INHERITANCE OF QUANTITATIVE TRAITS OF EGYPTIAN COTTON (*G. barbadense* L.) (B-Earliness and Fiber traits) El-Adl, A.M.*; Z.M. El-Diasty*; A.A. Awad**; A.M. Zenia** and A.M.Abd El-Bary**

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ABSTRACT

Six Egyptian cotton varieties were set up in diallel cross mating design to produce 15 F₁ hybrids and 15 F_{1r} reciprocal hybrids at 1996 growing season. In 1997 growing season, two experiments were carried out at both Sakha, Kafr El-Sheikh Governorate (L₁) and Kafr Saad, Damietta Governorate (L₂). Each experiment was designed in a randomized complete blocks with four replications. The 36 entries were evaluated for earliness and fiber traits: First fruiting node (F.F.N.), days to first opening boll (D.F.O.B.), earliness index (E.I.), fiber fineness (F.F.), fiber strength (F.S) and fiber length at (2.5% S.L) under two location. The results of the analyses of variance indicated that differences among population means were present and highly significant for all studied traits at the two locations and combined data except (D.F.O.B) at (L₁). Also the genotypes by location interactions were significant or high significant for all studied traits except fiber fineness (F.F) trait, indicating the presence of interaction between genotypes and locations. The lowest amount of heterosis versus mid- parents was (-0.64 %) for days to first opening boll and the largest amount was (4.60 %) for earliness index. Heterosis versus better-parent was not of economical importance. Tests of significant of the mean squares of general combining ability (G.C.A.) were larger in magnitudes than those specific combining ability (S.C.A.) and showed highly significance for all studied traits. In the same time specific combining ability by location variance (σ^2 s L) were larger than the other genetic components general combining ability by location variance (σ^2 g L) and reciprocal by location variance $(\sigma^2 r L)$ for all studied traits. The magnitudes of dominance genetic variance (σ^2 D) were larger than those additive genetic variance (σ^2 A) and reciprocal genetic variance (σ^2 r) for all studied earliness and fiber traits with the except of earliness index (E.I) trait. The estimates of broad sense heritabilities were larger in magnitude than their corresponding estimates of narrow sense heritabilities for all studied traits at two locations and from combined data except (F.F.N.) and (D.F. O.B) traits at location (L_1) , (F.S.) trait at (L_2) and (E.I.) trait from combined data.

INTRODUCTION

Breeding for earliness and fiber traits is an important objective in most cotton breeding programes, therefore, understanding the nature of gene action is useful to determine the breeding method must be followed to improve such these quantitative traits. Syiam *et al.*(1982), Rady and Gomaa (1983), Kajjidoni *et al.* (1984), Awad *et al.* (1986), Thomson and Luckett (1988), Tomer *et al.* (1988), Okasha (1989), El-Helw (1990), Kosba *et al.* (1991), Fahmy *et al.* (1994), Hendawy (1994c) and Gomaa (1997) obtained significant heterosis versus mid-parents for most earliness and fiber traits, while heterosis versus better-parent was different. Zaitoon *et al.* (1982), Rady and Gomaa (1983), Kosba *et al.*(1991) and Gomaa (1997) investigated types of gene action, they reported the additive types were more important than non-additive types for earliness and fiber traits.Kassem *et al.*(1981a),Singh and Singh(1981),Awad *et al.*(1986), Okasha (1989), Awad (1991), Kosba *et*

al. (1991), Zeina (1991), Amer (1995) and Gomaa (1997) obtained different estimates for both broad and narrow sense heritabilities.

The heritability in both broad and narrow senses are of great importance to plant breeders in selecting the most suitable breeding programs .The general objectives of this study are to investigate the amount of heterosis for the important economic traits of cotton in intra-specific crosses of *G. brbadense* L. The investigation of the nature of gene action with respect to the relative magnitudes of additive and non-additive genetic variances is accomplished through evaluating general and specific combining ability of the complete diallel crosses.

