

## **ESTIMATION OF GENETIC COMPONENTS AND GENETIC DIVERGENCE IN DIALLEL HYBRIDS OF COTTON**

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### **ABSTRACT**

Successful breeding requires genetic diversity to be sustained to maximize improvement potential and to minimize the inheritance of genetic vulnerability .Nine diverse cotton genotypes were hybridized following half diallel crossing system in order to investigate the genetic mechanism controlling variation and to estimated the genetic diversity among parents .

Analysis of combining ability revealed significant GCA and SCA for most studied characters indicating importance role of additive and non-additive effects in the inheritance these characters .Simple additive-dominance model was found adequate for analyzing  $F_1$  data sets .

The property of regression coefficient indicated intra-allelic interaction . The additive and non-additive gene effects were significant and involved in the inheritance of all studied characters .

A greater magnitude of  $(H_1+H_2)$  items for all studied characters revealed the importance of non-allelic gene effects which resulting in  $(H_1/D)^{1/2}$  more than unity indicated that over dominance for most characters, and consequently estimation of heritability in narrow were low for earliness index and lint yield to moderate and high for the rest characters . A moderate to high narrow-sense heritability for fiber characters suggest that there was potential in the plant material for improving these characters through single plant selection .

Analysis of divergence among parents revealed a significant dissimilarity coefficient more 85% of values . The genetic divergence among the parents based on Euclidean distance revealed existence of five major groups .

Hybridization between the wide divergence dusters showed significant SCA in most studied characters .

**Key words :** genetic component - genetic divergence –cluster analysis cotton .

## INTRODUCTION

Breeders of cotton are principally interested in improving the genetic potential of their materials to maximize economic gain. Therefore, they require information to identify and select desirable genotypes efficiently, and to concentrate their genes in a line and variety that is commercially acceptable. This usually over come by crossing unrelated strains to create variation followed by phenotypic screening. Parental selection for creating genetic variability for cotton improvement requires knowledge of the likelihood or improving traits of interest. This is based on the amount and type of genetic control of the trait. The amount of genetic control is influential because improvement of a trait with very small genetic control relative to environmental influences will be difficult ( Murtaza, 2005).

Several genetic mating designs exist to facilitate dissection of environmental and genetic control underlying quantitative traits in plants. Among the most common mating designs in crop improvements was the diallel analysis. This design used extensively in cotton to clarify the parental lines in terms of their ability to be combined in hybrid combinations. ( El Adl et al., 2001; El-Feki and Abd El-Gelil, 2001; Hemaida et al, 2006 and Basal and Turgut, 2003).

Exploiting heterosis is one of the methods used to increase yield potential in cotton. The superiority of a hybrid depends on heterosis over the better parent rather than over the mid parents

The success of the hybridization is largely dependent on the correct selection of parents. Heterosis and degree of dominance have been reported by several workers. ( Tuteja et al, 2003; Yehia, 2005 as well as El-Mansy and El-Lawendy, 2008 ).

The present study was planned to investigate the inheritance pattern of yield and its contributing characters as well as fiber properties. Diallel crossing technique has been used to create variability and to know the genetic parameters controlling the inheritance of the studied characters.

## MATERIAL AND METHODS

This study was initialed in 2006 in Sakha Agricultural Research Station. Nine diverse cotton genotypes i.e.; Pima S<sub>6</sub> as American Egyptian cotton, Karshenky<sub>2</sub> as Russian genotypes, Suven as Indian genotype and six Egyptian genotypes i.e. Monoufi, dandara. Giza 86, Giza87, Giza 89 x Pima S<sub>6</sub> and Giza 92, were selected and

crossed in all possible combinations excluding reciprocals to produce their F<sub>1</sub> crosses.

The nine parents and their 36 F<sub>1</sub>'s were evaluated by using randomized complete block design with three replications during 2007 cotton growing season. The experimental plots were 4.5 meter single row with intra and inter row distances of 25 and 70 cm, respectively. Data were recorded on five randomly selected plants per row in each of the three replications of the following characters:

Earliness index , boll weight , lint yield / plant , lint percentage , seed index, Lint index , upper half mean length, uniformity index , fiber strength , Elongation, micronaire reading and Yellowness were estimated. Fiber characters were determined using HVI Spectrum instrument system according to (ASTM: D4605-1986).

