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GENETIC ANALYSIS OF SOME QUANTITATIVE CHARACTERS IN TWO COTTON CROSSES (*Gossypium barbadense* L.)

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ABSTRACT

The present investigation was carried out to evaluate the six generations of the two crosses of G. barbadense L. (CB 58 × G80) and (CB 58 × G90) to estimate the type of gene action, heterosis, inbreeding depression, heritability estimates and genetic advance under selection. Scaling test indicated that the additive – dominant gene effects were not adequate in controlling these characters. Therefore, the interaction of genes must be taken into account. The additive gene effects (a) were significant for all of the studied traits in both crosses, except NB/P and L% in cross I, and L%, SI and FL in cross II. Moreover, dominance gene effects (h) were significant for all traits in cross I (CB 58 × G80), except for Mic and PL. Meanwhile the traits L% and Fiber properties were significant in cross II (CB 58 × G90). The interaction of additive × Additive (i) type of epistasis was significant for all studied traits, except for L%, Mic and FL in cross I and BW, SI, LI and PI in cross II. The interaction additive × dominance (j) gene effects were highly significant for BW, SCY/P, LY/P, Mic, PI, FL and UR in cross I. While in crosses II, the traits BW, PI, FL and UR recorded highly significant additive × dominance epistatic gene effects (j). Dominance × dominance (l) types of epistasis gene effects were highly significant for all traits except for L% only in crosses I. The traits NB/P, SCY/P, LY/P, Mic, PI and UR recorded significant or highly significant epistasis gene effects (j) in cross II. Heterosis relative to better parent was highly significant and positive for PI, FL and UR in both crosses, while Mic value recorded positive and negative significant effects in cross I and cross II, respectively. On the other hand heterosis relative to mid-parent was highly significant for PI, FL and UR in both crosses, while SCY/P and LY/P recorded highly significant and significant heterotypic effects relative to mid-parent in cross I and cross II, respectively. Inbreeding depression for both crosses was insignificant for all traits. High values of broad-sense heritability (over 50%) were detected for BW, L%, PI, FL and UR in cross I and BW, LI, Mic and PI in cross II. Moderate broad-sense heritability estimates were found for LI and Mic in cross I and SI and UR in cross II. Low broad sense heritability values (< 30%) were obtained for NB/P, SCY/P, LY and SI, and NB/P, SCY/P, LY, L% and FL in cross I and cross II, respectively. High narrow-sense heritability estimates (> 50%) were obtained only for UR in cross I and Mic and UR in cross II. Moderate heritability estimates were observed for BW, L%, LI, PI and FL in cross I. Low heritability in narrow sense values were obtained for NB/P, SCY/P, LY, SI and Mic in cross I and all traits under study except Mic and UR in cross II. The expected genetic advance values from selecting the desired 5% of F_2 population indicated that the improvement by selection could be effective for SCY/P and L% in cross I and BW, PL, FL and UR in cross II.

Key words: ***Cotton (Gossypium barbadense L.), Additive, Dominance, Heritability.***

INTRODUCTION

Improvement of yield and fiber quality of Egyptian cotton varieties is the main goal in cotton breeding program. Therefore, knowledge of type and magnitude of genetic variance affecting important economical traits in cultivated plants is essential for the development of efficient selection and breeding procedures.

The progress of any breeding program depends on the available genetic information. Among the basic information required by the cotton breeders is the estimation and partitioning of genetic variance, for yield and its components.

The main objectives of this investigation were to study type of gene action, heterosis, inbreeding depression, heritability estimates and genetic parameters in two cotton crosses of *Gossypium barbadense*.

Several works studied genetic effects in cotton, (Hassan 2018) showed significant additive and dominance gene effect for (SCY/P), (L %) and (UR). (Amer 2017) reported that additive gene effects were significant for (BW), (SCY/P), (LC/P) and (L %), while dominance gene effects were presence for all traits and (Yehia 2015), noticed that the epistatic gene effects additive × additive and dominance × dominance were highly significant in most studied traits. Also, the inheritance of all studied traits was controlled by additive and non-additive genetic effects

MATERIALS AND METHODS

The procedure used in the study started by a cross between the commercial varieties Giza 80, Giza 90, and C.B 58 all are belonging to *G. barbadense* L. in 2014 season at Sids Experiment Station to obtain F_1 generation of the crosses Giza 80 × C.B 58 and Giza 90 × C.B 58.

