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Generation Mean Analysis for some Traits in Two Egyptian Cotton Crosses

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Cross Mark



ABSTRACT

Six cotton populations; P₁, P₂, F₁, F₂, BC₁ as well as BC₂ via two cotton crosses (Giza 92 x Giza 96) and (Giza 94 x Giza 96) were employed in the study, at Sakha Agricultural Research Station, Kafr El-Shiekh, Egypt. The results indicated that mean values for most studied traits in F₁ was better than parents, F₂, BC₁ and BC₂ populations. Heterosis values versus mid-parents and better parents were significant and positively for SCY/P, LCY/P, L% as well as LI with respect to the two studied crosses. High significantly inbreeding depression was showed in the case of cross I for SCY/P, LCY/P and BW, while, in the case of cross II was for PI. Phenotypic coefficient of variance (PCV) values were higher than the corresponding values of Genotypic coefficient of variance (GCV) for all studied characteristics in both two studied crosses. Dominance gene effects, demonstrated higher values than additive for all studied traits in both crosses, which indicates predominant role of dominance gene action in the inheritance of these traits. This finding indicated the hybrid production is a proper breeding program for improvement of these traits with respect to the parents involved in the present study. Highly broad sense heritability in two crosses was found for all traits, except for SI at cross II. Expected genetic advance ($\Delta g\%$) with 10% selection intensity of individual plants ranged from 5.37% to 93.37% for L% and LI of cross I, respectively in the F₂ generation.

Keywords: *Gossypium barbadense* L., Heterosis, Inbreeding depression, Heritability.

INTRODUCTION

Plant breeders should understand the relationships between breeding materials for improving crops. Mather and Jinks (1982) revealed that the quantitative genetic method for estimating additive, dominance, and epistasis effects is generation mean analysis. In cotton breeding, genetic analysis of generation means has been employed to determine the sort of gene action that controls quantitative traits. Conversely, heterosis is an essential genetic tool for cotton yield improvement; considerable positive heterosis versus mid or better parent was identified for seed cotton yield /plant. Abd-El-Haleem et al., (2010) demonstrated that in most studied crosses, highly significant gene effects found for the traits of number of bolls per plant, boll weight, fiber length as well as fiber fineness. On the other side, dominance, (additive x dominance) as well as (dominance x dominance) interaction showed significantly for most yield and fiber traits. With the exception for monopodia, both additive as well as dominance genetic effects were found significantly for all traits studied. For all characters studied, the (additive x additive (i)) as well as (dominance x dominance (l)) gene interactions were found significant. Al-Hibbiny et al., (2019) indicated that some crosses had significantly and negative inbreeding depression for some studied traits, although the other crosses had significant and positively inbreeding depression. Data showed that non-additive genetic variance was larger than as compared with additive genetic variance in F₁ and F₂ generations for all traits with exception, for number of bolls/plant as well as seed/ lint cotton yield in F₂ crosses. Mabrouk et al., (2018) demonstrated that best heterosis over to both mid as well as better parent were found for crosses

(Giza 70 x Giza86), (Giza70 x Australy 13) as well as (Australy 13 x Pima S₄) for more yield studied traits, while the crosses (Giza 70 x Giza 92) as well as (Giza 70 x Giza 86) were showed best heterosis versus to mid parent for uniformity ratio. Data showed higher non-additive genetic variances as compared with additive genetic variance ones, for studied traits with the exception, for lint %, fiber length as well as fiber strength characters. On the other side, the heritability in broad sense were showed larger values than narrow-sense heritability for all studied traits with the, exception for fiber length. El-Shazly (2013) reported higher contribution of additive variance for most yield traits; lint %, uniformity ratio and lint index in each of BIP as well as selfed populations of F₃ generation. Both crosses were largely in magnitude of non-additive in BIP as compared with F₃ selfed for yield component traits and fiber strength. Most characters in BIP demonstrated high values in broad sense heritability as a result of increasing portion of genetic variance to the total phenotypic variance.

