the studied traits of the two crosses, except for number of bolls/plant, lint cotton yield/plant, lint percentage and seed index of the cross I.

Phenotypic and genotypic coefficients of variation

Table (2) showed that, the values of phenotypic coefficient of variation (PCV) were higher than the values of genotypic coefficient of variation (GCV) for all the traits studied of the two crosses. These results indicated that, the environment had an important role in the expression of these traits. The PCV and GCV recorded the highest values for number

Table 2. Heterosis as percentage from mid-parents, better-parent, inbreeding depression %, phenotypic (PCV) and genotypic (GCV) coefficient variability for all traits studied in the Cross I (Giza 96 x 10229) and Cross II (Giza 89 x 10229).

Traits	crosses	Mid-parent	Better parent	Heterosis (%)		Inbreeding depression	P.C.V (%)	G.C.V (%)
				Better parent	Mid-parent			
Number of bolls/plant	I	40.96	42.57	12.40**	8.15	-2.15**	3.99	3.25
	II	40.24	41.14	4.86**	2.58**	-5.57**	6.62	5.07
Seed cotton yield/plant (g)	I	128.63	149.13	27.48**	9.96	1.56**	2.37	2.17
	II	133.25	158.38	21.86**	2.53**	0.17**	3.27	1.50
Lint cotton yield/plant (g)	I	50.12	56.44	34.66**	19.58**	1.89**	2.78	2.34
	II	53.51	63.23	25.90**	6.56	0.89**	3.74	3.18
Lint percentage	I	39.18	40.51	5.06**	1.60**	0.34**	1.81	1.27
	II	40.23	40.51	3.16	2.44	0.73**	1.69	1.22
Boll weight (g)	I	3.13	3.51	13.91**	1.64**	3.38**	3.17	2.16
	II	3.30	3.86	16.58**	-0.13**	5.71**	4.63	3.17
Seed index (g)	I	9.83	10.43	8.14**	1.92**	2.35**	2.14	1.57
	II	10.50	11.78	13.33**	1.06**	2.31**	2.15	1.54
Micronaire reading	I	3.95	3.78	-4.43**	1.18**	4.64**	3.93	3.17
	II	4.05	3.78	-7.41**	-0.66**	-5.33**	5.27	3.43
Upper half means	I	34.93	37.20	6.89	0.40	4.22**	2.10	1.64
	II	33.71	34.78	3.597	0.43	4.51**	2.79	2.45
Fiber strength	I	11.01	11.68	7.60**	1.50**	2.11**	2.54	2.02
	II	9.84	10.35	6.23**	0.97	4.07**	2.49	1.61
Uniformity index	I	87.20	87.95	1.43	0.57	0.17**	1.25	1.02
	II	86.40	86.45	0.46	0.40	0.26**	0.88	0.54

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

of bolls/plant and micronaire reading traits of cross II (Giza 89 x 10229). Results indicated also that both PCV and GCV values were much close, this revealed that the major proportion of the observed variation was contributed by the genetic factors in additive genetic variance in most values for phenotypic and genotypic coefficient of variability, which were moderate for the traits studied in the two crosses. There is enough scope for selection based on these characters, and the diverse genotypes can provide materials for a sound breeding programme. Ahsan *et al*., (2015) noticed that, the highest genotypic (GCV) and phenotypic (PCV) coefficients of variation were exhibited by the number of bolls/plant, lint index and seed cotton yield/plant. GCV had similar trend as PCV. Kumar and Katageri (2017) found that PCV and GCV percent were recorded higher (> 20 %) for boll weight (25.69 and 22.99) and seed cotton yield (32.80 and 20.51) while moderate (10 - 20 %) for lint yield (13.09 and 11.43) but high PCV and moderate GCV observed for number of bolls per plant (25.40 and 14.19).