In 2015 season, F_1 hybrid was crossed to both parents to produce backcrosses, in addition to selfing the F1 hybrid pants to produce F_2 seeds.

In 2016 season, the six populations P_1, P_2, F_1, F_2, BC_1 and BC_2 of the two crosses were grown in a randomized complete block design with three replications. Plots were single rows of 6 m length and 0.6 m apart, at Sids Experiment Station of Agricultural Research Center.

Data were taken on plants of the six populations in each cross. The following characters were recorded as follows

1 - Yield components

1.1. Number of bolls per plant (NB/P).
1.2. Boll weight in grams (B.W).
1.3. Seed cotton yield per plant in grams (S.C.Y).
1.4. Lint cotton yield/plant (L.C.Y.).
1.5. Lint percentage (L %)

1.6. Seed index in grams (S.I).
1.7. Lint index (L.I.).

2 - Fiber quality properties

2.1. Micronaire reading (Mic.), this trait was expressed as fiber fineness.
2.2. Fiber strength (F.S.) (P.I.), this trait was expressed as pressley index values.
2.3. Fiber length (F.L.) (mm), this trait was expressed as upper half mean length (U.H.M.) in (mm).
2.4. Uniformity ratio % (U.R. %); this trait was determined by the following formula:

U.R.% = [(50% span length/2.5% span length) × 100)]

Fiber properties were measured in the laboratory of Cotton Technology Research Division, Cotton Research Institute, ARC, Egypt.

Statistical and Genetic Analyses

The statistic method used was generations mean analysis. A, B and C scaling test of Mather and Jinks (1971) was used to test the adequacy of additive, dominance model. Percentage heterosis, inbreeding depression, degree of dominance, heritability in narrow and broad sense and genetic advance under selection were determined according to Allard (1960) and Miller *et al* (1964). The formulas used were as follows;

1. Heritability in broad sense (H_{bs})

$$h^2b = \frac{½ D + ¼ H}{½ D + ¼ H + E} \times 100 = \frac{VF_2 - VE}{VF_2} \times 100$$

2. Heritability in narrow sense (H_{ns})

$$h^2n = \frac{½ D}{½ D + ¼ H + E} \times 100 = \frac{2VF_2 - (VBC_1 + VBC_2)}{VF_2} \times 100$$

3. Estimation of genetic advance from selection (ΔG)

a) $\Delta G = 1.76 \times H^2n \times (VF2)^{1/2}$

b) $\Delta G\% = \frac{\Delta G}{\overline{F2}} \times 100$

RESULTS AND DISCUSSION

The mean performance and scaling test of six generations of the two crosses (CB 58 × G80) and (CB 58 × G90) for different traits are presented in Table (1). In cross I (CB 58 × G80), the variety G80 (P_2) showed higher mean performance than the variety CB 58 (P_1) for BW, SCY/P, LY/P, L%, Mic, FL and UR.

Table 1. Mean performance and scaling test ± standard error of six population for yield components and fiber properties of the two intraspecific crosses.