The current study intended to explore heterosis, phenotypic PCV as well as genotypic GCV coefficients of variability, inbreeding depression, gene effects, heritability, and genetic advances for yield, it's components as well as fiber quality characteristics in both cotton crosses combinations (Giza 92 x Giza 96) and (Giza 94 x Giza 96).

MATERIALS AND METHODS

1. Genetic material

Three Egyptian cotton varieties i.e, Giza 92, Giza 94 as well as Giza 96 were used in this study. The experimental study was executed at Sakha Agricultural Research Station-

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Kafr El-Shiekh Governorate, Egypt during 2021 to 2023 growing seasons.

2. Field experiment

In 2021 growing season, parental cultivars were crossed to generate F₁ hybrid seeds for two crosses (Giza 92 x Giza96) as well as (Giza 94 x Giza 96). In 2022, each of F₁ was also backcrossed to both original parental cotton varieties to produce BC₁ and BC₂ generations. On the other side, F₁ plants were selfed to obtain F₂ seeds. Whereas six populations (P₁, P₂, F₁, F₂, BC₁ and BC₂) for each of the two crosses were evaluated separately in a randomized complete blocks design (RCBD) with four replications in 2023 growing season. Each replicate consisted of 29 rows, (3 rows for each non-segregating generations P₁,P₂ and F₁ progenies, 10 rows for F₂ population and 10 rows for BC₁ and BC₂ crosses (segregating generations). Each row was 4.0 meter in length and 70 cm in width. Seeds were planted in hills spaced 40 cm apart and one plant was left per hill at thinning time.

The studied traits were:-

- Seed cotton yield (g) / plant (SCY/P)
- Lint cotton yield (g) /plant (LCY/P)
- Lint percentage % (L%)
- Boll weight (g) (BW)
- Seed index (g) (SI)
- Lint index (g) (LI)
- Micronaire reading (MR)
- 2.5% Span length (mm) (2.5% SL)
- Pressely index (PI)
- Uniformity index (UI)

All fiber properties were measured in the Cotton Technology Research Division's Laboratories - Cotton Research Institute, Giza.

3. Statistical and genetic procedures

Heterosis as well as inbreeding depression (%) were estimated in accordance with Miller et al., (1958). The

phenotypic (PCV) and the genotypic (GCV) coefficient of variation were calculated applying the formula suggested by Dudley and Moll (1969). Research was carried out to estimate the several gene effects using Jinkes and Jones (1958) and Hayman (1958) six parameter genetic models. The scaling tests (A, B, and C) were utilized to determine the adequacy of the additive dominance model or the presence of non-allelic gene interactions for each characteristic, as described by Mather and Jinks (1982) . Allard (1960) estimated genetic advance as ΔG (10% selection intensity) as well as ΔG% as a percent of the F₂ mean.

RESULTS AND DISCUSSION

1. Mean Performances:-

Table (1) shows mean ± standard errors values for the six generations in both crosses for all studied attributes. The results showed that P₂ (Giza 96) performed better than P₁ (Giza 92) for all yield as well as fiber quality traits, except MR of the cross I (Giza 92 x Giza 96), and that P₁ (Giza 94) performed better than P₂ (Giza 96) for all yield traits of the cross II, (Giza 94 x Giza 96), while P₂ (Giza 96) performed better than P₁ for all fiber quality traits of cross II (Giza 94 x Giza 96).

On the other side, F₁ population recorded better means ± standard errors than the respective parents, F₂, BC₁ as well as BC₂ populations for most studied traits of the two crosses (Giza 92 x Giza 96) as well as (Giza 94 x Giza 96). Also, the relation between F₂ and F₁ demonstrated that there is several behavior, where the F₁ generation was better than as compared with F₂ for all the studied traits except, L%, 2.5% SL, PI and UI in the cross I (Giza 92 x Giza 96). Mean values of the segregating generations were higher than the better parents for all traits in the two crosses combinations, demonstrating a significant level of genetic diversity for these traits in the relevant crosses.