Gene effects

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). The results showed that the estimated Parameters of scaling tests A, B and C gave significant and highly significant deviated from zero for number of bolls/plant in the two crosses. The values of the Parameters of scaling tests A, B and C were deviated highly significant for seed cotton yield/plant, lint cotton yield/plant and boll weight in cross I, both B and C were highly significant in cross II in the same traits. The values A, B and C were significant and highly significant for lint percentage in cross I only. The estimates of the scaling test A, B and C deviate highly significant from zero for seed index in the cross II, whereas, the value B was highly significant in cross I. The values of scaling test A and C deviated highly significant from zero for micronaire reading in cross I. The value of the parameters A deviated highly significant from zero for upper half means in the cross I. Both A and B were highly significant in the cross II. The values of the parameters B and A deviated significant from zero for fiber strength in the cross I and cross II, respectively. The values of the parameters A and B deviated significant from zero for uniformity index in the cross I and cross II, respectively. The data revealed that the mean of F_2 performance (m) was highly significant for all traits studied in the two crosses except boll weight and micronaire reading traits of cross II (Giza 89 x 10229). The additive gene effects (*d*) were highly significant positive for upper half mean in cross II (Giza 89 x 10229), negatively significant for seed cotton yield/plant at the two crosses, lint cotton yield/plant, lint percentage, boll weight, seed index and micronaire reading in cross I (Giza 96 x 10229). On the other hand, the estimate of dominance gene effects (h) were highly significant and positive for seed cotton yield/plant, seed index and fiber strength at the two crosses, also highly significant and positive for number of bolls/plant, lint cotton yield/plant, lint percentage and micronaire reading in cross I (Giza 96 x 10229), but uniformity index was highly significant and negative in cross I (Giza 96 x 10229). Additive x additive epistatic type of gene effects (i) was positively and highly significant for boll weight and micronaire reading in cross I (Giza 96 x 10229) and fiber strength in cross II (Giza 89 x 10229). The epistatic effects interaction of additive x dominance (j) was positively and highly significant for lint percentage in the two crosses, also highly significant and positive for fiber

Table 3. The scaling test and estimates of six-parameter gene effects for yield, yield components and fiber traits of Cross I (Giza 96 x 10229) and Cross II (Giza 89 x 10229).

Scaling test and parameters	Number of bolls/plant		Seed cotton yield/plant (g)		Lint cotton yield/plant (g)		Lint percentage		Boll weight (g)	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
A	4.84±0.93**	6.33±2.27**	8.05±1.38**	-7.13±5.33	7.99±1.44**	-3.50±1.88	3.15±0.79**	-0.39±0.63	-0.19±0.07**	-0.71±0.15
B	8.70±1.88**	7.98±2.43**	54.65±3.61**	48.60±4.06**	24.12±1.37**	18.23±1.933**	1.22±0.51*	-0.90±0.50	0.64±0.11**	0.54±0.14**
C	14.12±3.96**	13.32±6.21*	60.50±8.07**	57.17±11.61**	29.64±4.03**	25.34±5.19**	3.41±1.71*	1.33±1.49	0.39±0.23*	0.21±0.37**
(m)	47.03**	44.55**	161.43**	162.11**	66.21**	66.78**	41.02**	41.20**	3.43**	3.63
(d)	-0.32	0.07	-2.80**	-2.74**	-1.74**	-1.15	-0.37**	-0.02	-0.04**	-0.07
(h)	4.50**	2.95	37.55**	13.42**	19.84**	3.25	2.89**	-1.35	0.49	0.16
(i)	-0.58	1.00	2.20	-15.71**	2.47	-10.61**	0.96	-2.62**	0.06**	-0.38
(j)	-1.93**	-0.82	-23.30**	-27.87**	-8.06**	-10.86**	0.96**	0.26**	-0.42	-0.62
(l)	-12.96**	-15.31**	-64.90**	-25.76**	-34.57**	-4.11**	-5.32**	3.91**	-0.50**	0.55

Table 3. Cont.

Scaling test and parameters	Seed index (g)		Micronaire reading		Upper half means		Fiber strength		Uniformity index	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
A	-0.20±0.14	-0.53±0.20**	-0.45±0.07**	-0.23±0.16	-4.00±0.72**	-3.80±0.64**	-0.53±0.30	0.58±0.24*	-2.40±0.75**	-0.85±0.83
B	1.20±0.21**	1.83±0.22**	0.10±0.14	0.18±0.18	0.22±0.40	-2.67±0.68**	1.05±0.16**	-0.25±0.18	-0.55±0.82	-1.05±0.52*
C	0.60±0.49	1.70±0.55**	-1.05±0.30**	0.20±0.44	-1.45±1.59	-3.87±1.91	0.67±0.65	-0.48±0.54	1.90±2.40	-0.10±1.75
(m)	10.38**	11.63**	3.60**	3.95	35.78**	33.35**	11.60**	10.03**	88.30**	86.58**
(d)	-0.10**	0.10	-0.10**	0.07	0.16	0.50**	-0.13	-0.10	-0.17	0.05
(h)	1.20**	1.00**	0.53**	-0.55	0.10	-1.39	0.69**	1.41**	-3.60**	-1.40
(i)	0.40	-0.40	0.70**	-0.25	-2.33**	-2.60**	-0.15	0.80**	-4.85**	-1.80**
(j)	-0.70**	-1.18**	-0.28**	-0.20	-2.11**	-0.56**	-0.79**	0.41**	-0.92**	0.10**
(l)	-1.40**	-0.90**	-0.35	0.30	6.10**	9.07**	-0.38	-1.13**	7.80**	3.70**