Cross 1	CB58 × G 80				
	Characters				
	NB/P	Bw	SCY/P	LY/P	L%
P_1	61.09 ± 1.88	2.99 ± 0.05	180.20 ± 4.56	72.32 ± 2.10	40.03 ± 0.30
P_2	56.70 ± 3.36	3.35 ± 0.06	187.88 ± 10.4	76.39 ± 4.09	40.74 ± 0.20
F_1	75.27 ± 4.74	3.36 ± 0.06	251.1 ± 14.64	101.4 ± 6.32	40.23 ± 0.21
F_2	55.69 ± 1.26	3.27 ± 0.04	180.44 ± 3.53	71.48 ± 1.41	39.62 ± 0.16
BC_1	48.85 ± 1.48	3.51 ± 0.04	170.23 ± 4.47	68.53 ± 1.90	40.21 ± 0.16
BC_2	45.99 ± 1.46	3.32 ± 0.04	151.59 ± 4.48	60.40 ± 2.01	39.78 ± 0.44
A	-38.65 ± 5.89	0.67 ± 0.11	-90.9 ± 17.75	-36.66 ± 7.67	0.15 ± 0.49
B	-39.97 ± 6.50	-0.08 ± 0.12	-135.8 ± 20.1	-56.98 ± 8.54	-1.40 ± 0.93
C	-45.55 ± 11.4	-0.001 ± 0.2	-148.6 ± 34.4	-65.6 ± 14.59	-2.76 ± 0.85
Cross 2	CB58 × G 90				
P_1	61.09 ± 1.88	2.99 ± 0.050	180.20 ± 4.56	72.32 ± 2.10	40.03 ± 0.30
P_2	48.56 ± 1.78	3.21 ± 0.045	154.18 ± 5.38	63.15 ± 2.30	40.90 ± 0.19
F_1	66.50 ± 1.98	3.37 ±0.061	222.18 ± 3.85	86.58 ± 1.72	38.94 ± 0.23
F_2	58.43 ± 1.88	3.27 ± 0.046	188.15 ± 5.11	76.78 ± 2.23	40.71 ± 0.17
BC_1	56.04 ± 1.87	3.30 ± 0.048	183.14 ± 5.52	72.86 ± 2.25	39.75 ± 0.14
BC_2	50.17 ± 1.36	3.15 ± 0.043	156.94 ± 4.03	63.02 ± 1.63	40.17 ± 0.22
A	-15.52 ± 4.63	0.24 ± 0.125	-36.15 ± 12.6	-13.19 ± 5.26	0.52 ± 0.472
B	-14.72 ± 3.8	-0.27 ± 0.114	-62.47 ± 10.4	-23.69 ± 4.35	0.51 ± 0.531
C	-8.92 ± 8.87	0.14 ± 0.230	-26.18 ± 22.9	-1.51 ± 10.04	4.02 ± 0.881

Table 1. Cont.

Cross 1	CB58 × G 80					
	Characters					
	SI	LI	Mic	PI	F L	UR
P_1	9.90 ± 0.27	6.62 ± 0.19	4.03 ± 0.03	9 ± 0.06	30.7 ± 0.11	83.52 ± 0.1
P_2	9.45 ± 0.23	6.49 ± 0.16	4.22 ± 0.03	8.88 ± 0.05	30.9 ± 0.05	83.57 ± 0.1
F_1	10.20 ± 0.22	6.86 ± 0.13	4.17 ± 0.03	9.35 ± 0.07	31.8 ± 0.08	84.22 ± 0.2
F_2	9.42 ± 0.14	6.19 ± 0.11	3.89 ± 0.05	9.06 ± 0.06	31.1 ± 0.12	83.79 ± 0.1
BC_1	10.74 ± 0.18	7.22 ± 0.12	4.15 ± 0.03	8.76 ± 0.04	30.2 ± 0.07	83.9 ± 0.04
BC_2	10.18 ± 0.18	6.76 ± 0.18	3.69 ± 0.03	8.9 ± 0.05	31.5 ± 0.15	84.6 ± 0.08
A	1.37 ± 0.49	0.97 ± 0.33	0.09 ± 0.07	-0.84 ± 0.12	-2.1 ± 0.19	0.12 ± 0.21
B	0.71 ± 0.48	0.16 ± 0.42	-0.98 ± 0.07	-0.43 ± 0.14	0.37 ± 0.31	1.49 ± 0.25
C	-2.07 ± 0.80	-2.07 ± 0.57	-0.99 ± 0.20	-0.36 ± 0.28	-0.84 ± 0.54	-0.34 ± 0.5
Cross 2	CB58 × G 90					
P_1	9.90 ± 0.271	6.62 ± 0.189	4.03 ± 0.03	9 ± 0.064	30.7± 0.11	83.52 ± 0.1
P_2	10.40 ± 0.31	7.20 ± 0.205	4.18 ± 0.06	8.65 ± 0.02	30.2 ± 0.07	82.9 ± 0.03
F_1	10.81 ± 0.27	6.89 ± 0.181	3.93 ± 0.04	9.15 ± 0.04	31.3 ± 0.10	84.1 ± 0.13
F_2	9.57 ± 0.185	6.58 ± 0.140	4.18 ± 0.03	8.98 ± 0.04	30.3 ± 0.13	83.55 ± 0.1
BC_1	9.55 ± 0.262	6.29 ± 0.168	3.87 ± 0.02	9 ± 0.027	30.2 ± 0.05	83.75 ± 0.1
BC_2	10.08 ± 0.20	6.77 ± 0.138	4.09 ± 0.1	9.13 ± 0.03	30.9 ± 0.08	84.8 ± 0.06
A	-1.62 ± 0.65	-0.93 ± 0.43	-0.23 ± 0.07	-0.15 ± 0.1	-1.2 ± 0.18	-0.13 ± 0.3
B	-1.04 ± 0.57	-0.55 ± 0.39	0.06 ± 0.21	0.47 ± 0.08	0.3 ± 0.197	2.48 ± 0.2
C	-3.66 ± 1.01	-1.27 ± 0.72	0.62 ± 0.17	-0.043 ± 0.2	-2.3 ± 0.58	-0.49 ± 0.5

