ESTIMATION OF SOME GENETIC PARAMETERS AND GENE ACTION FOR YIELD, YIELD COMPONENTS AND FIBER PROPERTIES IN TWO INTER-VARIETAL COTTON CROSSES

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ABSTRACT

This investigation was carried out during the three growing seasons of 2004, 2005 and 2006 at Sids Agricultural Experiment Station (Beni-Swief), the two inter-varietal crosses [Dandara x {Giza 83 x (Giza 75 x 5844}] and [Giza 90 x {Giza 83 x (Giza 75 x 5844)}] with its six populations P_1, P_2, F_1, F_2, BC_1 and BC_2 were grown in a randomized complete block design with four replications. The obtained results showed significant positive heterosis relative to mid-parents, in both the two crosses for all studied characters except PI in cross I and L % and 2.5% SL in cross II. Positive significant better parent heterosis were found for PFN, BW, SCY/P, LY/P, LI, Mic and 2.5% SL while showed negative significant PI in cross I. In cross II, the values of better parent heterosis were positive and significant for BW (g) and PI and negative for L%. The inbreeding depression values were significant and positive for BW, SCY/P and LI in both crosses and PFN and 2.5% SL in cross I as well as LY/P, Mic and PI in cross II, while negative value was recorded for PI in cross I. Potence ratio values showed partial-dominance or over-dominance for all studied characters in both crosses. Significant additive gene effects were found for PFN, L %, St, LI and PI in both crosses, also 2.5% SL in cross I and B/P, SCY/P and LY/P in cross II. Significant dominance gene effects were detected for B/P, SCY/P, LY/P, SI and Mic in both crosses, as well as PFN and LI in the first cross, BW (g) and PI in the second cross.

The values of epistatic gene effect additive x additive (i), were significant for B/P, SCY/P, LY/P, L% and PI in both crosses. Significant additive x dominance (j) values of epistasis were observed for most studied characters in the two crosses.

Relative high values of heritability in broad sense (over 50%) were noticed for all studied characters in both crosses except for B/P, SCY/P, LY/P, and L%, in cross I and for B/P, BW and LUR %, in cross II. High heritability values in narrow sense (over 50%) were recorded for PI in cross II, while moderate hertability values (ranged from 30 to 50%), in narrow sense, were recorded for PFN, BW, 2.5% SL and LUR % in the first cross and for PFN, L %, SI, Mic, PI and 2.5% SL, in the second cross. The other character showed low heritability values in narrow sense. Maximum predicted genetic character showed low heritability values in narrow sense. Maximum predicted genetic advance from selecting the desired 5% of F_2 population were achieved for PFN and BW in cross I and for PFN and SCY/P in cross II.

The exerted values of genotypic coefficients between most characters were higher than the corresponding values of phenotypic correlation coefficients in both crosses.

Both phenotypic and genotypic correlations were highly significant between (B/P and each of BW, SCY/P, LY/P), (SCY/P and LY/P) and between (SI and LI) in both crosses. The coefficients of genotypic correlation were significant between (BW and each of SCY/P, LY/P, L%, SI and 2.5% SL), as well as between (SCY/P and each of L %, SI, LI and LUR) in the first cross. While, in the second cross, highly significant positive genotypic correlations were detected between (BW and each of L%, SI, LI and LUR), (SCY/P and each of SI, LI and Mic).

INTRODUCTION

Egyptian cotton has international reputation because of the extraordinary characteristics of its fiber qualities. It played an important role in the national income of Egypt. Improvement of yield and fiber quality of cotton varieties is the main target in any cotton breeding program. The progress of any breeding program depends on the magnitude of genetic variability present in the genetic materials and the extent of heritability of desirable characters. A basic understanding of nature of the action and interaction of gene involved in the inheritance of quantitative characters is very essential for cotton breeders. Therefore, partitioning of variance, into additive, dominance and epistatic effects, as well as heritability estimates in both broad and narrow sense and also expected genetic advance upon selection are genetic parameters, which enable the breeder to foresee the reliability of selection for yield components and fiber properties. Gene action and epistatic effects in cotton were studied in intra-specific crosses among Egyptian varieties by El-Disouki and Ziena (2001), Hemida *et al.* (2001), Abd El-Zaher *et al.* (2003) and Eissa (2004a).

Most published studied on correlation in cotton have not yielded information on the genetic correlation between yield and its components. Most reported studies have dealt with correlation determined in established varieties. This type of association is of a little value to the breeder dealing with a segregating population. Performance of phenotypic and genotypic correlations were studied by several investigators i.e., El-Adly (1996) and El-Ameen *et al.* (2004) and Eissa (2004b).

Therefore, the present investigation was conducted to estimate the heterosis, inbreeding depression, partitioning of variance, heritability estimates and expected genetic advance upon selection for yield components and fiber properties. Moreover, the calculation of the phenotypic and genotypic correlations between characters in the two intra-specific crosses of cotton. [Dandara x {Giza 83 x (Giza 75 x 5844)}] and [Giza 90 x {Giza 83 x (Giza 75 x 5844)}].

MATERIALS AND METHODS

This investigation was carried out at Sids Agricultural Experiment Station, Agricultural Research Centre, during the seasons 2004, 2005 and 2006.