#### **Statistical Analysis:**

The data for each measurement was tabulated and analyzed on plot mean basis. The diallel analysis was used to evaluate characters that had a significant variation among parents. Significant differences in phenotypic were assumed to imply that genetic differences were present. Simple additive dominance model approach of (*Hayman, 1954 and 1958*) and as modified by (*Mather and Jinks, 1982*) was followed for genetic analysis and for estimation of components of genetic variation. The significance of components of variation in F<sub>1</sub> generation was tested by *Jink, (1956); Hayman (1958)*; when the value of a parameter divided by its standard error, exceeded 1.96, then it was significance.

Estimates of both general combining ability (GCA) and specific combining ability (SCA) were computed according to (*Griffing, 1956*) designated as method (2) model (1).

Hierarchical clustering procedure using ward's minimum variance method, which minimize within group sum of squares across all partitions, was applied to determine genetic diversity and distances. This procedure used a method performing a disjoint duster analysis on the basis of Euclidean distances as outlined by (*Anderberg, 1973*) and developed by (*Johnson and Wichern, 1988*). In this application of ward's method the Euclidean distances were computed and the results from clustering analysis are presented as dendrograms. All these computations were performed using SPSS (1995) computer procedure

## RESULTS AND DISCUSSION

The results indicated significant differences between parental cotton genotypes and their progenies for all studied characters providing evidence for the presence of fair amount of genetic variability. This due to their partial different genetic backgrounds and origins as shown in Table 1. The results also revealed that this variability could be transmitted to the progeny consequently. Thus validated the genetic analysis of the traits following the technique of Mather and Jinks (1982).

**Table ( 1 ) Analysis of variance for combining ability of the studied characters**

S.O.V	D.F	EI	LY	LP	SI	LI	FL	UN	STR	ELO	MC	B
Replication	2	0.3421	1627.306	1.0051	6.8062	2.0401	0.1836	2.0205	0.0890	0.1343	0.0156	1.0605
Genotypes	44	88.268**	326.0455*	9.4001**	2.7675**	2.4033**	4.8497*	3.5194**	8.4269**	0.3939**	0.3198**	2.452**
GCA	8	128.1201	1470.5**	1.005	6.80622	3.5428*	51.13**	24.08**	75.53**	3.39**	3.5893**	26.139**
SCA	36	1166.379*	337.2	9.400**	2.76752**	2.1345**	20.00**	27.53**	49.09**	2.38**	1.1017**	14.451**
Error	88	4.6849	204.2093	0.5254	0.3229	0.8016	0.5577	1.3101	1.3102	0.0664	0.0267	0.1418

\* and \*\* P < 0.05 and 0.01 respectively

Ei = earliness index, L.Y= lint yield, L.P = lint percentage, SI = seed index, LI= lint index

F.L= fiber length, U.N = uniformity ratio, STR = strength, ELO = elongation, MC= micronaire value

B= yellowness

The combining ability variances further revealed that variances due to general combining ability and specific combining were highly significant for most characters. These results indicated that the importance of additive and non-additive (epistasis and/or dominance) effects in the inheritance of such characters. These findings were supported those by (*Ahuja and Tuteja (2000), Mert et al.,(2003) and Tuteja et al.,( 2003)*).

The ultimate choice of parents in a breeding program is generally based on performance of parents and their F<sub>1</sub>'s, however, GCA and SCA effects are more informative than performance, since, it also reveals the type of gene effects, i.e., additive or non-additive effects.

Table 2. Showed the GCA effect of nine parental genotypes. The data revealed that the parental cotton genotypes (P7) Giza87 and (P9) G 92 as well as (P5) Monoufi exhibited positive and significant GCA effects for most fiber characters. These genotypes could be considered good combiners for these characters. On the other hand, the American variety Pima S<sub>6</sub> proved to be good ones for seed index and lint index. Giza86 was the best combiner for lint percentage and lint index. These results showed that exploiting these cotton genotypes

in multiple crosses may result in accumulation of additive gene effects and consequently raise the population mean. In this regard *Hassan and Awad (1997) and El-Adl et al., (2001)* obtained similar results.