MATERIALS AND METHODS

The cotton varieties used in this study included six Gossypium barbadese L. cultivators Giza 85 (P₁), Giza 86 (P₂), Giza 89 (P₃), Giza 76 (P₄), Giza 77 (P₅) and Giza 87 (P₆) representing a wide range of variability in most of the studied traits, were utilized. The experiments reported herein were carried out at two locations, Sakha, Kafr El-Sheikh Governorate (L1) and Kafr Saad, Damietta Governorate (L2) during the two successive seasons 1996 and 1997 growing seasons. A diallel cross set was carried out among the six cotton varieties in 1996 growing season. The parental varieties and their possible 30 F₁ hybrids (including reciprocal) were sown in 1997 at the two locations, i.e. Sakha (L1) and Kafr Saad (L2). The two experiments were arranged in a randomized complete blocks design with four replications per each location. Each plot was one row 4.0 m. long and 0.6 m. wide. Hills were 0.2 m. apart to insure 20 hills per row. At seedling stage, plants were thinned to keep a constant stand of two plants per hill with 40 plants per row. Ordinary cultural practices were followed as usual for the cotton crop in the two locations. Data were recorded on an individual guarded plants of the 36 genotypes for the following traits first fruiting node (F.F.N.), days to first opening boll (D.F.O.B.), earliness index (E.I.), fiber fineness (F.F.), fiber strength (F.S.) and fiber length at (2.5% S.L) under the two locations.

Estimates of both general combining ability (G.C.A.) and specific combining ability (S.C.A.) were computed according to Griffing (1956) designated as method (I), model (II). The combined analysis was calculated over the two locations to test the interactions of the different genetic components with the two locations. Heterosis was expressed for all studied traits as percent increase of the F_1 performance above the mid-parents and better- parent.

The estimates of heritabilitias were determined according to the following equations:

1- From single location:

a- h²b (broad sense heritability) =
$$\frac{2 \sigma^2 g + \sigma^2 s}{2 \sigma^2 g + \sigma^2 s + \sigma^2 e} \times 100$$

b- h²n (narrow sense heritability) =
$$\frac{2 \sigma^2 g}{2 \sigma^2 g + \sigma^2 s + \sigma^2 \frac{e}{r}} \times 100$$

2- From combined data over locations:

$$a - h^{2}b = \frac{2 \sigma^{2}g + \sigma^{2} s}{2 \sigma^{2}g + \sigma^{2} s + \sigma^{2} r + 2 \frac{\sigma^{2}gL}{L} + \frac{\sigma^{2}rL}{L} + \frac{\sigma^{2}e}{rL}} \times 100$$

b-
$$h^{2}_{n}$$
 = $\frac{2 \sigma^{2}g}{2 \sigma^{2}g + \sigma^{2} s + \sigma^{2} r + 2 \sigma^{2}gL + \sigma^{2}sL + \sigma^{2}rL + \sigma^{2}e}{L} \times 100$

RESULTS AND DISCUSSION

The analysis variance of each location and combined data for all studied traits are given in Tables 1 and 2. The results indicated that earliness and fiber traits showed highly significant differences between all genotypes except (D.F.O.B.) at (L₁), also the genotypes by locations interactions were significant except (F.F.) trait. The amounts of heterosis values could be expressed as the percent deviation of F1 hybrids versus the average of midparents (M.P) or the means of the better-parent (B.P). Heterosis values were obtained from the (M.P) and the (B.P) for earliness and fiber traits and the results are cleared in Table 3. Similarly, heterosis values were also calculated over the two locations and the results are presented in Table 4. The results of F1's, F1r s and F1. 1rs showed desirable and significant heterosis versus mid-parents (M.P) for days to first opening boll (D.F.O.B.) and earliness index (E.I) at (L2). In the same time, the F 1r's showed desirable and significant heterosis versus mid-parents (M.P.) at (L₁) for the same two previous traits and 2.5% span length (2.5%S.L.). While, heterosis for fiber fineness (F.F) was significant positive (undesirable) at (L2). On the other hand, the calculated values of heterosis versus the better-parent (B.P.) were significant and not of economical importance for (F.F.N), (F.F.) and (2.5% S.L) traits at the two locations. The combined data showed insignificant heterosis values versus mid-parents (M.P) for all studied traits except of days to first opening boll (D.F.O.B.). and (2.5% S.L.) traits. On the other hand heterosis versus better-parent (B.P) were undesirable and significant for all studied earliness and fiber traits except for days to first opening boll (D.F.O.B), earliness index (E.I). and (F.S.) traits. In this respect, a guite number of authors obtained similar results among them Rady and Gomaa (1983) Khajjidoni et al. (1984), El-Helw (1990), Okasha (1989), Kosba et al. (1991) and Hendawy (1994c).

Table 2: The combined analysis of variance and mean squares for earliness fiber traits for parents, F₁'s hybrids and F_{1r}'s reciprocal hybrids

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S.O.V.	d. f.	F.F.N	D.F.O.B	E.I	F. F.	F. S.	2.5 % S. L.
Rep.	6	0.2132	18.0694**	311.3982	0.2841**	0.2376	0.6481
Locations	1	18.0977**	20336.000**	19134.0625**	4.4006**	0.6055	140.7813 ^{**}
Genotypes	35	2.4062**	9.8875**	107.4787**	0.8647**	1.0687**	8.5856**
G × L	35	0.5847**	5.5642**	64.4725*	0.0798	0.5746*	1.5064**
Error	210	0.1930	2.8465	41.4816	0.0794	0.3621	0.5949

^{*} significant at 5% level .