In 2004 season, the parental genotypes were crossed as follows: cross I: [Dandara x {Giza 83 x (Giza 75 x 5844)}] and cross II [Giza 90 x {Giza 83 x (Giza 75 x 5844)}] to produce F_1 hybrid seeds.

In 2005 season, the parents were again crossed to obtain more F_1's hybrid seeds. Moreover, the F_1 plants were backcrossed for both parents to obtain BC_1 and BC_2 and the F_1 plants were self-pollinated to produce F_2 generation seeds.

In 2006 season, the six populations i.e., (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the two crosses were widely spaced sowing as individual plants in a complete randomized block design with four replicates. Each replicate included two rows for each parent, four rows for F_1 population and six rows for each of BC_1 and BC_2, in addition to sixteen rows for F_2 population. Rows were 7.0 m long and 60 cm apart, hills per row were spaced 70 cm. One row was left between every two planted rows. After word, about 5 weeks from sowing date, the hills were thinned to single healthy plant per hill. Cultural practices for growing cotton as well as the pest control were applied among the three seasons.

The following measurements were taken on the individual plants of the six populations: position of the first node (PFN), number of harvested bolls per plant (B/P), boll weight in grams (BW), seed cotton yield per plant (SCY/P), lint yield per plant (LY/P), lint percentage (L %), seed index in grams (SI), lint index in grams (LI), fiber fineness as micronaire reading (Mic), fiber strength as Pressley index (PI), fiber length at 2.5% span length (2.5% SL) and length uniformity ratio (LUR).

Type of gene effects was estimated by using the relation between generations mean as outlined by Mather and Jinks (1971). The significance of the above estimates were tested by the "t".

Heritability values in broad and narrow senses and expected genetic advance under selection were determined according to Warner (1952) and Allard (1960), respectively. A, B and C scaling tests of Mather and Jinks (1971) were used to test the adequacy of additive dominance model. Estimation of genetic variance and its components were calculated using Mather (1949) procedures.

Both phenotypic and genotypic correlations among traits were estimated concerning the simple phenotypic correlation in F_1 and F_2. The following formula was used to estimate simple phenotypic correlation r(Ph):

$$r(Ph) = \frac{Cov.\ XY}{\sqrt{VX.VY}}$$

Where:

r(Ph)	=	simple phenotypic correlation
Cov.XY	=	phenotypic covariance between character x and character Y.
VX and VY	=	variance of character x and Y, respectively.

Concerning the genotypic correlation in F_2 generations, Burton (1951) used a formula in which some of the non-heritable effects might be eliminated by calculating the genetic correlation as follows:

$$\text{Genotypic correlation} = \frac{Cov.\ XY\ F_2 - Cov.\ XY\ F_1}{\sqrt{(VX\ F_2 - VX\ F_1)\ (VY\ F_2 - VY\ F_1)}}$$

Where:

Cov. and V	=	covariance and variance.
X	=	measurement of one character.
Y	=	measurement of the other character.
F_1 and F_2	=	first and second generation, respectively.

RESULTS AND DISCUSSION

The means of the six populations and their standard error for the studied characters are shown in Table 1. The results indicated that the parental genotypes revealed significant differences for PFN, L%, SI, LI, in the two crosses and 2.56% SL, LUR % in cross I, B/P, SCY/P, LY/P, SI and LI in cross I. Meanwhile, F_1 population means was higher than F_2 generations for most studied characters in both crosses except PI in cross I, PFN, B/P, SI and 2.5% SL in cross II. On the other hand, BC_2 population means surpassed BC_1 for all characters studied except PFN, BW, L% and PI in cross I, while BC_1 population means exceeded BC_2 population means for all characters studied except SI in cross II.

Heterosis, inbreeding depression and potence ratio are presented in Table 2. Highly significant or significant positive heterotic values relative to better parent were found for PFN, BW, SCY/P, LY/P, LI, Mic and 2.5% SL and highly significant negative value for PI in the first cross. Likewise, highly significant or significant positive heterosis values relative to better parent was recorded for SI, PI and LUR %, while highly significant negative value was found for L % in the second cross. Significant heterosis relative to better parent indicated that the main cause of heterosis effects were over-dominance and epistatic gene effects. In this respect, Hassan (2007) recorded positive significant heterosis relative to better parent for number of bolls/plant and seed cotton yield/plant.

Highly significant or significant positive heterosis values relative to mid-parents were found for all studied characters in both crosses except for PI in cross I and for PFN, L% and 2.5% SL in cross II. The remaining characters in both crosses showed insignificant heterosis relative to mid-parents, indicated that additive gene effect play a major role in the inheritance of these characters. Similar results were reported by Khattab *et al.* (1984), El-Disouqi *et al.* (2000) and Eissa (2004a).

Inbreeding depression values were positive and significant for all studied characters in both crosses except B/P, LY/P and Mic in cross I and for PFN, L%, SI and 2.5% SL in cross II. In theory, inbreeding depression is caused by decreased in the heterozygosity, which conditions strong dominance or over-dominance gene action. Awad *et al.* (1986) concluded that inbreeding depression estimates were significant for first fruiting node, boll weight and seed index.

Both heterosis and inbreeding depression are coinciding to the same particular phenomenon.

Potence ratio indicated over-dominance towards the better parent or the lower parent for all most characters in the two crosses except for PFN, SI and 2.5% SL in cross I and for PFN, LI and 2.5% SL in cross II which showed partial dominance. These results were in accordance with the findings obtained by Abou-Zahra *et al.* (1987), Eissa (2004a) and El-Adly (2004).