A = additive, B = dominance and C = non-allic interaction.

Moreover, the variety CB 58 (P_1) revealed higher mean performance than G80 (P_2) for NB/P, SI, LI and PI. Moreover the F_1 generation showed higher mean performance value than other generation for NB/P, BW, SCY/P, LY/P, SI, PI and FL, (Table 1). Backcross 1 (BC1) showed higher mean performance than (BC_2) for all studied traits, except for PI, FI and UR.

In cross II (CB 58 × G90), data on the mean performance for most of the studied traits showed that the variety CB 58 (P_1) recorded higher values than G90 (P_2) for NB/P, SCY/P, LY/P, PI and FL compared with the variety G90 (P_2). On the other hand, G90 (P_2) revealed higher mean performance than CB 58 (P_1) for BW, L% and Mic. F_1 generation showed higher mean performance than other generations for NB/P, BW, SCY/P, LY, SI, PI and

FL. Backcross (BC_1) has higher values than (BC_2) for BW, SCY/P and LY/P. While, (BC_2) gave higher values for the other traits, (Table 1).

Mather's scaling test A, B and C of the two crosses is given in (Table 1). It is worthy to mention that A, B and C values were deviated from Zero and were significant for all studied traits, except for L%, Mic and UR which were insignificant for A value, BW, L%, SI, LI and FL which were insignificant for B value and BW, PI and UR which were insignificant for C value, respectively in cross I. Scaling test results of the cross II, showed that A, B and C showed different values for all studied traits and deviated from Zero. A values were significant for all traits, except for BW, L%, PI and UR. Whereas, B values were significant for NB/P, BW, SCY/P, LY, PI and UR. While C values were significant for L%, SI, LI and FL.

Significant of any one of the scaling tests suggested the presence of non-allelic interaction. Meanwhile, insignificant scaling test suggested that the additive and dominance effects are adequate and important for these traits. These results are in agreement with those reported by El-Adly (2004), Esmail (2007), Haleem et al (2010), Nassar (2013) and Srinivas and Bhadru (2015).

The gene effects using generations' means are presented in (Table 2). It could be clearly observed from that the constant mean values (m) were highly significant for all studied traits in both crosses. Additive gene action (d) was significant for all studied traits in both crosses except NB/P and L% in cross I and L%, and SI in cross II. Meanwhile, the dominance gene effects (h) were significant or highly significant for NB/P, BW,SCY/P, SI, LI and UR in cross I, whereas, L% character and fiber properties were only highly significant in cross II.

The Additive × Additive (i) type of epistasis gene effects was significant for all studied traits, except for L%, Mic and FL in cross I and BW, SI, LI and PI in cross II. The additive × dominance (j) gene effects were highly significant for BW, SCY/P, LY/P, Mic, PI, FL and UR in cross I. While in cross II, the traits BW, PI, FL and UR recorded highly significant additive × dominance epistatic gene effects (j). Dominance × dominance (l) type of epistasis gene effects were highly significant for all traits, except for L% only in crosses I. The traits NB/P, SCY/P, LY/P, Mic, PI and UR recorded significant or highly significant epistasis gene effects (j) in crosses II.

Table 2. Type of gene action ± standard error for studied traits of the two intraspecific crosses (CB58 × G 80) and (CB58 × G 90.