Table 1. Means ± standard errors of six populations for all studied traits in two crosses.

Traits	crosses	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
SCY/P (g)	I	141.63±0.15	150.73±0.61	197.45±0.25	191.55±1.79	190.58±0.24	193.18±1.52
	II	161.03±0.73	150.73±0.61	172.23±0.33	171.48±1.52	171.75±0.52	170.75±1.20
LCY/P (g)	I	50.19±0.14	53.72±0.17	73.94±0.20	71.76±0.78	72.44±0.17	72.73±0.60
	II	61.51±0.35	53.72±0.17	67.90±0.07	67.57±0.82	68.34±0.41	67.54±0.67
L%	I	35.44±0.07	35.64±0.03	37.45±0.12	37.46±0.15	38.01±0.08	37.65±0.12
	II	38.20±0.06	35.64±0.03	39.42±0.07	39.40±0.25	39.79±0.12	39.56±0.16
BW (g)	I	3.09±0.07	3.33±0.05	3.50±0.04	3.33±0.10	3.41±0.06	3.39±0.08
	II	3.22±0.04	3.33±0.04	3.58±0.06	3.58±0.10	3.50±0.06	3.54±0.07
SI (g)	I	9.55±0.06	10.40±0.04	10.50±0.11	10.31±0.11	10.48±0.08	10.65±0.06
	II	10.52±0.07	10.40±0.04	10.55±0.06	10.53±0.06	10.65±0.05	10.62±0.03
LI (g)	I	5.24±0.04	5.76±0.02	6.29±0.08	6.18±0.10	6.42±0.05	6.43±0.07
	II	6.52±0.04	5.76±0.02	6.87±0.05	6.84±0.08	7.04±0.06	6.95±0.03
MR	I	3.60±0.04	4.08±0.03	2.90±0.04	3.50±0.07	3.65±0.03	3.73±0.06
	II	4.50±0.04	4.08±0.03	3.95±0.06	4.03±0.10	4.08±0.05	4.06±0.08
2.5% SL (mm)	I	34.40±0.09	36.15±0.10	36.30±0.13	36.45±0.26	35.60±0.18	35.61±0.08
	II	33.40±0.08	36.15±0.10	36.60±0.09	36.35±0.46	35.95±0.30	35.45±0.30
PI	I	10.20±0.04	10.60±0.04	11.23±0.11	11.58±0.15	11.50±0.13	11.63±0.05
	II	9.53±0.09	10.60±0.04	10.95±0.06	10.53±0.13	10.70±0.07	10.78±0.09
UI	I	85.60±0.08	86.43±0.13	86.48±0.14	87.50±0.47	86.18±0.18	86.25±0.27
	II	85.48±0.05	86.43±0.13	87.50±0.15	87.43±0.26	87.40±0.18	87.10±0.09

2. Heterosis as well as inbreeding depression:-

Table (2) shows heterosis as a percent of mid as well as better- parents, and inbreeding depression values. High significant positively heterosis versus to mid as well as better parents were showed for SCY/P, LCY/P, L% as well as LI

in two cotton crosses and UI at cross II, (Giza 94 x Giza 96), while, for fiber quality traits, 2.5% SL and PI it was significant and positive heterosis over mid-parents at two cotton crosses. Cotton has significant heterobeltiosis due to the major combined effects of (additive x dominance) as

well as (dominance x dominance) gene effects. In other cases, the absence of considerable heterosis could be caused by internal cancellation of heterosis components.

Considering the inbreeding depression in F₂ relative to F₁ (Table 2), the data for cross I (Giza 92 x Giza 96) exhibited highly significant and positive inbreeding depression for the traits of SCY/P, LCY/P and BW, while, it was highly significant and negative inbreeding for PI at cross II (Giza 94 x Giza 96). Most traits in the two crosses showed a coincidence of sign and magnitude of heterosis as well as inbreeding depression. This is logical and expected, because the expression, of heterosis in F₁ progenies is followed by a significant decrease in F₂ due to homozygosity. Similar results are in accordance with Abd-El-Haleem *et al.*, (2010), El-Shazly, (2013) and Orabi *et al.*, (2018).