Mather's scaling test A, B and C values for studied characters are given in Table (3). The estimates of parameter A, B and C (one or more of these parameter), were deviated highly significantly or significantly form zero for all studied characters in both crosses. It is interesting to note that, the significant of any one or more of these tests indicates epistasis on the scale of characters used. Therefore the results confirmed the presence of non-allelic interaction in the inheritance of all studied characters in the two crosses. These results are supported by Awad *et al.* (1989), El-Okkia *et al.* (1989), Ismail *et al.* (1991), Abd El-Zaher (1999), Eissa (2004a) and El-Adly (2004).

Table (1): Means of P_1, P_2, F_1, F_2, BC_1 and BC_2 and their standard errors for studied characters of the two intra-specific crosses Dandara x [G. 83 x (G. 75 x 5844)] and Giza 90 x [G. 83 x (G. 75 x 5844)].

Generation	Characters											
	PFN	B/P	BW (g)	SCY/P	LY/P	L %	SI (g)	LI	Mic	PI	2.5% SL	LUR %
Cross I: Dandara x [G. 83 x (G. 75 x 5844)]												
P_1	7.45±0.17	33.8±2.586	2.65±0.036	90.32±7.47	34.25±2.61	38.2±0.3**	7.69±0.124	4.76±0.086	2.99±0.042	10.3±0.1**	30.7±0.1**	88.0±0.3**
P_2	6.65±0.1**	35.05±2.57	2.64±0.033	92.08±6.79	33.33±2.36	36.29±0.17	10.5±0.1**	5.96±0.1**	3.10±0.062	9.45±0.08	28.76±0.15	83.86±0.25
F_1	7.35±0.98	39.73±1.98	2.81±0.031	112.1±6.27	43.61±2.48	38.85±0.17	10.44±0.11	6.62±0.076	3.95±0.035	9.82±0.073	31.24±0.14	87.82±0.32
F_2	6.89±0.080	37.39±1.12	2.66±0.024	100.89±3.3	38.5±1.26	38.34±0.11	9.46±0.064	5.87±0.046	3.89±0.031	10.03±0.06	30.83±0.09	86.29±0.17
BC_1	7.92±0.112	39.58±1.91	2.80±0.031	112.05±5.7	43.48±2.25	38.65±0.16	9.35±0.097	5.89±0.06	3.93±0.049	10.11±0.10	30.42±0.14	85.19±0.27
BC_2	6.92±0.112	44.58±1.66	2.64±0.035	119.53±4.8	44.18±1.75	37.07±0.18	10.18±0.10	6.03±0.079	3.95±0.048	9.57±0.101	30.01±0.13	85.34±0.22
Cross II: G. 90 x [G. 83 x (G. 75 x 5844)]												
P_1	7.30±0.128	41.7±2.2**	2.74±0.053	113.9±4.8**	46.14±1.99**	40.53±0.2*	9.19±0.1**	6.27±0.1**	4.06±0.02	9.27±0.075	30.50±0.29	85.03±0.34
P_2	6.75±0.1**	33.75±1.25	2.63±0.039	89.36±3.65	34.94±1.53	39.74±0.24	8.4±0.087	5.54±0.78	3.95±0.052	10.3±0.1**	30.16±0.30	84.15±0.44
F_1	7.00±0.095	45.45±1.87	2.81±0.35	126.76±4.5	50.38±1.81	39.71±0.18	9.44±0.087	6.22±0.079	4.09±0.026	10.79±0.06	30.27±0.20	86.19±0.26
F_2	7.11±0.064	36.47±0.98	2.68±0.23	99.64±2.84	38.42±1.13	38.45±0.12	9.51±0.057	5.97±0.047	3.82±0.026	10.23±0.05	30.49±0.15	87.00±0.19
BC_1	7.37±0.101	44.57±1.74	2.69±0.035	120.41±5.1	47.63±2.07	39.46±0.17	9.38±0.088	6.12±0.078	3.81±0.038	10.34±0.07	31.08±0.16	86.54±0.27
BC_2	6.98±0.090	40.80±1.35	2.57±0.036	105.12±3.7	40.71±1.50	38.69±0.18	9.58±0.081	6.07±0.068	3.69±0.039	10.53±0.08	30.22±0.27	87.12±0.30

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

Table (2): Heterosis inbreeding depression and potence ratio for studied characters of the two intra-specific crosses Dandara x [G. 83 x (G. 75 x 5844)] and Giza 90 x [G. 83 x (G. 75 x 5844)].