**Table 2. Estimates of general combining ability effects for different characters in cotton crosses**

Parent	EI	LY	LP	SI	LI	FL	UN	STR	ELO	MC	B
Pima S <sub>6</sub> (1)	- 0.155	0.09	-0.390	1.1949	0.524	0.47	0.267	- 0.234	- 0.089	- 0.087	- 0.763
Kar <sub>2</sub> (2)	- 1.178	-3.16	-1.828	- 0.8141-	- 0.964	0.11	- 0.242	- 0.540	- 0.310	- 0.374	- 0.114
Suv. (3)	2.535	- 0.198	-1.015	0.0384	0.344	1.20	0.521	1.228	0.204	0.071	0.434
Dandara (4)	0.285	0.50	0.344	0.2374	0.383	1.07	- 0.975	- 0.843	- 0.113	0.098	0.754
Monoufi (5)	0.535	-1.38	0.775	-0.2323	0.221	0.42	0.261	1.157	0.202	0.123	0.448
Giza 86 (6)	- 1.314	3.10	1.569	0.1192	0.461	0.17	0.682	0.457	0.272	0.259	- 0.579
Giza 87 (7)	- 1.200	- 0.305	-0.741	-0.3929	- 0.472	1.17	0.503	0.481	-0.04	0.129	0.125
Ps6 XG.89 (8)	- 0.034	3.36	1.340	-0.002	0.307	-0.39	- 0.142	- 0.685	0.175	0.247	- 0.437
Giza 92 (9)	0.527	2.52	0.054	-0.0717	- 0.115	0.32	0.158	1.433	0.069	- 0.065	- 0.504
CD	0.695	4.50	0.1233	0.121	0.225	0.192	0.368	0.368	0.083	0.052	0.182

On the basis of SCA effects revealed that most of combinations having SCA effects are between geographically diverse parents which may be related to their genetic diversity. SCA for earliness index in relation to significant positive heterosis over mid-parent revealed that the crosses with each of PimaS<sub>6</sub> and Karshenky<sub>2</sub> exhibited the highest magnitude of positive significant SCA effect and exhibited the highest magnitude of significant positive heterosis over mid-parents (Table 3) No cross combinations were superior in all yield characters. In general, three cross combinations showed significant positive SCA effects for lint yield, five for lint index, two for lint percentage and seven for seed index. As regard to fiber characters, the cross combinations Kar<sub>2</sub> x G92, dandra x G92, Pima S<sub>6</sub> x Monoufi exhibited higher mean performances for fiber length, although showed the maximum significant SCA for fiber length. On the other hand, the combination which involved Monoufi or/and G92 as a common parent gave higher mean performance for fiber strength (Table 3 ) indicated that some of these combinations exhibited significant positive SCA.

It is interest to note that the crosses showing good specific combining ability were having of either good x good or good x poor general combining ability as reported by *Tuteja et al (2003)* The crosses showing high specific combing ability effect, involving one

good and one poor GCA could produce desirable transgressive segregants if fixable gene complex in good combiners and complementary epistatic effect in poor combiner acted in the same direction to maximize the desirable attributes. In this connection (*El-Mansy and El-Lawendey, 2008*).

The parental lines in this study were having divers genetic background of their source populations and hence exhibited SCA effects for earliness and fiber characters as well as some yield attributes (*Tuteja et al (2003)* and *Verma et al (2004)*) indicating equale importance of non-additive gene effects along with additive effects.

From the present study it can be concluded that the performance of parents does not seem to be index of GCA in the material. However, on the basis of GCA effects, the parental lines Giza86 and Pima S<sub>6</sub> may be used as breeding lines for improvement of most yield characters. On the other side, the parental lines G87, G.92 and Monoufi can be used for improvement of most fiber characters. As the selection of parents for a crossing programme on the basic of phenotypic performance may not prove useful, a modified selection types, which involved intermating, i.e. recurrent selection can be successfully used for crossing among breeding material for the desirable characters of both yield and fiber quality characters **Tuteja et al., (2003)**.

#### ***Genetic component***

Assessment of the genetic components of variance using Hayman diallel method (1954) data in Table 5 showed that the estimates of  $t_2$  were non-significant for most studied characters suggesting fulfillment of the assumption underlying diallel analysis (Table 4). The regression coefficients of most characters were significantly from zero and from unity. Significantly from zero and not from unity suggesting no non-allelic interaction and an independence of genes distribution among the parents.

Thus, the additive dominance model did provide fair basis for interpreting the results, while significantly from unity but not from zero, indicated, non allelic interaction included epistasis and correlated genes distributed among the parents. Therefore, the data did not fulfill the diallel assumptions. This property of the regression coefficient indicated intra-allelic interaction.