The results of the analyses of variance and the mean squares of the diallel crosses for the F₁ hybrids and F_{1r} reciprocal hybrids for two locations and their combined data are presented for earliness and fiber traits in Tables 5 and 6 respectively. The results indicated those tests of significant showed that the mean squares of general combining ability (G.C.A) showed highly significant for all studied traits for two locations except days to first opening boll (D. F.O.B) trait at (L1). In this respect, the mean squares of specific combining ability (S.C.A) were also significance for all studied traits except (D.F.O.B.) and (E.I.) traits at the two locations, (F.F.N.) at (L₁) and (F.S.) trait at (L2). From the combined data, the F-test showed that the magnitudes of the mean squares of (G.C.A.) were larger than that (S.C.A) and showed highly significance for all studied traits. On the other hand, the mean squares of (S.C.A) and reciprocal were insignificant for all studied traits except (2.5% S.L.). In general, the results indicated that the major portion of the genetic variance in these populations were due to (G.C.A.) rather than (S.C.A) and (Rec.) for all studied traits. The magnitudes of (G.C.A) by locations interactions (G.C.A.×L.) (S.C.A.) by locations interaction (S.C.A.×L.) and reciprocal by locations interaction (Rec. x L.) showed highly significance for all studied earliness and fiber traits. Many authors investigated similar results among them Zaitoon et al.(1982), Dawwam and Hendawy (1989), El-Helw (1990), Hassoub (1991), Hendawy (1994a, 1994b) and El-Tabbakh and El-Nakhlawy (1995).

^{**} significant at 1% level .

Table 4: Percentage of heterosis over both mid-parents (M.P) and betterparent (B.P) for eraliness and fiber traits form the combined data.

P	ai eiit (D.F	<i>)</i> ioi eraililes	s and inci	ei traits form the combined data.				
Entries and Comparisons	F.F.N	D.F.O.B.	E.I.	F.F.	F.S.	2.5% S.L.		
M.P	7.32	142.24	57.40	3.34	11.20	32.51		
Range	5.88-8.40	140.86-143.56	49.57-60.90	2.76-3.80	10.77-11.64	30.75-34.23		
F ₁	7.43	141.51	29.71	3.44	11.35	33.06		
Range	6.66-8.03	139.21-142.92	53.18-64.66	2.99-4.13	10.54-11.82	31.14-34.16		
F _{1r}	7.38	141.17	60.38	3.37	11.42	32.92		
Range	6.31-8.19	139.5-140.42	56.07-66.32	3.00-3.99	10.50-11.99	30.46-34.06		
F _{1.1r}	7.41	141.33	60.04	3.41	11.38	32.99		
Range	6.31-8.19	139.21-142.92	53.18-66.32	2.99-4.13	10.5-11.82	30.46-34.06		
H(F _{1,} M.P)	1.50	- 0.51	4.02	2.99	1.34	1.69**		
H(F _{1r} , M.P)	0.82	-0.75**	5.19	0.90	1.96	1.26*		
L.SD 0.05	0.208	0.799	3.049	0.133	0.285	0.365		
0.01	0.273	1.050	4.007	0.175	0.374	0.480		
H(F _{1.1r} , M.P)	1.23	-0.64*	4.60	2.10	1.61	1.48**		
L.S.D 0.05	0.193	0.739	2.823	0.124	0.264	0.338		
0.01	0.253	0.972	3.710	0.162	0.347	0.444		
H(F ₁ , B.P.)	26.36**	0.46	-1.95	24.64**	-2.49	-3.42**		
H(F _{1r} , B.P.)	25.51**	0.22	-0.85	22.10**	-1.89	-3.83**		
L.S.D 0.05	0.445	1.0708	6.519	0.285	0.609	0.781		
0.01	0.584	2.244	8.268	0.375	0.801	1.026		
H(F _{1.1r} , B.P.)	26.02**	0.33	-1.41	23.55**	-2.23	-3.62**		
L.S.D 0.05	0.438	1.681	6.416	0.281	0.600	0.768		
0.01	0.575	2.209	8.433	0.369	0.788	1.010		

Table 5: The analysis of variance and mean squares of complete diallel crosses for earliness and fiber traits at the two locations.