Estimates		Characters											
		PFN	B/P	BW (g)	SCY/P	LY/P	L %	SI (g)	LI	Mic	PI	2.5% SL	LUR %
Cross I: Dandara x [G. 83 x (G. 75 x 5844)]													
Heterosis	H.P.	10.53**	13.35	6.04**	21.74*	27.33**	1.65	-0.19	11.07**	27.42**	-4.47**	1.92**	-0.25
	M.P.	4.26*	15.41*	6.24**	22.92**	29.06**	4.28**	15.04**	23.51**	29.72**	-0.46	5.17**	2.18**
Inbreeding depression	I.D.%	6.67**	5.89	5.34**	10.00**	11.72	1.31*	9.39**	11.33**	1.52	-2.14*	1.31*	1.74**
Potence ratio	P.R.	0.75	-8.49	0.75	-23.75	21.35	1.65	-0.99	-2.10	-16.45	-0.11	1.62	0.89
G. 90 x [G. 83 x (G. 75 x 5844)]													
Heterosis	H.P.	3.70	8.99	2.55	11.27	9.19	-2.02**	2.72*	-0.80	0.74	4.35**	-0.75	1.36**
	M.P.	-0.36	20.48**	4.66**	24.71**	24.27**	-1.06	7.33**	5.33**	2.12*	10.05**	-0.20	1.89**
Inbreeding depression	I.D.%	-1.57	19.76**	4.63**	21.39**	23.74**	3.17	-0.74	4.02**	6.60**	5.19**	-0.73	-0.94*
Potence ratio	P.R.	-0.09	1.94	2.27	2.05	1.76	-1.08	1.63	0.86	1.55	-1.84	-0.35	3.64

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

Table (3): Scaling test for studied characters studied in two intra-specific crosses.

Characters	Cross I Dandara x [G. 83 x (G. 75 x 5844)]			Cross II G. 90 x [G. 83 x (G. 75 x 5844)]		
	A	B	C	A	B	C
PFN	1.04±0.302**	-0.16±0.277	-1.36±0.43**	0.44±0.257	0.21±0.266	0.39±0.358
B/P	5.63±5.02	14.38±4.64**	1.25±6.996	1.99±4.512	2.40±3.514	-20.5±5.97**
BW (g)	-0.14±0.078	-0.17±0.08**	0.27±0.124*	-0.17±0.95	-0.3±0.089**	-0.27±0.133*
SCY/P	21.68±15.011	34.88±13.4**	-3.04±20.842	0.14±12.075	-5.88±9.485	-58.2±15.7**
LY/P	9.100±5.761	11.42±4.90*	-0.80±7.897	-1.26±4.934	-3.90±3.815	-28.16±6.3**
L %	0.23±0.47	-1.00±0.435*	1.15±0.649	-1.32±0.43**	-2.07±0.47**	-5.89±0.68**
SI (g)	0.57±0.253*	-0.54±0.247*	-1.19±0.37**	0.13±0.214	1.32±0.203**	1.57±0.312**
LI (g)	0.40±0.166*	-0.52±0.19**	-0.48±0.262	-0.25±0.195	0.38±0.176*	0.37±0.272
Mic	0.92±0.112**	0.85±0.12**	1.57±0.161**	-0.53±0.09**	-0.66±0.10**	-0.91±0.13**
PI	0.12±0.255	0.13±0.229	0.75±0.332*	0.62±0.169**	0.07±0.174	-0.27±0.258
2.5 % SL	-1.05±0.34**	0.02±0.322	1.43±0.498**	1.39±0.476**	0.01±0.641	0.76±0.836
LUR %	-5.48±0.69**	-1.00±0.59	-2.38±1.00**	1.86±0.692**	3.90±0.788**	6.44±1.065**

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

The results in Table 4, illustrated type of gene effects using generation mean analysis for studied characters in the two intra-specific crosses. It could be clearly observed that the constant mean (m) values were highly significant for all studied characters in the both crosses except SCY/P and LY/P in cross I. The additive gene effects (d) were highly significant and positive or negative for PFN, L%, SI, LI and PI in both crosses, 2.5% SL and LUR % in cross I, B/P, SCY/P and LY/P in cross II. While the remaining characters in both crosses computed insignificant and negligible values.

The dominance gene effects (h) appeared to be of very important role in the inheritance of B/P, SCY/P, LY/P, SI, Mic and LUR% in both crosses, PFN, LI and 2.5 SL in cross I, BW and PI in cross II, which had positive or negative significant values. These results indicated that improvement of these characters could be achieved through recurrent selection.

The additive x additive type of epistatic gene effects (i) values, were positive and highly significant for B/P, SCY/P, LY/P, L% and PI in both crosses, in addition to PFN, SI, 2.5% SL and LUR % in cross I. Whereas, the remaining studied characters were insignificant and of positive or negative values.

Most studied characters were significantly affected by one or two types of epistatic gene effects (j and L) in both crosses except PI in cross I and PFN, SCY/P, LY/P, L%, and 2.5% SL in cross II.

These results are in accordance with the findings obtained by Khattab *et al.* (1984) for (L%); El-Okkia *et al.* (1989) for (B/P, L% and SI); El-Adly (1996**)** for (BW, B/P, SI and LI); Abd El-Zaher (1999) for (L %, SI and LI in both crosses and LYP in cross II); Hassan (2007) for (BW, B/P and SI in cross I); Eissa (2004a) for (BW and SI) and El-Adly (2004) for (BW, SCY/P, LY/P and L%), who observed that additive, dominance gene effects and epistatic action played a major role in the inheritance of their studied characters.

Heritability estimates in broad and narrow senses as well as expected genetic advance upon selection are presented in Table 5. High broad sense heritability values (over 50%) were detected for all studied characters in both crosses except for SCY/P, LY/P and L% in cross I and for B/P, BW and LUR% in cross II which recorded moderate heritability estimates (from 30% to 50%).

Table (4): Type of gene effect for characters studied of the two intra-specific crosses Dandara x [G. 83 x (G. 75 x 5844)] and Giza 90 x [G. 83 x (G. 75 x 5844)].