**Table 3. Estimates of specific combining ability effects for different characters in cotton crosses**

Parent	EI	LY	LP	SI	LI	FL	UN	STR	ELO	MC	B
P1 X 2	4.012	1.725	0.240	-0.642	-0.169	0.513	-0.104	0.290	0.031	0.062	-0.410
P1 X P3	4.550	11.271	0.151	0.124	0.471	0.195	-0.025	-0.989	-0.042	0.193	0.748
P1 X P4	-2.950	17.776	0.337	0.802	0.747	0.958	2.196	0.993	0.634	0.323	1.339
P1 X P5	5.800	0.5573	-0.256	-0.192	0.524	0.540	0.193	0.759	0.052	0.132	1.242
P1 X P6	-0.602	-3.814	-2.737	-0.998	-0.515	-0.551	-0.961	0.559	-0.284	0.0338	0.357
P1 X P7	0.035	13.155	0.054	-0.352	0.319	0.688	0.984	0.368	-0.08	0.083	0.502
P1 X P8	2.868	-18.22	-0.988	-0.540	-0.311	0.179	0.596	-0.465	0.046	0.075	-0.155
P1 X P9	3.308	9.382	0.149	-0.407	0.668	-0.233	-1.437	0.850	0.085	-0.313	1.105
P2 X P3	-2.677	-2.195	-0.059	0.405	-0.122	0.019	0.493	-2.016	-0.254	0.014	-0.310
P2 X P4	-0.927	-8.928	0.025	0.684	-0.314	-0.218	-1.185	-1.501	-0.478	0.011	-0.219
P2 X P5	-7.677	-0.8827	-0.662	-0.210	-0.320	0.798	-0.488	-0.801	-0.427	-0.180	0.051
P2 X P6	0.421	-0.565	-1.299	-0.349	0.973	-0.193	-0.443	0.865	-0.63	-0.50	2.366
P2 X P7	10.308	0.952	-1.328	0.730	-0.287	-0.221	-0.864	1.608	-0.021	-0.162	-0.122
P2 X P8	4.391	4.109	0.497	-0.425	0.792	-0.396	0.981	-0.092	0.334	0.062	1.154
P2 X P9	4.330	0.724	-0.720	-0.592	0.049	1.692	0.815	0.656	0.107	0.075	0.357
P3 X P4	3.694	0.239	0.855	-0.667	0.044	0.564	-0.307	-0.080	0.216	-0.092	-0.028
P3 X P5	3.611	13.051	0.426	0.872	-0.034	0.213	0.457	1.620	0.001	-0.150	0.042
P3 X P6	3.459	7.265	0.160	-0.001	0.013	0.622	0.702	-0.280	-0.002	-0.153	-0.076
P3 X P7	-4.405	-3.367	-0.464	-0.188	0.0103	-0.272	-0.619	-1.571	-0.193	-0.098	0.064
P3 X P8	-1.571	7.053	0.749	0.357	0.120	1.219	-0.507	-0.204	0.039	0.059	-0.188
P3 X P9	0.967	2.333	-2.396	-0.464	-0.612	-2.539	-1.143	-3.041	-0.375	-0.125	0.024
P4 X P5	-0.3639	-0.527	0.106	0.384	1.627	-0.490	-0.055	-2.032	0.010	0.047	-0.301
P4 X P6	-5.291	0.690	-0.321	-0.388	-0.252	0.552	-0.843	-0.332	-0.127	-0.156	-0.019
P4 X P7	0.7095	1.832	0.447	-0.076	0.088	0.125	-0.164	0.278	0.016	0.032	0.260
P4 X P8	-0.3071	-2.930	0.473	0.102	-0.166	0.416	0.348	2.111	0.170	0.056	-0.264
P4 X P9	2.868	3.988	0.589	-0.398	-0.167	1.237	0.715	-0.707	0.110	-0.232	-0.295
P5 X P6	-1.041	-0.947	-0.228	-0.416	0.070	0.167	0.654	0.468	0.092	0.087	0.218
P5 X P7	-7.405	-2.242	0.056	-0.304	-0.493	0.173	1.199	-0.289	0.367	-0.025	-0.570
P5 X P8	1.012	6.515	-0.625	0.108	-0.216	-0.536	-1.222	1.411	0.155	-0.035	0.172
P5 X P9	-11.882	2.008	0.954	-0.158	-0.182	-0.781	1045	0.393	0.028	-0.256	-0.458
P6 X P7	6.444	-2.761	0.394	0.157	0.060	-0.051	-0.188	0.478	0.298	-0.028	-0.008
P6XP8	-2.473	0.488	0.221	0.229	-0.164	-0.027	0.357	-0.027	0.357	-0.122	0.085
P6XP9	2.717	-4.834	1.107	0.269	-0.049	-0.405	-0.43	-0.1374	-0.308	0.041	-0.643
P7X 8	6.414	11.347	0.643	-0.319	0.119	-0.487	-0.631	0.320	0.261	0.184	-0.134
P7X 9	-7.647	-3.401	0.588	-0.252	0.092	-0.199	0.969	1.035	0.001	0.262	-0.164
P8X 9	2.936	7.332	-0.172	-0.107	-0.010	0.758	-0.685	-0.598	-0.312	-0.113	-0.022
CD	2.00	13.1	0.926	0.344	0.642	0.547	1.05	1.05	0.236	0.149	0.519