0.014	S.O.V d.f		F.F.N.		D.F.O.B		E.I.		F.F.		F.S.		2.5% S.L	
S.O.V	d.f	L ₁	L ₂	L ₁	L ₂	L ₁	L ₂	L ₁	L1	L ₁	L ₂	L ₁	L ₂	
G.C.A	5	0.9586**	3.2145**	1.2250	15.9000**	43.9562**	70.5250**	0.7243**	0.5861**	0.7225**	0.7096**	4.9844**	7.6250**	
S.C.A	15	0.0368	0.2063**	0.5042	1.1542	15.6500	12.9260	0.0239*	0.0594 [*]	0.2020**	0.0917	0.6990**	0.4148**	
R.ec.	15	0.0347	0.0759	0.8649	0.7837	26.0057 [*]	7.5656	0.0088	0.0221	0.1006	0.0868	0.3770**	0.1956	
Error	105	0.0409	0.0557	0.6623	0.7609	12.1481	8.5927	0.0121	0.0276	0.0842	0.0968	0.1439	0.1535	

L₁ Sakha.

Table (6): Combined analysis of variances and mean squares for general and specific combining ability for complete diallel crosses analysis for earliness and fiber traits.

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S.O.V.	d.f.	F.F.N.	D.F.O.B.	E.I.	F.F.	F.S.	2.5% S.L.						
G.C.A	5	1.8672**	2.5500**	46.8219**	0.6504**	0.5777**	6.0609**						
S.C.A	15	0.0513	0.6458	8.1859	0.0262	0.0899	0.3555**						
Recop.	15	0.0282	0.3849	7.5605	0.0093	0.0293	0.1265						
G.C.A × L	5	1.7550**	24.1000**	83.3500**	0.0386	1.1062**	1.9500**						
S.C.A × L	15	0.5624**	1.4667**	48.8166**	0.1237**	0.4555**	1.6115**						
Rec. × L	15	0.2140**	3.5153**	73.8011**	0.0496**	0.5153**	1.2788**						
Error	210	0.0483	0.7116	10.3704	0.0199	0.0905	0.1487						

^{*} significant at 5% level . ** significant at 1% level .

L₂ Kafr Saad.

^{*} significant at 5% level.

^{**} significant at 1% level .

The estimates of (G.C.A.) effects for earliness and fiber traits at the two locations were determined and the results are presented in Table 7. In the same time, the combined data over the two locations were also investigated and the results are shown in Table 8. From combined data, the variety Giza-85 (P₁) showed significant (desirable) (G.C.A.) effect for (E.I.), the variety Giza-89 (P3) was negative (desirable) (G.C.A.) effects and high significant for first fruiting node (F.F.N.) and days to first opening boll (D.F.O.B.). In the same time, the variety Giza -86 (P2) showed significant and undesirable (G.C.A.) effect for all earliness and fiber traits. The variety Giza-77 (P₅) showed highly significant (undesirable) (G.C.A.) effect for most studied traits except (2.5 % S.L.), the varieties Giza -76 (P₄) and Giza -87(P₆) showed (desirable) and significant (G.C.A.) effect for fiber traits.

The specific combining ability (S.C.A.) effects (Sij) were calculated for all earliness and fiber traits at (L₁) and (L₂) and the results are presented in Table 9. The (S.C.A.) effects (Sij) were also estimated over the two locations and the resultes are cleared in Table 10. The results indicated that the cross (P₂×P₅) at (L₁) exhibited significant negative (S.C.A.) effect for first fruiting node (F.F.N.) trait. In the same time, the crosses [(P₁×P₆), (P₃ ×P₄) and (P₅ x P₆)] showed significant negative (S.C.A.) at (L₂) for the same above trait. On the other hand, the cross (P1xP2) exhibited significant positive (S.C.A.) at (L₂) for the same trait. The crosses $[(P_1 \times P_6)]$ and $(P_4 \times P_5)$ showed significant negative (S.C.A) effect for fiber fineness (F.F.) at (L₁), while the crosses [(P₃×P₅) and (P₁×P₂)] showed significant positive (S.C.A.) effect for the same trait at (L₁) and (L₂), respectively. Concerning fiber length

Table 7: Estimates of parental general combining ability effects for earliness and fiber traits at the two locations.