Generation	Characters											
	PFN	B/P	BW (g)	SCY/P	LY/P	L %	SI (g)	LI	Mic	PI	2.5% SL	LUR %
Cross I: Dandara x [G. 83 x (G. 75 x 5844)]												
m	4.81**	15.66*	2.41**	31.6	12.47	39.17**	7.85**	5.00**	2.85**	10.63**	32.16**	90.05**
d	0.40**	-0.62	0.00	-0.88	0.46	0.97**	-1.38**	-0.60**	-0.50	0.41**	0.94	2.09**
h	5.66**	62.84**	0.61	196.66**	72.98**	-3.01	3.84**	1.86**	3.07**	-1.58	-4.41**	-12.81**
i	2.24**	18.76**	0.24	59.60**	21.32**	1.92**	1.22**	0.36	0.20	0.76*	-2.46**	-4.10**
j	1.20**	-8.75	0.31**	-13.20	-2.32	1.23*	1.11**	0.92**	0.07	-0.25	-1.07*	-4.48**
L	-3.12**	-38.77	-0.21	-116.2**	-41.84**	2.69*	-1.25	-0.24	-1.97	0.77	3.49**	10.58**
Cross II: G. 90 x [G. 83 x (G. 75 x 5844)]												
m	6.77**	12.84*	2.89**	49.14**	17.54*	37.64**	8.92**	5.40**	4.28**	8.98**	29.69**	85.27*
d	0.28**	3.98**	0.05	12.28**	5.60**	0.39*	0.39**	0.37*	0.05	-0.53**	0.17	0.44
h	1.14	61.83**	-0.75*	124.38**	50.68	1.18	1.86*	1.45	-1.66**	3.18**	2.62	6.00*
i	0.26	24.86**	-0.20	52.5**	23.00**	2.50**	-0.12	0.50	-0.28	0.82**	0.64	-0.68
j	0.23	-0.41	0.13	6.02	2.64	0.75	-1.19**	-0.63	0.13	0.69**	1.38	-2.04*
L	-0.91	-29.25**	0.67**	-46.76	-17.84	0.89	-1.33*	-0.63	1.47**	-1.37**	-2.04	-5.08**

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

On the contrary, low broad sense heritability value (less than 30%) was obtained for B/P in cross I. The relative high value of heritability in broad sense could be due to dominance and epistatic effects. This indication means that the selection for high expression of that on the basis of phenotype could be highly effective. While, low or moderate values of heritability in broad sense may be due to the effect of environment, which had a considerable share in the inheritance of these characters.

Moderate or low narrow sense heritability estimates (less than 50%) were calculated for all studied characters, could be due to the relative great amount of environmental and dominance effects. These findings were in harmony with those obtained by Ismail *et al.* (1991) and Mohamed *et al.* (2001).

Table (5): Heritability in broad and narrow senses and the expected genetic advance upon selection for characters studied in the two crosses.

Characters	Cross I Dandara x [G. 83 x (G. 75 x 5844)]			Cross II G. 90 x [G. 83 x (G. 75 x 5844)]		
	Heritability		Genetic advance %	Heritability		Genetic advance %
	Broad sense	Narrow sense		Broad sense	Narrow sense	
PFN	57.46	49.25	14.97	55.53	33.69	7.94
B/P	29.22	7.31	5.69	41.68	9.76	6.81
BW (g)	67.64	49.68	11.48	47.96	28.34	6.40
SCY/P	31.22	8.13	6.95	60.12	16.73	12.45
LY/P	34.98	7.61	6.48	57.98	7.60	5.81
L %	38.65	13.59	1.01	55.62	43.91	3.64
SI (g)	50.97	22.95	4.04	61.80	35.76	5.60
LI (g)	53.52	24.47	4.97	51.21	19.74	4.06
Mic	63.47	13.18	2.69	69.31	31.11	5.35
PI	64.85	8.62	1.43	77.45	50.22	6.72
2.5 % SL	60.39	41.11	3.15	54.38	41.90	5.43
LUR %	52.10	40.20	2.08	46.59	23.40	1.32

The expected genetic advance values from selection of the 5% superior plants in the F_2 generation were high (over 7%) for PFN (in both crosses), BW (in cross I) and SCY/P (in cross II). The high values of the predicted gain upon selection were also linked with high estimates of heritability indicating the possibility improvement of those characters through selection. While, moderate or low values of expected genetic advance under selection (less than 7%) were obtained for the remaining characters in both crosses, indicating that the improvement of these characters has low effect through selection.

In general, it could be concluded that the traits, which controlled by additive gene effect and high heritability values, could be improved by simple selection. On the other hand, the existence of high dominance gene effect would need hybrid program.

Phenotypic and genotypic correlation coefficients between all possible pairs of studied characters in cross I [Dandara x {Giza 83 x (Giza 75 x 5844)}] are presented in Table (6). The results of Phenotypic and genotypic correlation revealed positive or negative and highly significant coefficients between (B/P with each of BW and LY/P), (SCY/P with both of B/P and LY/P), (LI with each of L% and SI) and between (LUR % with each of Mic and 2.5% SL).

Table (6): Phenotypic (P) and genotypic (G) correlations between yield and its components and fiber properties for the intra-specific cross I Dandara x [G. 83 x G. 75 x 5844)].