Cross 1	CB58 × G 80					
	Characters					
	NB/P	Bw	SCY/P	LY/P	L%	SI
m	55.69 ± 1.26	3.27 ± 0.038	180.44 ± 3.530	71.48 ± 1.412	39.62 ± 0.16	9.42 ± 0.143
d	2.86 ± 2.08	0.19 ± 0.059	18.64 ± 6.332	8.13 ± 2.768	0.42 ± 0.472	0.56 ± 0.252
h	-16.71 ± 8.29	0.78 ± 0.202	-11.04 ± 24.624	-1.01 ± 10.381	1.35 ± 1.175	4.68 ± 0.812
i	-33.08 ± 6.52	0.59 ± 0.191	-78.10 ± 18.967	-28.06 ± 7.908	1.51 ± 1.14	4.15 ± 0.763
j	0.66 ± 2.83	0.37 ± 0.070	22.46 ± 8.503	10.16 ± 3.601	0.77 ± 0.506	0.33 ± 0.309
l	111.7 ± 14.10	-1.18 ± 0.309	304.83 ± 42.75	121.70 ± 18.31	-0.26 ± 2.06	-6.23 ± 1.29
Cross 2	CB58 × G 90					
m	58.43 ± 1.88	3.27 ± 0.046	188.15 ± 5.105	76.78 ± 2.226	40.71 ± 0.17	9.57 ± 0.185
d	5.87 ± 2.309	0.15 ± 0.064	26.19 ± 6.832	9.84 ± 2.783	-0.43 ± 0.26	-0.54 ± 0.33
h	-9.65 ± 9.13	0.085 ± 0.234	-17.48 ± 25.118	-16.53 ± 10.75	-4.52 ± 0.89	1.66 ± 1.046
i	-21.31 ± 8.82	-0.18 ± 0.224	-72.45 ± 24.570	-35.38 ± 10.5	-2.10 ± 0.84	1.002 ± 0.99
j	-0.39 ± 2.65	0.26 ± 0.073	13.16 ± 7.689	5.25 ± 3.191	0.0064 ± 0.32	-0.29 ± 0.39
l	51.55 ± 12.81	0.23 ± 0.345	171.07 ± 35.67	72.26 ± 14.99	1.98 ± 1.365	1.66 ± 1.652
Cross 1	CB58 × G 80					
	Characters					
	LI	Mic	PI	F L	UR	
m	6.19 ± 0.108	3.89 ± 0.05	9.06 ± 0.06	31.07 ± 0.12	83.79 ± 0.1	
d	0.47 ± 0.216	0.49 ± 0.04	-0.14 ± 0.07	-1.24 ± 0.16	-0.71 ± 0.09	
h	3.51 ± 0.639	0.14 ± 0.20	-0.51 ± 0.27	0.21 ± 0.60	2.64 ± 0.43	
i	3.19 ± 0.612	0.10 ± 0.20	-0.92 ± 0.26	-0.84 ± 0.59	1.96 ± 0.39	
j	0.40 ± 0.249	0.54 ± 0.04	-0.20 ± 0.08	-1.21 ± 0.17	-0.69 ± 0.11	
l	-4.33 ± 1.03	0.79 ± 0.25	2.19 ± 0.38	2.52 ± 0.84	-3.59 ± 0.61	
Cross 2	CB58 × G 90					
m	6.58 ± 0.140	4.18 ± 0.03	8.98 ± 0.04	30.29 ± 0.13	83.55 ± 0.1	
d	-0.48 ± 0.22	-0.22 ± 0.1	-0.13 ± 0.04	-0.47 ± 0.09	-1.017 ± 0.1	
h	-0.22 ± 0.75	-0.97 ± 0.3	0.69 ± 0.19	2.32 ± 0.57	3.74 ± 0.49	
i	-0.21 ± 0.71	-0.79 ± 0.2	0.36 ± 0.19	1.45 ± 0.56	2.85 ± 0.47	
j	-0.19 ± 0.26	-0.15 ± 0.1	-0.31 ± 0.05	-0.75 ± 0.11	-1.31 ± 0.13	
l	1.69 ± 1.133	0.97 ± 0.44	-0.68 ± 0.26	-0.59 ± 0.69	-5.19 ± 0.68	

m = mean, d = additive, h = dominance, i = additive × additive, j = additive x dominance and l = dominance x dominance

From the above results, it could be concluded that the additive and dominance gene effects as well as some epistasis gene effects could be contributed in the inheritance of the studied characters. In this respect, many authors reported similar results, such as Ali *et al* (2007), Iqbal *et al* (2013), Mohsen and Amein (2016) and Baloch *et al* (2016).