Par-	F. F	. N.	N. D. F. O. B.		E.	I.	F.	.F	F	.S	2.5% S.L	
ents	L ₁	L	L ₁	L	L	L	L	L	L	L	L	L ₂
P ₁	0.0271	- 0.0882	- 0.0806	- 0.5930	2.3160	1.0695	0.1729**	0.1007*	- 0.4750**	- 0.2444**	- 1.0222**	- 1.4562**
P ₂	0.0562	0.3889	0.0340	1.4528	- 2.7586	- 4.6492	0.2437**	0.2319**	0.0937	- 0.1465	0.1236	- 0.1000
P ₃	- 0.5229"	- 0.9903**	- 0.2868	- 1.8868 ^{**}	- 0.3599	1.7399	0.2146**	0.2278**	0.0063	- 0.2590**	- 0. 4681**	- 0.1167
P ₄	0.0896	0.1576	- 0.2993	- 0.0305	0.8991	1.8172	- 0.1979**	- 0.1743**	0.2271**	0.2514**	0.4840**	0.5354**
P ₅	0.0125	0.1368	0.5944	0.6694	- 1.5319	0.3953	- 0.0879**	- 0.0847	0.1187	0.1514	0.1465	0.3458**
P ₆	0.3375	0.3951"	0.0382	0.3882	1.4353	- 0.3728	- 0.3458**	- 0.3014**	0.0292	0.2472**	0.7361**	0.7917**
S.E	0.0533	0.0622	0.2145	0.2299	0.9185	0.7725	0.0290	0.0438	0.0765	0.0820	0.1000	0.1033

Sakha.

Table 8: Estimates of parental general combining ability effects for earliness and fiber traits from the combined data.

Variety	F.F.N.	D.F.O.B	E.I.	F.F.	F.S.	2.5% S.L.
P ₁	-0.0306	-0.3368	1.6927 [*]	0.1368**	-0.3597**	-1.2392**
P ₂	0.2226**	0.7434**	-3.7039**	0.2378**	-0.0264	0.0118
$P_{_3}$	-0.7566**	-1.0868**	0.6900	0.2212**	-0.1264	-0.2924**
P ₄	0.1236 [*]	-0.1649	1.3582	-0.1861**	0.2392**	0.5097**
P ₅	0.0747	0.6319**	-0.5683	-0.0861**	0.1351	0.2462*
P ₆	0.3663**	0.2132	0.5313	-0.3236**	0.1382	0.7639**
S.E.	0.0579	0.2223	0.8486	0.0371	0.0793	0.1016

significant at 5% level . ** significant at 1% level .

L₂ Kafr Saad. significant at 5% level.

^{**} significant at 1% level.

at (2.5% S.L.), some crosses like [($P_1 \times P_4$) ($P_2 \times P_4$), ($P_3 \times P_5$) and ($P_3 \times P_6$)] showed significant positive (S.C.A) effect. From the combined data, the cross ($P_1 \times P_2$) exhibited significant positive (S.C.A) effect for fiber fineness (F.F.) trait . Three crosses [($P_1 \times P_4$), ($P_3 \times P_5$) and ($P_3 \times P_6$) showed significant positive (S.C.A) effect for fiber length at (2.5% S.L.) trait, while the cross ($P_1 \times P_2$) exhibited significant negative (S.C.A) effect for the same trait.

In this investigation, the different genetic parameters were obtained for (L₁) and (L₂) and over both two locations for earliness and fiber traits. In addition heritability values in both broad h2b % and narrow h2n % senses were also calculated and the results are presented in Tables 11 and 12, respectively. The estimated values of genetic parameters from the combined data showed that the magnitudes of dominance variance (σ^2 D) were larger than those of additive variances (σ^2 A) and reciprocal (σ^2 r) for all studied traits with the except of $(\sigma^2 A)$ for (E.I.). In the same time, $(\sigma^2 s L)$ were larger than the other genetic components (σ^2 g L) and (σ^2 r L) for all studied traits. Concerning hertability, the results revealed that heritability values in broad sense ranged from (13.50%) for (D.F.O.B.) trait at (L₁) to (91.08%) for (F.F.) trait at the same location. In the same time, the highest values of narrow sense heritability was (86.07%) for fiber fineness (F.F.) at (L₁). From the combined data the estimated values of heritability in broad (h2b %) sense ranged from (1.70%) to (78.66%) for (E.I.) and (F.F.), respectively. In the same time, the highest values of heritability in narrow sense was (21.86 %) for (F.F.) trait, these findings indicated that the studied traits would be obtained through selection programs. Similar results were obtained by Kassem et al. (1981a), Singh and Singh (1981), Awad et al. (1986), Kosba et al.(1991), Zeina (1991) and Amer (1995).

Table 9: Estimates of specific combining ability effects for the crosses studied for earliness and fiber traits at the two locations.