Characters		B/P	BW (g)	SCY/P	LY/P	L %	SI (g)	LI	Mic	PI	2.5% SL	LUR %
PFN	P.	0.112	0.096	0.129	0.145	0.111	0.054	0.112	0.129	0.117	0.201	0.276
	G.	-0.142	-0.088	-0.068	-0.079	-0.014	-0.313**	-0.251*	0.093	-0.149	-0.215*	-0.263**
B/P	P.		-0.524**	0.942**	0.931	-0.058	0.018	-0.009	0.073	0.054	0-0.171	-0.084
	G.		1.943**	1.53*	1.169**	1.312**	0.412**	1.447**	0.24	0.176	0.486**	0.448**
BW	P.			-0.227	-0.222	-0.012	-0.093	-0.079	-0.049	0.034	0.239	0.057
	G.			1.073**	1.05**	0.376**	0.438**	0.093	0.156	0.149	0.302**	-0.032
SCY/P	P.				0.991**	-0.057	-0.009	-0.027	0.037	0.086	-0.106	-0.104
	G.				0.997**	0.522**	0.248*	0.647**	0.083	0.028	0.132	0.205*
LY/P	P.					0.067	0.014	0.057	0.021	0.073	-0.085	0.107
	G.					0.609**	0.198*	0.685**	0.111	-0.006	0.120	0.206*
L %	P.						0.193	0.694**	-0.055	-0.021	0.125	0.006
	G.						-0.261**	0.660**	0.103	-0.185	-0.058	-0.088
SI	P.							0.838**	-0.010	-0.236	0.219	0.197
	G.							0.472**	0.310**	0.413**	0.137	-0.231*
LI	P.								-0.030	-0.171	0.228	0.137
	G.								0.347**	0.236*	-0.167	0.258**
SI	P.									-0.112	0.067	0.330
	G.									0.180	0.102	0.016
2.5% SL	P.										-0.108	-0.171
	G.										0.193	0.119
LUR %	P.											0.499**
	G.											0.279**

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

Table (7): Phenotypic (P) and genotypic (G) correlations between yield and its components and fiber properties for the intra-specific cross II G. 90 x [G. 83 x G. 75 x 5844)].

Characters		B/P	BW (g)	SCY/P	LY/P	L %	SI (g)	LI	Mic	PI	2.5% SL	LUR %
PFN	P.	-0.030	0.054	0.001	0.022	0.178	0.165	0.260	0.055	0.311	0.266	0.156
	G.	-0.278**	-0.108	-0.489	-1.044**	-0.023	-0.183	-0.210*	0.089	0.140	-0.293	-0.145
B/P	P.		0.327*	0.984**	0.982**	0.139	-0.171	-0.068	-0.249	0.307	0.068	-0.039
	G.		-0.310**	0.906**	1.144**	-0..54**	1.318**	0.715**	0.951**	-0.742**	-0.278**	-0.201*
BW	P.			0.474**	0.463**	-0.037	0.135	0.094	0.045	0.108	0.012	0.137
	G.			0.110	0.189	0.298**	0.358**	0.470**	0.045	-0.044	0.164	0.454**
SCY/P	P.				0.997*	0.128	-0.158	-0.063	-0.220	0.304	0.069	-0.051
	G.				1.035**	-0.587**	2.095**	1.299**	1.306**	-1.064**	-0.338**	0.135
LY/P	P.					0.202	-0.170	-0.028	-0.195	0.293	0.085	-0.043
	G.					-1.041**	4.048**	2.462**	2.564**	-2.119**	-0.760**	-0.273**
L %	P.						-0.194	0.446**	0.224	-0.063	0.120	0.018
	G.						-0.108	0.313**	-0.151	0.018	-0.389**	0.146
SI	P.							0.785**	0.102	-0.082	0.068	0.068
	G.							0.666**	0.415**	-0.270**	0.306**	-0.023
LI	P.								0.229	-0.131	0.101	0.049
	G.								0.145	-0.089	0.061	0.407**
SI	P.									-0.075	-0.059	0.287
	G.									-0.145	-0.030	-0.764**
2.5% SL	P.										-0.037	-0.147
	G.										-0.083	0.290**
LUR %	P.											0.537**
	G.											0.573**

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

Genotypic correlation in cross I, revealed positive and highly significant or significant correlation coefficients between (B/P with each of BW, L %, SI, LI, 2.5% SL, LUR %) (BW with each of L%, SI and 2.5% SL), (SCY/P with B/P, BW, LY/P, L%, SI, LI and LUR %), (LY/P with each of B/P, BW, L %, SI, LI and LUR %) (L % with both of SI and LI), (SI with both of LI, Mic and PI), (LI with each Mic, PI, and LUR %) and (2.5% SL with LUR). The remaining relationships under study gave insignificant phenotypic and genotypic correlation coefficients. The relationship between SCY/P and other traits might be useful for cotton breeder who desires to improve seed cotton yield, to select plants superior in number of bolls per plant, consequently. These results are in harmony with those reported by El-Adl *et al.*(1981), El-Beily (1983), Allam (1992), Hassan (2007) and Eissa (2004b).

Regarding the second cross [Giza 90 x {Giza 83 x (Giza 75 x 5844)}], it could be clearly observed from Table (7) that, positive and highly significant phenotypic correlation coefficients were obtained between (B/P and BW), as well as between (SCY/P with each of B/P, BW and LY/P), (LY/P with each B/P and BW), (LI with each of L% and SI), and (2.5% SL with LUR %).