Heterosis, inbreeding depression and average degree of dominance are presented in (Table 3). Highly significant and positive heterotic effects relative to better parent (H.BP) that are useful for the cotton breeder, were detected for PI, FL and UR in both crosses, while the Mic value showed highly significant, positive and negative effects in cross I and cross II, respectively.

Table 3. Heterosis, inbreeding depression (ID) and average degree of dominance ($\bar{a}$) for yield components and fiber properties of the two intraspecific crosses.

Parameters		NB/P	Bw	SCY/P	LY/P	L%	
Cross1		**CB58 × G 80**					
Heterosis	**BP %**	**61.09**	**3.35**	**187.88**	**76.39**	**40.74**	
	MP %	**58.90**	**3.12**	**184.04****	**71.71****	**38.97**	
ID %		**26.00**	**2.87**	**28.15**	**29.50**	**1.52**	
$\bar{a} = \sqrt{H/D}$		**2.42**	**2.42**	**0.77**	**0.35**	**1.79**	
Cross2		**CB58 × G 90**					
Heterosis	**BP %**	**8.85**	**-0.88**	**23.30**	**32.58**	**0.25**	
	MP %	**21.28**	**6.98**	**32.89***	**36.53***	**3.76**	
ID %		**12.13**	**2.97**	**15.32**	**11.32**	**-4.55**	
$\bar{a} = \sqrt{H/D}$		**1.28**	**0.75**	**0.82**	**1.30**	**3.26**	
Parameters		**SI**	**LI**	**Mic**	**PI**	**F L**	**UR**
Cross1		**CB58 × G 80**					
Heterosis	**BP %**	**9.45**	**6.62**	**3.90****	**9.00****	**30.78****	**83.57****
	MP %	**9.67**	**6.55**	**4.06**	**8.90****	**30.75****	**83.55****
ID %		**7.65**	**9.78**	**6.71**	**3.10**	**2.31**	**0.51**
$\bar{a} = \sqrt{H/D}$		**2.89**	**2.74**	**0.57**	**1.88**	**0.41**	**1.93**
Cross2		**CB58 × G 90**					
Heterosis	**BP %**	**9.19**	**-4.31**	**-5.13****	**8.89****	**5.83****	**4.53****
	MP %	**6.50**	**-0.29**	**-8.42**	**11.05****	**6.80****	**4.90****
ID %		**11.47**	**4.46**	**-6.36**	**1.86**	**3.23**	**0.68**
$\bar{a} = \sqrt{H/D}$		**1.76**	**0.68**	**2.09**	**2.27**	**2.23**	**1.92**

BP = better parent   MP = parent mid-parent
***, ** significant at the 0.05 and 0.01 probability levels, respectively.**

Highly significant heterosis relative to mid parents (H.MP) were obtained for PI, FL and UR in both crosses. Moreover SCY / P and LY/P recorded highly significant and significant heterotic effects relative to mid-parent in cross I and cross II, respectively.

Inbreeding depression values (ID%) in (Table 3), were insignificant for all traits in both crosses. Insignificant ID % may be due to the presence of linkage between genes controlling these characters in these materials. In general, the present investigation revealed that not only additive but also non-additive genetic variance components were important in the inheritance of these characters of cotton material used in this study.

Average degree of dominance $\bar{a} = \sqrt{H/D}$ (Table 3), revealed an over dominance effects for NB/P, BW, L%, SI, LI, PI and UR traits in cross I and for NB/P, L%, SI, LI, PI and UR traits in cross II. While, partial dominance controlled SCY/P, LY/P, Mic and FL traits in cross I and BW, SCY/P and LI traits in cross II. The above results indicated that the main cause of heterotic effects was due to both over dominance and epstatic gene effects for PI and UR and all fiber traits in cross I and cross II respectively, toward the better parent. Also partial dominance effects were detected for SCY/P, LY/P and FL in cross I, towards the lower parent.

Heritability estimates in broad and narrow senses ($H_{b.s}$ and $H_{n.s}$) and genetic advance as percentage as the mean upon selecting the highest 50% for studied traits are presented in Table (4). The values of heritability in broad sense (> 50%) were detected for BW, L%, PI, FL and UR in cross I and BW, LI, Mic and PI in cross II. Moderate broad sense heritability estimates (from 30% to 50%) were found for LI and Mic in cross I and SI and UR in cross II. However, low broad sense heritability values (< 30%) were obtained for (NB/P, SCY/P, LY/P and SI) and (NB/P, SCY/P, LY/P, L% and FL) in cross I and cross II, respectively, (Table 4).