Crosses	F.F	.N.	D.F.	O.B	Е	.l.	F.	F.	F.	S.	2.5%	S.L.
	L	L	L	L	L	L	L	L	L	L	L	L
$P_1 \times P_2$												
P ₁ × P ₃	0.0292	0.0507	-0.1111	-0.4674	2.6088	4.2513 [*]	-0.0312	0.0431	0.2167	-0.4764 [*]	-0.6903**	-0.4625
$P_1 \times P_4$												
P ₁ × P ₅												
$P_1 \times P_6$												
P ₂ × P ₃												
P ₂ × P ₄												
P ₂ × P ₅												
P ₂ × P ₆												
P ₃ × P ₄												
P ₃ × P ₅												
P ₃ × P ₆												
P ₄ × P ₅												
$P_4 \times P_6$												
P ₅ × P ₆												
S.E.	0.1215	0.1418	0.4891	0.5242	2.0945	1.7615	0.0662	0.0998	0.1744	0.1870	0.2279	0.2355

Table 10: Estimates of specific combining ability effects for the crosses studied for vegetative and earliness traits from the combined data.

Crosses	F.F.N.	D.F.O.B.	E.I.	F.F.	F.S.	2.5% S.L.
P ₁ × P ₂	0.1608	0.6118	0.7947	0.2892**	-0.1653	-0.1243
P ₁ × P ₃	0.0399	-0.2892	3.4301	0.0059	-0.3465	-0.2764*
P ₁ × P ₄	-0.0340	-0.7548	1.7494	0.0132	0.1066	0.5840*
P ₁ × P ₅	0.1212	0.0483	-0.5554	-0.0806	0.1920	0.0726
$P_1 \times P_6$	-0.1705	-0.3580	-0.2006	-0.1618	0.0701	-0.2764
P ₂ × P ₃	-0.0382	-0.0632	-0.5058	0.0486	0.0951	-0.1649
P ₂ × P ₄	0.2253	0.1400	0.4249	-0.0628	0.0858	0.1205
P ₂ × P ₅	-0.0319	-0.1694	-0.2512	-0.0253	-0.1163	0.3403
P ₂ × P ₆	0.0076	-0.0632	2.1599	-0.0441	0.2868	0.1851
P ₃ × P ₄	-0.2330	-0.6423	-2.6928	-0.0587	0.1795	0.3684
P ₃ × P ₅	0.1972	-0.2330	-0.5476	0.0913	-0.0788	0.5569*
$P_3 \times P_6$	0.0368	-0.3267	0.4028	-0.0524	0.2993	0.5142*
P ₄ × P ₅	0.0858	0.2736	3.2136	-0.0326	0.0993	-0.1764
P ₄ × P ₆	0.0441	0.2952	-0.7835	0.1361	-0.2788	-0.1816
P ₅ × P ₆	-0.1944	-0.1892	-0.0283	0.1049	0.0253	-0.0306
S.E.	0.1320	0.5069	1.9352	0.0847	0.1808	0.2317

Table 11: Estimates of different genetic parameters in addition to heritability values in broad (h²b%) and harrow (h²n%) senses for F1 and F1r reciprocal hybrids for earliness and traits at the two location.

Genetic	F.F	.N.	D.F.	O.B.	Е	.l.	F.	F.	F.	S.	2.5%	S.L.
Parameters	L	L ₂	L	L ₂	L ₁	L ₂	L ₁	L ₂	L ₁	L ₂	L	L ₂
2	0.0768	0.2511	0.0596	1.2299	2.3683	4.8116	0.0584	0.0440	0.0437	0.0515	0.3586	0.6015
σg												
2	-0.0023	0.0874	-0.0918	0.2283	2.0333	2.5162	0.0068	0.0185	0.0683	-0.0030	0.3223	0.1517
σs												
	-0.00308	0.01010	0.10126	0.01138	6.92878	-0.51353	-0.00165	-0.00276	0.00817	-0.00502	0.11658	0.02103
σr												
2	78.97	89.96	13.50	77.68	26.19	58.55	91.08	79.42	62.77	51.55	79.96	88.59
h ♭%												
h _n %	78.97	76.63	13.50	71.09	21.11	46.42	86.07	65.62	35.23	51.55	55.17	78.67

σ² g general combining ability variance .

Table 12: Estimates of different genetic parameters addition to hertability values in broad (h²b%) and narrow (h²n%) senses for F₁ and F_{1r} reciprocal hybrids for earliness and fiber traits from combined data.

Genetic Parameters	F.F.N.	D.F.O.B.	E.I.	F.F.	F. S.	2.5% S. L.
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 $[\]sigma^2$ s specific combining ability variance.

 $[\]sigma^2$ r reciprocal variance.

h²_n narrow sense heritability.

h_b broad sense heritability.