Positive and highly significant phenotypic correlation coefficients were found between (B/P and each of BW, SI, LI and MIC), (BW and each of L%, SI, LI and LUR %), (SCY/P and each of LY/P, SI, LI and Mic), as well as (LY/P with each of SI, LI and Mic) and between (LI with both L % and SI). Furthermore, highly significant or significant negative genotypic correlations were detected between (PFN and each of B/P, LY/P, LI and 2.5% SL), (B/P with each of L%, and 2.5% SL), (SCY/P with L%, PI and 2.5% SL), LY/P and each of L%, PI, 2.5% SL and LUR%), (L % with both Mic and 2.5% SL) and between (SI with PI). The remaining relationships under study gave insignificant phenotypic and genotypic correlation coefficients.

It is clear from the results of both crosses that genotypic correlation coefficients for most characters studied were higher than the phenotypic correlation coefficients. It seemed that the environmental factors had depressed the phenotypic correlation estimates.

In this connection, our results are supported by Ismail *et al.* (1991), El-Adly (1996), Eissa (2004) and El-Ameen *et al.* (2004). In contrary, El-Adl *et al.* (1981), Ismail *et al.* (1991), Allam (1992), who pointed out that genotypic correlation coefficients were less than phenotypic correlation coefficients or equal to zero value with most characters.

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تقدير بعض القياسات الوراثية وفعل الجين للمحصول ومكوناته والصفات التكنولوجية فى هجينين صنفين من القطن

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أجريت هذه الدراسة فى مزرعة محطة البحوث الزراعية فى سدس بمحافظة بنى سويف خلال مواسم 2004 ، 2005 ، 2006 وذلك لدراسة هجينين صنفين من القطن المصرى وهما [{جيزة 83 × (جيزة 75 × 5844)} × دندرة] و [{جيزة 83 × (جيزة 75 × 5844)} × جيزة 90] وقد تم تقييم ستة عشائر الخاصة بكل هجين (الابوين والجيل الاول والجيل الثانى والجيل الرجعى الاول والجيل الرجعى الثانى) فى تجربة قطاعات كاملة العشوائية باربعة مكررات ، وقجد أظهرت النتائج ما يلى:

1- أعطت قيم معدل قوة الهجين (منسوبة لاحسن الاباء) قيما موجبة وعالية المعنوية لصفة عقدة اول فرع ثمرى ، متوسط وزن اللوزة ، محصول القطن الزهر والشعر للنبات ، معامل الشعر ، والنعومة ، وطول التيلة عند 2.5% ، بينما كانت معنوية وسالبة لمتانة التيلة فى الهجين الاول. وأعطت فى الهجين الثانى قيما موجبة ومعنوية لصفات معامل البذرة ومتانة التيلة ، ومعنوية وسالبة لتصافى الحليج ، بينما أعطت باقى الصفات فى كلا الهجينين قيما غير معنوية لقوة الهجين منسوبة لاحسن أب.

2- أظهرت قيم معدل قوة الهجين (منسوب لمتوسط الابوين) فى كلا الهجينين قيما معنوية وموجبة لجميع الصفات فيما عدا متانة التيل فى الهجين الاول ، وطول التيلة عند 2.5% وتصافى الحليج فى الهجين الثانى حيث أظهرت قيما سالبة عالية المعنوية. أما باقى الصفات الاخرى فى كلا الهجينين فى كلا الهجينين فقد أعطت قيما غير معنوية لقوة الهجين (منسوبة لمتوسط الابوين) مما يدل على وجود تأثير للفعل الجينى المضيف على وراثة هذه الصفات.

3- كان الانخفاض الراجع للتربية الداخلية عالى المعنوية وموجبا لصفات متوسط وزن اللوزة ، محصول القطن الزهر للنبات ومعامل الشعر فى كلا الهجينين ، عقدة أول فرع ثمرى ، وطول التيلة عند 2.5% فى الهجين الاول ، ومحصول القطن الشعر للنبات ، النعومة والمتانة فى الهجين الثانى ، ومن جهة أخرى كانت القيم سالبة ومعنوية لصفة متانة التيلة فى الهجين الثانى.

4- أظهرت جميع الصفات المدروسة فى كلا الهجينين سيادة فائقة أو سيادة جزئية.

5- باختبار معنوية مدى تطابق نموذج الاضافة والسيادة بين الصفات المدروسة ، نستطيع ان نقرر ان معنوية واحد او اكثر من هذه المفردات (A, B, C) تدل على انحراف هذه القيم عن الصفر فى أغلب

الصفات المدروسة فى كلا الهجينين ، وهذا يؤكد أن هذا النموذج غير كافى للتعبير عن نموذج الاضافة والسيادة لهذه الصفات.

6- كان لتأثير الفعل الوراثى المضيف دورا كبيرا فى وراثة صفات عقدة أول فرع ثمرى ، تصافى الحليج ، معاملى البذرة والشعر ، متانة التيلة (فى كلا الهجينين) وفى توريث صفة طول التيلة عند 2.5% (فى الهجين الاول) وعدد اللوز على النبات ، محصول القطن الزهر والشعر للنبات (فى الهجين الثانى). مما يدل على أهمية الانتخاب لتحسين هذه الصفات.