**Table 4. Values of  $r^2$  regression coefficient of covariance ( wr ) on ( vr ) and t values for b = 0 and b=1**

Characters	$r^2$	Regression coefficient		t value	
				b = 0	b = 1
Earliness index	0.03	0.01	± 0.40	-0.03	1.52*
Lint yield / plant	9.69*	0.32	± 0.13	2.49*	5.41*
Lint percentage	1.44	1.06	± 0.28	2.83*	-0.25
Seed index	18.40*	0.27	± 0.10	2.65*	7.33*
Lint index	2.74*	0.33	± 0.19	1.71	3.50*
Fiber length	0.05	0.71	± 0.24	3.01*	1.22
Uniformity	0.99	0.13	± 0.26	0.50	3.37*
Fiber strength	0.19	0.76	± 0.31	2.44*	0.75
Elongation	1.21	0.47	± 0.21	2.21	2.51*
Micronaire value	0.001	0.85	± 0.19	4.53*	0.78
+b	14.14*	0.59	± 0.08	7.33*	5.08*

B=0 and b=1 indicate difference of regression coefficient value from 0 and 1, respectively.

\*, \*\* significant at 0.05 and 0.01 respectively.

With regard to genetic components estimated by the diallel analysis (Table 5 ). The data showed both additive (D) and dominance ( $H_1$  and  $H_2$  ) components of genetic variation were significant for all characters except lint yield and seed index for additive ones and lint index for dominance components ( $H_1$ ). These results indicated that the importance of both additive and dominance gene effects in the inheritance of these characters. But the higher magnitude of dominance components than additive ones indicated the predominance of non-additive type of gene action for such characters. Moreover, values of  $H_2$  were relatively smaller than those of  $H_1$ , indicating that the positive and negative alleles, at the loci of the characters, are not equal in the proportion to the parents. Similar findings were obtained by (Murtaza, 2005). Domiance effects as algebraic sum over all loci ( $h^2$  ) in heterozygous phase in all crosses were significant for lint yield, seed index and fiber length and its magnitude was lower than  $H_1$  and  $H_2$  suggesting that dominance was unidirectional.



**Table 5. Estimates of genetic components of variation for the studied characters in half diallel crosses**

Characters	D	H <sub>1</sub>	H <sub>2</sub>	h <sup>2</sup>	F	E
Earliness Index	51.21 ±17.01	175* ± 37.53	105.50* ±32.27	14.78± 21.62	98.29* ±39.67	1.53± 5.38
Lint Yield	28.45± 25.53	213.84*± 56.35	221.31*± 48.44	661.19*± 32.45	44.76± 59.56	78.61*± 8.07
Lint Percentage	5.07*± 0.41	3.25*± 0.91	2.19*± 0.78	0.31*± 0.52	0.98± 0.96	0.18± 0.13
Seed Index	0.25± 0.16	1.67± 0.34	0.91*± 0.29	0.56*± 0.20	-0.48± 0.36	0.16*± 0.05
Lint Index	0.73*± 0.29	0.91± 0.65	0.57*± 0.56	0.22± 0.37	0.02± 0.69	0.28*± 0.09
Fiber length	3.63*± 0.23	2.07*± 0.50	1.64*± 0.43	1.36*± 0.29	1.98*± 0.53	0.12*± 0.07
Uniformity	0.83*± 0.30	2.10*± 0.66	2.01*± 0.57	-0.37± 0.38	-0.10± 0.70	0.44*± 0.09
Strength	2.84*± 0.40	5.75*± 0.89	3.75*± 0.77	-0.12± 0.51	1.05± 0.94	0.43*± 0.13
Elongation	0.14*± 0.03	0.27*± 0.06	0.18*± 0.05	-0.01± 0.03	0.06± 0.06	0.02*± 0.01
Micronaire	0.16*± 0.01	0.12*± 0.02	0.09*± 0.02	-0.01± 0.01	0.02± 0.03	0.01*± 0.001
+b	0.89*± 0.12	1.24*± 0.26	0.83*± 0.22	-0.02 ±0.15	0.01± 0.27	0.05± 0.04