3. Phenotypic and Genotypic Coefficients of Variation: -

The results displayed that the phenotypic coefficient of variation (PCV) was higher than as compared with

genotypic (GCV) coefficient of variation for all studied attributes in both crosses, these findings suggested that the environment played a significant role in the expression of these characteristics. Also, PCV as well as GCV were demonstrated highest BW and MR values of the two crosses (Table 2). Both of PCV as well as GCV values were much close, revealed that the genetic factors contributed the majority of the detected variation of most values for phenotypic as well as genotypic coefficients of variability was moderate for the traits in both crosses. Similar results are in accordance with El-Shazly, (2013). Kumar and Katageri (2017) showed that higher values for PCV% as well as GCV% more than (> 20 %) for boll weight which were (25.69 and 22.99), while for SCY/P it were (32.80 and 20.51) respectively, whilst, it was moderate (10 - 20 %) for LCY/P (13.09 and 11.43).

Table 2. Heterosis, inbreeding depression %, phenotypic and genotypic coefficient variability for all studied traits in two crosses.

Traits	Crosses	Mid-parents	Better parent	Heterosis (%)		Inbreeding depression	P.C.V (%)	G.C.V (%)
				Mid-parent	Better parent			
SCY/P (g)	I	146.18	150.73	35.08**	31.00**	2.99**	1.87	1.82
	II	155.88	161.03	10.49**	6.96**	0.43	1.77	1.64
LCY/P (g)	I	51.95	53.72	42.31**	37.63**	2.94**	2.17	2.11
	II	57.62	61.51	17.84**	10.38**	0.49	2.44	2.34
L%	I	35.54	35.64	5.36**	5.06**	-0.05	0.80	0.66
	II	36.92	38.20	6.78**	3.20**	0.06	1.27	1.24
BW (g)	I	3.21	3.33	9.08	5.26	5.00**	6.20	5.19
	II	3.21	3.22	11.37**	11.02**	-0.07	5.35	4.64
SI (g)	I	9.98	10.40	5.26	0.96	1.79	2.11	1.50
	II	10.48	10.55	0.72	0.00	0.31	1.13	0.27
LI (g)	I	5.50	5.76	14.27**	9.13**	1.70	3.14	2.68
	II	6.14	6.52	11.82**	5.29**	0.33	2.31	2.01
MR	I	3.84	3.60	-24.43	-19.44	-20.69**	4.04	3.47
	II	4.29	4.08	-7.87	-3.07	-1.90**	5.12	4.57
2.5% SL (mm)	I	35.28	36.15	2.91**	0.41	-0.41	1.44	1.32
	II	34.78	36.15	5.25**	1.24	0.68	2.56	2.51
PI	I	10.40	10.60	7.93**	5.90**	-3.12**	2.58	2.26
	II	10.06	10.60	8.82**	3.30	3.88**	2.38	2.02
UI	I	86.01	86.43	0.54	0.06	-1.19	1.08	1.05
	II	85.95	86.43	1.80**	1.24**	0.09	0.59	0.52

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

4. Gene Effects

Table (3) shows the results of testing for nonallelic interactions (A, B, and C), as well as six-parameter model and type of epistasis. The data demonstrated that the parameters estimated of scaling tests A, B and C were highly significantly veered from zero (0) for SCY//P, LCY/P, L% and LI in both crosses; while it was deviated highly significant for PI in cross I. Both A as well as B had been significant for SI and MR in cross (Giza 92 x Giza 96). The values of the parameter A deviated highly significant from zero for 2.5% SL, PI and UI in the cross II, (Giza 94 x Giza 96). On the other side, values of parameter C deviated significantly from zero for 2.5% SL and PI for cross I, (Giza 92 x Giza 96) and UI in both crosses. The value of the parameter B also showed highly significant from zero for SI in cross II (Giza 94 x Giza 96). Mean performance for F₂ was highly significant for all the studied traits in both crosses. The additive gene effects (d) were positive significantly for L% in cross I, (Giza 92 x Giza 96). On the opposite side, the estimate of dominance gene effects (h)