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

m=Mean of F2 d= Additive effect h= Dominance effect

i=Additive x Additive type of gene interaction j=Additive x Dominance type of gene interaction

l=Dominance x Dominance type of gene interaction

strength and uniformity index in cross II (Giza 89 x 10229), but was highly significant and negative seed cotton yield/plant, lint cotton yield/plant, seed index and upper half mean in the two crosses, also was highly significant and negative for number of bolls/plant, micronaire reading, fiber strength and uniformity index in cross I (Giza 96 x 10229). The epistatic effects interaction of dominance x dominance (l) were highly significant and negative for number of bolls/plant, seed cotton yield/plant, lint cotton yield/plant and seed index in the two crosses, also highly significant and negative for lint percentage and boll weight in cross I (Giza 96 x 10229) and fiber strength in cross II (Giza 89 x 10229), but was highly significant and positive for upper half means and uniformity index in the two crosses and lint percentage in cross II (Giza 89 x 10229).

The dominance gene effect, were higher than additive gene effects for all traits studied in the two crosses, indicating predominant role of dominant component of gene action in the inheritance of these traits, so the selection for these traits should be delayed to later segregating generations when dominant effect is diminished. Estimates of additive effects found to be small due to a high degree of dispersion of increasing alleles between parents, and dominance can be small due to its bi-directional nature.

EL-Refaey and Abd El-Razek (2013) found that the estimated mean effects (m) were highly significant for all the traits studied 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 x dominance and dominance x dominance were 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. AL-Hibbiny *et al*., (2015) found that six parameters gene effects exhibited that non-additive genetic effects was greater than the additive genetic effects for most studied traits of the two crosses. The pietistic effects, additive x additive, additive x dominance and dominance x dominance were significant or highly significant in some cases at the two crosses. The dominance gene effects played the major role in controlling the genetic variation of the most studied traits in the two crosses.

Heritability and expected genetic advance

Heritability estimates in broad and narrow senses as well as the expected genetic advance for traits studied in the two crosses are presented in Table (4). The broad-sense heritability (h^2_{bs}%) values were higher than the narrow sense heritability (h^2_{ns}%) values for all traits studied, thus suggesting that improvement for these traits can be made through selection. The results demonstrated that high heritability in broad-sense estimates (>50%) were detected for all traits studied at the two crosses except seed cotton yield/plant at cross II (Giza 89 x 10229). The heritability in narrow-sense estimates ranged from 3.29% to 35.70% for boll weight and uniformity index of cross I (Giza 96 x 10229), respectively. Narrow sense heritability is a reflection of the amount of additive, fixable, heritable variation.

Table 4. Heritability and expected genetic advance for all traits studied in the Cross I (Giza 96 x 10229) and Cross II (Giza 89 x 10229).

Traits	h^2_{bs}%		h^2_{ns}%		ΔG		ΔG%	
	I	II	I	II	I	II	I	II
Number of bolls/plant	88.25	84.07	4.79	6.08	15.80	31.56	33.61	70.84
Seed cotton yield/plant (g)	89.93	47.66	13.65	8.19	91.86	76.42	56.91	47.15
Lint cotton yield/plant (g)	88.86	90.74	18.88	5.22	61.10	22.97	92.28	34.39
Lint percentage	78.32	80.40	6.89	3.80	8.98	4.65	21.90	11.29
Boll weight (g)	76.99	69.57	3.29	4.39	0.63	1.30	18.33	36.72
Seed index (g)	79.07	77.64	20.16	15.85	7.87	6.98	75.81	60.01
Micronaire reading	87.56	72.22	5.97	9.26	1.49	3.39	41.28	85.88
Upper half means	84.57	92.21	13.14	12.31	17.34	20.13	48.48	60.37
Fiber strength	86.06	72.54	9.45	6.29	4.90	2.77	42.23	27.60
Uniformity index	84.42	69.27	35.70	6.69	69.40	8.98	78.60	10.37

H^2_{bs}%: Heritability in broad sense. H^2_{ns}%: Heritability in narrow sense.
ΔG: Expected genetic advance. ΔG%: Expected genetic advance (% of F_2 mean).