L₁ Sakha. L₂ Kafer Saad.

σ ² g	0.02528	-0.73982	0.34899	0.02942	-0.00728	0.22193
σ^2 S	0.37881	1.18547	-0.57911	0.15291	0.03548	1.29176
σ^2 r	-0.04645	-0.78260	-16.56015	-0.01008	-0.12150	-0.28808
σ² gL	0.10103	0.14516	3.03689	-0.00671	0.05569	0.03294
σ ² sL	0.29851	0.43845	22.32360	0.06027	0.21194	0.84937
σ^2 rL	0.08285	1.40185	31.71540	0.01485	0.21240	0.56505
H ² b %	55.81	40.02	1.70	78.66	9.01	66.13
H ² n %	6.57	0.00	1.70	21.86	0.00	16.91

- $\sigma^2 g$ general combining ability variance.
- σ^2 s specific combining ability variance.
- σ^2 r reciprocal combining ability variance.
- σ²g L G.C.A by location variance.
- σ^2 sL S.C.A by location variance.
- σ^2 rL reciprocal by location variance.
- h² b broad sense heritability.
- h² n narrow sense heritability .

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وراثة الصفات الكمية فى القطن المصرى ب- صفات التبكير والتيله

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تـــم اســـتخدام ســـته اصــناف مــن القطــن المصـــرى والتابعــة للجــنس (Gossypium barbadense L.)

وقَّد تم اختيار هذه الأصناف لمَّا لها من تباين واضح في الصفات تحتُ الدراسة وتم إجراء جميع الهجن التبادلية بين الأباء في موسم ١٩٩٦. وفي موسم ١٩٩٧ أجريت تجربتان الأولى في محطة البحوث الزراعية بسخا كفر الشيخ ، والثانية بكفر سعد محافظة دمياط .

وقد صممت كل تجربة في قطاعات كاملة العشوائية ذات أربع مكررات لتقييم السلالات الأبوية والهجن الناتجة وتم دراسة صفات التبكير متمثلة في ارتفاع أول عقدة ثمرية ، تاريخ تفتح أول لوزة ومعامل التبكير . كذلك تم دراسته صفات التيله متمثلة في متانة التيله ، نعومة التيلة و طول التيلة عند نسبة التوزيع ٥٠٠٠.

أظهرت نتائج تحليل التباين وجود اختلافات عالية المعنوية للتراكيب الوارثية لجميع الصفات المدروسة في كلا المنطقتين وكذلك التحليل المشترك ما عداً صفة تاريح نفتح أول لوزة في المنطقة الأولى .

كما أظهر التحليل المشترك معنوية النفاعل بين التراكيب الوراثية والمناطق لجميع الصفات المدروسة ماعدا صفة نعومة التيلة.

كانت اقل قيمة لقوة الهجين مقدرة على متوسط الأباء -٢٤٠٠ الصفة تاريخ تفتح أول لوزة بينما كانت أعلى قيمة هي ٢٠٦٠ الاصفة معامل التبكير وكانت قوة الهجين مقدرة بالنسبة للآب الأفضل غير مرغوبة.

أظهرت النتائج أن تباين القدرة العامة على التألف عالي المعنوية لجميع الصفات المدروسة وكانت القيم أعلى من قيم تباين القدرة الخاصة على التألف.

كانت قيم معامل التوريث في المعنى الواسع أعلى من القيم في المعنى الضيق في كلا المنطقة ين والتحليل المشترك عداً صفتى ارتفاع أول عقدة ثمرية وتفتح أول لوزة في المنطقة الأولى وصفة متانه التيلة في المنطقة الثانية وصفة معامل التبكير في التحليل المشترك.

كانت قيمة التباين السيادى أعلى من قيم التباين الأضافي لجميع الصفات المدروسة عدا صفة معامل التبكير.

نستنتج من ذلك انه يمكن استخدام طريقه التهجين في تحسين الاقطان المصريه من خلال برامج تربيه القطن .