High narrow sense heritability estimates were obtained only for UR in cross I and Mic and UR which exceeded 50% values. Moderate heritability estimates were observed for BW, L%, LI, PI and FL in cross I. On the contrary, low heritability in narrow sense values were obtained for NB/P, SCY/P, LY/P, SI and Mic in cross I and all traits in cross II except Mic and UR.

Table 4. Heritability precentages, genetic advance (ΔG) expressed as percentage of mean for yield components and fiber properties of the two intraspecific crosses.

Parameters		NB/P	Bw	SCY/P	LY/P	L%	
Cross1		CB58 × G 80					
Heritability	H_{bs}	3.09	57.42	2.15	4.14	72.14	
	H_{ns}	0.60	44.81	1.22	1.60	35.62	
ΔG		11.7	17.3	51.8	9.1	95.5	
Cross2		CB58 × G 90					
Heritability	H_{bs}	0.91	79.18	0.23	0.77	25.17	
	H_{ns}	0.47	26.35	0.33	0.82	9.67	
ΔG		7.18	67.39	8.35	4.42	19.72	
Parameters		SI	LI	Mic	PI	F L	UR
Cross1		CB58 × G 80					
Heritability	H_{bs}	6.32	41.20	37.87	64.78	59.85	65.11
	H_{ns}	4.43	38.64	12.07	42.12	45.01	62.22
ΔG		13.6	17.8	14.5	27.1	26.0	11.2
Cross2		CB58 × G 90					
Heritability	H_{bs}	47.67	60.03	91.46	77.44	16.14	45.63
	H_{ns}	9.21	12.60	78.82	21.37	14.76	41.56
ΔG		20.75	36.96	11.96	64.39	90.46	74.50

H_{bs} = heritability in broad sense , H_{ns} = heritability in narrow sense

The expected genetic advance values from selecting the desired 5% of population in F_2 plants (Table 4) ranged from 9.1% for LCY/P to 95.5% for L% in cross I and ranged from 4.42 % for LY to 90.46% for FL in cross II. The results of expected genetic advance for SCY/P and L% in cross I and BW, PL, FL and UR in cross II were high, indicating that the improvement of these characters is highly effective through selection, while selection for the other characters would be less effective. It could be concluded from the previous results that selection in the F_2's of these hybrids will improve the characters which showed high genetic advance values and selected genetics should be evaluated in several environments through the cotton breeding program.

Breeding implication

The results suggested that these characters (SCY/P) and (L %) and (BW), (PI), (FL) and (UR) in cross (CB58 × G 80) and cross (CB58 × G 90) respectively, it could be improved through appropriate selection method or by hybrid development in cotton breeding program.

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التحليل الوراثي لبعض الصفات الكمية في هجينين من القطن (الباربادينس)