was highly significant for SCY/P, LCY/P, L% and LI at both crosses, also SI in cross I, (Giza 92 x Giza 96) and PI in cross II (Giza 94 x Giza 96) were highly significant and positive. Epistatic type (additive x additive) of gene effects (i) was positive and significantly for L%, LI as well as MR for cross I, (Giza 92 x Giza 96). Whereas, epistatic effects interaction of (additive x dominance (j)) was found positive and significantly for L%, LI and MR in cross I (Giza 92 x Giza 96), also, was positively and significant for 2.5% SL in both crosses and PI as well as UI for cross II, (Giza 94 x Giza 96). Epistasis effects interaction of (dominance x dominance (l)) on the other side, showed highly significantly and positive for 2.5% SL and UI in the cross I, (Giza 92 x Giza 96).

For all studied attributes in both crosses, the dominance gene effect, on the other side was higher than as compared with additive gene effect, indicating a predominant role of the dominant component of gene action in the inheritance of these attributes, and thus the selection for these attributes should be delayed until the dominant

effect is diminished. Results also showed that additive effects were being modicum because of the highest degree of dispersion of increasing alleles among parents.

EL-Refaey and Abd El-Razek (2013) noticed highly significant for additive as well as dominant genetic effects for the traits of NB/P, boll weight in the cross IV, fiber length in the cross II, fiber fineness in the crosses I and IV. Dominance, as well as the interaction (additive x dominance) as well as (dominance x dominance) were significant for NB/P in the cross I, as while, seed as well as lint cotton yield / plant in the crosses I and II, respectively,

boll weight in cross IV, fiber length and also fiber fineness in the cross I, indicated that dominance and their non-allelic interactions were greatly affected in the inheritance of these attributes.

Orabi *et al.* (2018) demonstrated that dominance effects for micronaire value as well as fiber length were higher as compared with additive effects. On the other hand, (additive x additive) as well as (dominance x dominance) interaction with complementary action with non-additive effect, highly significant epistasis values were discovered.

Table 3. Scaling test and estimates of six-parameter gene effects for all studied attributes.

Scaling test and parameters	SCYP (g)		LCYP (g)		L %		BW (g)		SI (g)	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
A	42.08±0.57**	10.25±1.32**	20.76±0.42**	7.27±0.89**	3.14±0.22**	1.95±0.25**	0.23±0.15	0.21±0.14	0.90±0.20**	0.20±0.14
B	38.18±3.11**	18.55±2.50**	17.80±1.24**	13.47±1.36**	2.21±0.27**	4.05±0.32**	-0.05±0.17	0.30±0.16	0.40±0.17*	0.28±0.10**
C	78.95±7.20**	29.72±6.18**	35.26±3.14**	19.24±3.32**	3.88±0.65**	4.91±1.02**	-0.12±0.43	0.74±0.41	0.30±0.49	0.05±0.28
(m)	191.55**	171.48**	71.76**	67.57**	37.46**	39.40**	3.33**	3.58**	10.31**	10.53**
(d)	-2.60	1.00	-0.29	0.79	0.36*	0.23	0.03	-0.04	-0.17	0.03
(h)	52.58**	15.43**	25.28**	11.78**	3.38**	3.59**	0.59	0.13	1.53**	0.51
(i)	1.30	-0.92	3.30	1.50	1.47*	1.09	0.30	-0.24	1.00	0.44
(j)	1.95	-4.15	1.48*	-3.10	0.46**	-1.05	0.14	-0.05	0.25	-0.04
(l)	-81.55	-27.88	-41.87	-22.23	-6.83	-7.08	-0.48	-0.26	-2.30	-0.92
Scaling test and parameters	LI (g)		MR		2.5% SL (mm)		PI		UI	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
A	1.32±0.13**	0.69±0.13**	0.80±0.08**	-0.30±0.12	0.50±0.40	1.90±0.61**	1.58±0.28**	0.93±0.18**	0.28±0.39	1.82±0.39**
B	0.82±0.16**	1.27±0.09**	0.48±0.13**	0.09±0.18	-1.23±0.23	-1.85±0.61	1.43±0.15**	0.00±0.19	-0.40±0.58	0.27±0.27
C	1.14±0.42**	1.36±0.34**	0.53±0.30	-0.37±0.43	2.65±1.09*	2.65±1.87	3.05±0.64**	0.07±0.53	5.02±1.92**	2.80±1.08**
(m)	6.18**	6.84**	3.50**	4.03**	36.45**	36.35**	11.58**	10.53**	87.50**	87.43**
(d)	-0.01	0.09	-0.07	0.02	-0.01	0.50	-0.13	-0.07	-0.07	0.30
(h)	1.78**	1.32**	-0.19	-0.18	-2.35	-0.78	0.78	1.74**	-4.69	0.85
(i)	1.00*	0.60	0.75*	0.16	-3.38	-2.60	-0.05	0.85	-5.15	-0.70
(j)	0.25**	-0.29	0.16*	-0.19	0.86**	1.88**	0.08	0.46**	0.34	0.77**
(l)	-3.13	-2.56	-2.03	0.06	4.10**	2.55	-2.95	-1.78	5.27*	-1.40