7- أما بالنسبة لتأثير الفعل السيادى للجين فأن له دورا هاما فى توريث عدد اللوز على النبات ، محصول القطن الزهر والشعر ، معاملة البذرة والنعومة (فى كلا الهجينين) ، وفى توريث عقدة أول فرع ثمرى ، معامل الشعر (فى الهجين الاول) ووزن اللوزة ، ومتانة التيلة (فى الهجين الثانى).

8- أظهرت النتائج أن التأثير الراجع للتفاعل بين العوامل (الاضافة × الاضافة) يتحكم فى صفة عدد اللوز على النبات ، محصول القطن الزهر والشعر ، تصافى الحليج ، والمتانة (فى كلا الهجينين).

9- وبالنسبة للتأثير الجينى للتفاعل بين (الاضافة × السيادة) فانه يتحكم فى وراثة معظم الصفات تحت الدراسة فى كلا الهجينين.

10- كان للتفاعل الجينى بين (السيادة × السيادة) دورا فى توريث معظم الصفات المدروسة ما عدا صفات وزن اللوزة ، ومعاملى البذرة والشعر ، والمتانة (فى الجيل الاول) ومحصول القطن الزهر والشعر ، تصافى الحليج ، ومتانة التيلة (فى الجيل الثانى) حيث كانت هذه القيم غير معنوية.

11- سجلت درجة التوريث (بمعناها العام) قيما عالية (أعلى من 50%) لكل الصفات المدروسة فى كلا الهجينين ما عدا صفات عدد اللوزة ، محصول القطن الزهر والشعر للنبات ، تصافى الحليج (فى الهجين الاول) , وعدد اللوز ، ومتوسط وزن اللوزة ، درجة انتظام طول التيلة (فى الهجين الثانى) حيث سجلت درجة توريث متوسطة.

12- أعطت درجة التوريث بمعناها الضيق قيما متوسطة او منخفضة (اقل من 50%) لكل الصفات المدروسة فى كلا الهجينين.

13- كانت قيم التحسين الوراثى المتوقع من انتخاب احسن 5% من نباتات الجيل الثانى عالية (اكبر من 7%) لصفات عقدة اول فرع ثمرى ، ووزن اللوزة (فى الهجين الاول) ، عقدة اول فرع ثمرى ، محصول القطن الزهر للنبات فى (الهجين الثانى). أما باقى الصفات فقد أظهرت قيما متوسطة او منخفضة للتحسين الوراثى.

14- تشير نتائج معامل الارتباط المظهرى فى الهجين الاول الى وجود ارتباط موجب وعالى المعنوية بين (محصولى القطن الزهر والشعر للنبات وكل من عدد اللوز على النبات) ، (معامل الشعر وكل من تصافى الحليج % ، معامل البذرة) ، (درجة انتظام الطول وكل من قراءة الميكرونير ، طول التيلة عند 2.5%) ، بينما كان معامل الارتباط المظهرى سالبا وعالى المعنوية بين (عدد اللوز على البنات ومتوسط وزن اللوزة). واظهر الاتباط الوراثى فى الهجين الاول ارتباطا موجبا وعالى المعنوية او معنويا بين (عدد اللوز على النبات مع متوسط وزن اللوزة ، وتصافى الحليج % ، ومعاملى البذرة والشعر ، طول التيلة عند 2.5% ، درجة انتظام الطول) ، (محصولى القطن الزهر والشعر للنبات مع كل من عدد اللوز على النبات ، متوسط وزن اللوزة وتصافى الحليج % ، ومعاملى البذرة والشعر ، ودرجة انتظام الطول) ، (معامل الشعر مع كل من تصافى الحليج % ، معامل البذرة ، قراءة الميكرونير ، متانة التيلة ، درجة انتظام طول التيلة). بينما كان معامل الارتباط الوراثى سالبا ومعنويا بين (عقدة اول فرع ثمرى وكل من معاملى البذرة والشعر ، طول التيلة عند 2.5% درجة انتظام الطول).

15- سجلت نتائج الارتباط المظهرى فى الهجين الثانى الى وجود ارتباط موجب وعالى المعنوية بين (محصولى القطن الزهر والشعر للنبات وكل من عدد اللوز على النبات ، متوسط وزن اللوزة) ، (معامل الشعر وكل من تصافى الحليج % ، معامل البذرة) ، (عدد اللوز على النبات ومتوسط وزن اللوزة). بينما كان معامل الاتباط المظهرى سالبا وعالى المعنوية وأظهر الاتباط الوراثى فى الهجين الثانى ارتباطا موجبا وعالى المعنوية او معنويا بين (عدد اللوز على النبات مع متوسط وزن اللوزة ، ومعاملى البذرة والشعر ، قراءة الميكرونير) ، (محصولى القطن الزهرى والشعر للنبات مع كل من عدد اللوز على النبات ، متوسط وزن اللوزة ، ومعاملى البذرة والشعر ، قراءة الميكرونير) ، (معامل الشعر مع كل من تصافى الحليج % ، معامل البذرة). بينما كان معامل الارتباط الوراثى سالبا وعالى المعنوية بين (عقدة اول فرع ثمرى وكل من عدد اللوز للنبات ، محصول الشعر للنبات ، معامل الشعر ، طول التيلة عند 2.5%).