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الهدف من البحث هو دراسة طبيعة الفعل الجيني وقوة الهجين ومعامل التربية الداخلية وكفاءة التوريث والتحسين المتوقع من الانتخاب لبعض الصفات الاقتصادية لهجينين من القطن (هجن صنفية) وهي (سي بي ٥٨ X جيزة ٨٠) و (سي بي ٥٨ X جيزة ٩٠) وذلك خلال ثلاثة مواسم هي ٢٠١٤ , ٢٠١٥ , ٢٠١٦ في تجربة قطاعات كاملة العشوائية من ثلاثة مكررات. تم زراعة المواسم الثلاث بمزرعة محطة بحوث سدس – مركز البحوث الزراعية – محافظة بني سويف. وكانت اهم النتائج المتحصل عليها هى. كان تأثيرالفعل الجيني المضيف معنوى لكل الصفات المدروسة فى كلا الهجينين عدا صفة عدد اللوز على النبات وتصافي الحليج في الهجين الاول ومعامل البذرة وتصافي الحليج وطول التيلة في الهجين الثاني بينما كان تأثير الفعل السيادى للجين معنوي في كل الصفات المدروسة في الهجين الاول ماعدا صفة نعومة التيلة ومتانة التيلة بينما كان تصافي الحليج وصفات الجوده معنوية في الهجين الثاني. وقد اوضحت النتائج ان تأثير التفوق الراجع الي تأثير الفعل الجيني المضيف × المضيف معنوي لكل الصفات المدروسة في الهجين الاول والثاني عدا صفات تصافى الحليج ونعومة التيلة وطول التيلة في الهجين الاول وصفات متوسط وزن اللوزة ومعامل البذرة ومعامل الشعر ومتانة التيلة في الهجين الثاني. اما تأثير التفوق الراجع الى الفعل الجيني المضيف × الفعل الجيني السيادى معنوى فى صفات متوسط وزن اللوز ومحصول القطن الزهر والشعر ونعومة التيلة ومتانة التيلة وطول التيلة ومعامل انتظام التيلة فى الهجين الاول بينما الهجين الثاني كان معنوى لصفات متوسط وزن اللوزه وطول التيلة ومعامل انتظام التيلة. كذلك اوضحت النتائج ان تفوق الفعل الجيني الراجع الي التفاعل بين الفعل الجيني السيادى × السيادى كان معنويا لكل الصفات المدروسة عدا صفة تصافى الحليج في الهجين الاول وبينما كانت معنوية لصفات عدد اللوز على النبات ومحصول القطن الزهر والشعر ونعومة التيلة ومتانة التيلة ومعامل انتظام التيلة في الهجين الثاني. كانت قوة الهجين منسوبة الي افضل الابوين موجبة وعالية المعنوية لصفات متانة التيلة وطول التيلة ومعامل انتظام التيلة في كلا الهجينين بينما سجلت صفة نعومة التيلة معنويه موجبة وسالبة في الهجين الاول والثاني علي التوالي. علي الجانب الاخر كانت قوة الهجين منسوبة الي متوسط الابوين عالية المعنوية لصفة متانة وطول التيلة ومعامل

انتظام التيلة لكلا الهجينين بينما كانت صفة محصول القطن الزهر والشعر عالية المعنوية لقوة الهجين منسوبة الي متوسط الابوين في كلا الهجينين. أوضحت النتائج ان معامل التربية الداخلية غيرمعنوى لكل الصفات المدروسة. أضهرت النتائج ان كفاءة التوريث في المعني الواسع عالية (أكثر من ٥٠%) لصفات متوسط وزن اللوزه وتصافى الحليج وطول التيله ومتانة التيله ومعامل انتظام التيلة في الهجين الاول بينما كانت عالية لصفات متوسط وزن اللوزه ومعامل الشعر ونعومة ومتانة التيلة في الهجين الثاني. كذلك كانت كفاءة التوريث في المعني الواسع متوسطه (من ٣٠- ٥٠%) لصفات معامل الشعر ونعومة التيلة للهجين الاول ولصفة معامل البذره ومعامل انتظام التيلة في الهجين الثاني. كذلك اوضحت النتائج ان كفاءة التوريث في المعني الواسع كانت منخفضة (أقل من ٣٠%) لصفة عدد اللوز علي النبات ومحصول القطن الزهر ومحصول القطن الشعر ومعامل البذره في الهجين الاول ولصفة عدد اللوز علي النبات ومحصول القطن الزهر ومحصول القطن الشعر وتصافى الحليج وطول التيلة في الهجين الثاني. كذلك اوضحت النتائج ان كفاءة التوريث في المعني الضيق كانت عالية (أكثر من ٥٠%) فقط لصفة معامل انتظام التيلة في الهجين الاول ولصفات نعومة التيلة ومعامل انتظام التيلة للهجين الثاني بينما كانت متوسطه (٣٠- ٥٠%) لصفات متوسط وزن اللوزة وتصافي الحليج ومعامل الشعر ومتانة التيلة وطول التيلة في الهجين الاول. بينما كانت كفاءة التوريث في المعني الضيق منخفضة (أقل من ٣٠%) لصفة عدد اللوز علي النبات ومحصول القطن الزهر والشعر ومعامل البذره ونعومة التيلة في الهجين الاول ولكل الصفات المدروسة فيما عدا نعومة التيلة ومعامل انتظام التيلة في الهجين الثاني. أظهر التحسين المتوقع من الانتخاب لنباتات الجيل الثاني أنه يمكن التحسين لصفة محصول القطن الشعروتصافى الحليج في الهجين الاول ولصفة متوسط وزن اللوزة ومتانة وطول التيلة ومعامل انتظام التيلة في الهجين الثاني.

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