*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) j : (additive x dominance) l : (dominance x dominance)

5. Heritability and Expected Genetic Advance:

Heritability in both of broad as well as narrow senses and additionally the expected genetic advance for the studied traits in both cotton crosses are shown in Table (4). Heritability in broad sense (h²_{bs}%) revealed higher values than narrow sense heritability (h²_{ns}%) for all studied traits, thus indicating that these characters can be improved through selection. The results revealed a highly (h²_{bs}%) estimates more than (>50%) were detected for all studied attributes at both crosses with the , exception of SI at cross II (Giza 94 x Giza 96). Narrow sense heritability ranged from 2.67% to 33.95% for MR at cross I, (Giza 92 x Giza 96) as well as SI at cross II, (Giza 94 x Giza 96), respectively.

Expected genetic advance, (Δg%) with 10% selection intensity of the individual plants in F₂ generation ranged from 5.37% to 93.37% for L% and LI of cross I (Giza 92 x Giza 96), respectively. Mabrouk *et al.* (2018) showed highest (h²_{bs}%) values were showed for LI 86.29% and the lowest h²_{bs}% value was for 2.5% SL about 22.20%, while the values of h²_{ns}%, ranged from zero for NB/P, SCYP and UI to 61.67% for L%, respectively. Orabi *et al.* (2018) indicated that broad sense heritability were high values for all studied attributes, whilst (h²_{ns}%) values were lower values for the traits of SCYP as well as LCYP/P.

Table 4. Heritability as well as expected genetic advances for all studied attributes

Traits	h ² _{bs} %		h ² _{ns} %		ΔG		ΔG%	
	I	II	I	II	I	II	I	II
SCYP (g)	98.58	95.17	15.55	17.03	97.95	91.04	51.13	53.09
LCYP (g)	98.50	97.85	21.99	5.05	60.19	14.64	83.88	21.67
L %	89.17	98.38	3.83	23.1	2.01	20.45	5.37	51.91
BW (g)	89.57	91.97	7.48	4.13	2.71	1.39	81.65	38.91
SI (g)	77.33	43.42	15.79	33.95	6.04	7.99	58.60	75.98
LI (g)	90.09	91.23	16.88	19.24	5.77	5.35	93.37	78.24
MR	91.56	93.43	2.67	10.02	0.66	3.64	18.96	90.35
2.5% SL(mm)	93.83	98.94	31.45	10.30	29.12	16.84	79.88	46.32
PI	92.21	89.76	9.97	15.61	5.24	6.87	45.26	65.26
UI	97.69	91.91	38.24	30.15	63.85	27.18	72.97	31.09

H²_{bs} %: Broad sense heritability.