The expected genetic advance (Δg%) under 10% selection of the individual plants in the F_2 generation ranged from 10.37% to 92.28% for uniformity index of cross II (Giza 89 x 10229) and lint cotton yield/plant of cross I (Giza 96 x 10229), respectively.

AL-Hibbiny *et al*., (2015) found that high heritability estimates in broad-sense (>50%) were detected for all traits studied at the two crosses, except seed cotton yield/plant of the cross II and fiber fineness of the cross I. Heritability estimates in narrow-sense ranged from 0.00 to 37.51% for boll weight of the cross I and 2.5% span length of the cross II, respectively. The expected genetic advance (Δg%) from selection ranged from 0.00 to 85.75% for boll weight of the cross I and number of bolls/plant of the cross II, respectively. Mabrouk *et al.,* (2018) found that the highest broad-sense heritability estimates was observed in case of lint index with values of 86.29% and the lowest value was for fiber length with value of 22.20%, while the values of narrow-sense heritability, it ranged from zero for No. of bolls/plant, seed cotton yield/plant and uniformity ratio to 61.67% for lint percentage, respectively.

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تحليل متوسطات العشائر لبعض الصفات الكمية في القطن

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الملخص العربى

الهدف الاساسى من هذا البحث دراسة تأثير الفعل الجيني باستخدام متوسطات الست عشائر الأب الأول ، الأب الثاني ، الجيل الأول ، الجيل الثاني ، الجيل الرجعي للاب الأول والجيل الرجعى للاب الثانى لعشرة صفات لهجينين من القطن الهجين الأول (جيزة ٩٦ x ١٠٢٢٩) والهجين الثانى (جيزة ٨٩ x ١٠٢٢٩) وقد أقيمت هذه التجربة باستخدام تصميم القطاعات الكاملة العشوائية فى اربع مكررات بمحطة البحوث الزراعية بسخا، محافظة كفرالشيخ مصر لمدة ثلاثة اعوام. وكانت أهم النتائج المتحصل عليها كالتالى:

أظهرت النتائج ان قيم متوسطات الجيل الاول كانت أعلى من الاباء، الجيل الثانى، الاب الرجعى الأول والاب الرجعى الثانى لمعظم الصفات محل الدراسة لكلا الهجينيين المدروسين. أظهرت نتائج قوة الهجين لمتوسط وأفضل الابوين معنوية عالية وموجبة لمعظم الصفات المدروسة فى كلا الهجينين، علي الجانب الاخر كانت قوة الهجين لمتوسط وأفضل الابوين عالية المعنوية وسالبة (مفيدة) لصفة قراءة الميكرونير فى كلا الهجينين. كانت قيم التربية الداخلية موجبة وعالية المعنوية لجميع الصفات المدروسة ما عدا صفة عدد اللوز/نبات فى كلا الهجينين وصفة قراءة الميكرونير فى الهجين الثاني. أشارت النتائج الى ان قيم معامل الاختلاف الظاهرى كانت اكبر من قيم معامل الاختلاف الوراثى فى كل الصفات المدروسة فى كلا الهجينين. أظهرت التاثيرات الجينية للست مقاييس ان التاثيرات الوراثية السيادية كانت اكبر من التاثيرات الوراثية المضيفة لكل الصفات المدروسة فى كلا الهجينين. وقد لعبت التاثيرات الجينية السيادية دورا رئيسياً فى التحكم فى التباين الوراثى لكل الصفات محل الدراسة لكلا الهجينين. كانت تقديرات كفاءة التوريث بالمعنى الواسع أكبر من ٥٠٪ لكل الصفات المدروسة فى كلا الهجينين ما عدا صفة محصول القطن الزهر/نبات للهجين الثانى وصفة وزن اللوزة للهجين الاول. وتراوحت تقديرات درجة التوريث بالمعنى الضيق من ٣,٢٩ % الى ٣٥,٧٠٪ لصفة متوسط وزن اللوزة ومعامل الانتظام للهجين الاول ، على التوالى. اشارت النتائج ان قيم التقدم الوراثى المتوقع تراوحت من ١٠,٣٧٪ الى ٩٢,٢٨٪ لصفة ومعامل الانتظام للهجين الثاني وصفة محصول القطن الشعر/نبات للهجين الاول ، على التوالى.

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