Table 3:Percentage of heterosis over both mid-parents (M.P) and better- parent (B.P) for vegetative and earliness traits at two locations.

traits at two locations.												
Entries and	F.F	.N.	D.F.	O.B.	E	.l.	F.	.F.	F.	S.	2.5%	S.L.
Comparisons	L ₁	L ₂	L ₁	L ₂	L ₁	L ₂	L ₁	L ₂	L ₂	L ₁	L ₂	L ₁
M.P	7.63	7.02	133.57	150.9	65.26	46.54	3.28	3.39	11.11	11.29	32.08	32.93
Range	6.32-820	5.43-8.60	132.43-134.82	148.45-152.60	57.74-70.40	41.40-57.88	2.63-3.72	2.90-4.00	10. 38-11.57	10.65-11.80	30.35-34.10	31.15-34.35
F ₁	7.70	7.016	133.21	149.80	67.25	52.17	3.29	3.58	11.50	11.20	33.06	33.06
Range	7.20-8.13	6.07-8.35	131.60-134.90	146.82-153.15	56.13-78.57	44.33-59.46	2.75-3.90	3.10-4.35	10.45-12.08	10.05-11.85	30.98-34.28	31.30-34.75
F _{1r}	7.59	7.17	132.75	149.56	69.25	51.50	3.24	3.50	11.41	11.41	32.63	33.21
Range	6.88-8.30	5.75-8.20	131.48-134.25	146-45- 151.68	63.50-75.07	44.62-58.06	2.75-3.75	3.10-4.28	10.40-12.02	10.60-11.95	30.10-34.28	30.83-34.88
F _{1.1r}	7.65	7.17	132.98	149.68	68.25	51.83	3.27	3.54	11.46	11.31	32.85	33.13
Range	6.88.8.30	5.75-8.35	131.48-134.90	146.45-153.15	56.13-78.57	44.33-59.46	2.75-3.90	3.10-4.35	10.40-12.08	10.05-11.92	30.10-34.28	31.30-34.88
H (F ₁ , M.P.)%	0.92	1.99	-0.27	-0.73*	3.05	12.10**	0.31	5.61*	3.51*	-0.80	3.065**	0.40
H (F _{1r} , M.P.)%	-0.52	2.14	-0.61*	-0.89**	6.11*	10.66**	-1.22	3.25	2.70*	1.06	1.72**	0.58
L.S.D 0.05	0.193	0.226	0.778	0.834	3.334	2.804	0.105	0.159	0.278	0.298	0.363	0.375
0.01	0.256	0.298	1.029	1.103	4.406	3.706	0.139	0.210	0.367	0.393	0.480	0.495
H(F _{1.1r} M.P.)%	0.26	2.14	-0.44	-0.81**	5.58	11.37**	-0.31	4.43*	3.15**	1.77	2.40**	0.61
L.S.D 0.05	0.179	0.209	0.721	0.772	3.086	2.596	0.98	0.147	0.257	0.276	0.336	0.347
0.01	0.237	0.276	0.953	1.021	4.079	3.431	0.129	0.194	0.340	0.364	0.444	0.459
H (F ₁ , B.P.) %	21.84**	31.86**	0.59	0.91	-4.47	-9.87	25.10**	23.45**	-0.61	-5.09	-3.05**	-3.76**
H (F _{1r} , B.P.) %	20.10	32.04**	0.24	0.75	-1.63	-11.02 [*]	23.19**	20.69**	-1.38	-3.31	-4.31**	-3.32**
L.S.D 0.05	0.413	0.482	1.664	1.784	7.128	5.994	0.225	0.340	0.594	0.636	0.776	0.801
0.01	0.546	0.638	2.200	2.358	9.421	7.923	0.298	0.449	0.785	0.841	1.025	1.059
H(F _{1.1r} , B.P.)%	21.04**	32.04**	0.42	0.83	-3.05	-10.45*	24.34**	22.09**	-0.95	-4.15	-3.67**	-3.55**
L.S.D 0.05	0.407	0.475	1.638	1.756	7.015	5.899	0.222	0.338	0.584	0.626	0.764	0.789
0.01	0.538	0.628	2.165	2.321	9.272	7.798	0.293	0.447	0.772	0.828	1.009	1.042

Table 1:The analysis of variance and mean squares for earlines and fiber traits at the two locations for the parents,

F₁ hybrid and F_{1r}'s reciprocal hybrids`1

i i nybria ana i ir a reciprocar nybrias i													
S.O.V	d.f.	F.F.N.		D.F.O.B.		E.I.		F. F.		F. S.		2.5 % S. L.	
		L ₁	L ₂										
Rep.	3	0.3081	0.1184	26.1667**	9.9722*	160.00232*	462.7940**	0.0761	0.4921**	0.1487	0.3265	0.1574	1.1389
Geno.	35	0.6704**	2.3205**	3.0679	12.3795**	96.5291**	75.4230**	0.4699**	0.4746**	0.9316**	0.7117*	4.6911**	5.4011**
Error	105	0.1634	0.2226	2.6493	3.0438	48.5925	34.3706	0.0485	0.1103	0.3370	0.3873	0.5756	0.6142

L₁ Sakha. L₂ Kafr Saad. * significant at 5% leval. ** significant at 1% level .