H²_{ns} %: Narrow sense heritability.

ΔG: Expected genetic advance.

ΔG%: Expected genetic advance (% of F₂ mean).

CONCLUSION

Dominance gene effects perform a significant role in controlling genetic variances for all studied attributes in both crosses. Low Inbreeding depression was showed for both crosses, on the other side, heterosis over both mid as well as better parent was highly significant for most studied traits. The opposite direction of additive as well as dominance variances resulted low narrow sense heritability for most

studied traits. Therefore, the present study could be suggested that the proper breeding program is hybrid production with respect the most of studied traits.

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تحليل متوسطات العشائر لأصناف المحصول ومكوناته وصفات الجودة في هجينين من القطن المصري

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المخلص

تم استخدام متوسطات العشائر الستة (الأب الأول ، الأب الثاني ، الجيل الأول ، الجيل الثاني ، الجيل الرجعي للأب الأول والجيل الرجعي للأب الثاني) لمجموعة من الصفات المحصولية و التكنولوجيا لهجينين من القطن ، الهجين الأول (أكسترا جيزة 92 x أكسترا جيزة 96) والهجين الثاني (أكسترا جيزة 94 x أكسترا جيزة 96) بهدف دراسة تأثير الفعل الجيني ، وقد أقيمت هذه التجربة باستخدام تصميم القطاعات الكاملة العشوائية في أربع مكررات بمحطة البحوث الزراعية بسخا - محافظة كفر الشيخ - مصر ، خلال مواسم الزراعة 2021-2023. وكانت أهم النتائج المتحصل عليها كالتالي: - أظهرت النتائج أن قيم متوسطات الجيل الأول كانت أعلى من الأباء، الجيل الثاني، الأب الرجعي الأول والثاني لمعظم الصفات المدروسة لكلا الهجينين. - أظهرت نتائج قوة الهجين لمتوسط وأفضل الأبوين معنوية عالية وموجبة لصفات محصول القطن الزهر/نبات ومحصول القطن الشعر/نبات ومعدل الحليج ومعامل الشعر في كلا الهجينين. - أظهرت قيم التربية الداخلية معنوية موجبة وعالية لصفات محصول القطن الزهر والشعر/النبات ووزن اللوزة في الهجين الأول وكذلك صفة متانة التيلة في الهجين الثاني ، بينما كانت سالبة وعالية المعنوية لصفة قراءة الميكرونير في كلا الهجينين و صفة متانة التيلة في الهجين الأول. - أشارت النتائج إلى أن قيم معامل الاختلاف المظهرى كانت أكبر من قيم معامل الاختلاف الوراثي في كل الصفات المدروسة في كلا الهجينين. - أظهرت دراسة التأثيرات الجينية للمقاييس الستة أن التأثيرات الوراثية السيادة كانت أكبر من التأثيرات الوراثية المضيقة لكل الصفات المدروسة في كلا الهجينين وقد لعبت التأثيرات الجينية السيادة دورا رئيسياً في التحكم في التباين الوراثي لكل الصفات المدروسة لكلا الهجينين. - كانت تقديرات كفاءة التوريث بالمعنى الواسع أكبر من 50% لكل الصفات المدروسة في كلا الهجينين ما عدا صفة معامل البندرة في الهجين الثاني، كما تراوحت تقديرات درجة التوريث بالمعنى الضيق من 2.67% إلى 33.95% لصفة قراءة الميكرونير في الهجين الأول و صفة معامل البندرة في الهجين الثاني ، على التوالي. - أشارت النتائج أن قيم التقدم الوراثي المتوقع تراوحت من 5.37% إلى 93.37% لصفة معدل الحليج و صفة معامل الشعر على التوالي في الهجين الأول. - وعليه فإن استخدام وحساب القيم والمقاييس الوراثية يعتبر أداة فعالة في تربية وتحسين الصفات الاقتصادية للقطن المصري.