\* Significant at 0.05 level of probability

The F value was positive and significant for earliness index and fiber length only, reflecting that dominance genes were more frequent than recessive ones among the parental genotypes. However, the insignificant values of F for the other characters may indicate the equality in the relative frequencies of dominant and recessive genes in the parents. These results agree with ( *El-Mansy 2005* and *Akhtar et al 2008* )

Several ratios were obtained to provide further genetic information about the studied characters as presented in Table 6. The ratio  $\sqrt{H_1/D}$  measured overall degree of dominance, which was in the range of over dominance for most characters.

The ratio  $H_2/4H_1$  estimated the frequency of negative versus positive alleles at loci exhibiting dominance, it was less than 0.25 for all characters except lint yield indicated that the additive components did not contain all the dominance effects in these characters, and

suggested that the positive and negative alleles at the loci were equal in proportion.

Estimates for the ratio of dominance to recessive genes in the parents ( $KD / KR$ ) were more than unity for most characters, indicated the presence of an excess of dominant genes for such characters, while seed index and uniformity index showed lower than 1, indicated the presence of an excess of recessive genes.

Regarding number of gene block ( $K$ ), the data showed that one gene blocks governed all studied characters except lint yield which was governed by two gene blocks.

The correlation coefficient of ( $wr+vr$ ) with parental measurements ( $Yr$ ) was positive and high for micronair value, indicating that the dominance was unidirectional i.e., increasing alleles were associated with one parent. However, the correlation coefficients were found to be negative and high for lint yield and lint index. The other characters were characterized by lower value suggesting that was ambidirectional in the parents ( Kearsy and Pooni, 1996 ).

Low heritability values were obtained for earliness index and lint yield moderate heritability value was obtained for uniformity ratio. High heritability value were obtained for the other studied traits , lint percentage, seed index , fiber length , fiber strength , fiber elongation ,micronaire reading and yellowness degree. High estimates of heritability in narrow sens represents fixable variation, which indicate that the response to selection should be rapid for these characters . This offers a lot of scope for improvement of the characters through individual plant selection . According to *Hayman (1957)*, epistasis can decrease or increase degree of dominance which also effect on heritability estimates .

**Table 6. Proportion of genetic components for the studied characters**

Characters	$\sqrt{H1/D}$	H2/4H1	KD/KR	$h^2/H_2 (K)$	r	g	$h^2_n$
EI	1.755	0.168	3.423	0.555	0.334	63.028	7.8
L.Y / P	2.742	0.259	0.521	2.988	-0.603	-189.575	3.2
L.P	0.801	0.168	1.273	0.144	-0.430	5.939	78.1
S.I	2.604	0.137	0.452	0.18	0.033	-1.026	65.8
L.I	1.121	0.155	1.029	0.391	-0.548	0.913	55.7
F.L	0.755	0.198	2.132	0.831	0.012	2.711	66.3
Un	1.588	0.238	0.924	-0.086	0.246	1.442	35.5
Str	1.422	0.163	1.297	-0.045	-0.120	-1.260	58.2
Elo	1.386	0.168	1.362	-0.049	0.033	0.169	55.3
M.C	0.857	0.194	1.165	0.058	0.622	0.029	72.3
+b	1.179	0.167	1.007	0.252	0.212	-1.678	71.3

**Genetic divergence among parental cotton genotypes:**

This analysis could provide useful additional information for studying interrelationships of genotypes and giving graphical assessment of genetic variability. Such information could be useful in identifying optimal breeding strategies for cotton improvement.

The actual values of Euclidean distances corresponding to 36 possible comparisons, taking two genotypes at time are giving in Table 7. These estimates, which treated as chi-square values, showed that about 85% of the value were significant, squared Euclidean distances were ranged from 3.748 between Giza 86 and Monoufi to 58.906 between Giza 86 and Russian genotype Karshinky2. In this regard *Abd EL-sayyed et al, (1998)* and *Goda, (2007)* found that the Egyptian cotton varieties were different from the American and Russian cottons.

**Table 7. Euclidean dissimilarity coefficient among studied cotton parental genotypes in matrix form**

	Pima S <sub>6</sub>	Kar2	Suv.	Dandara	Monoufi	Giza 86	Giza 87	PS <sub>6</sub> XG.89	Giza 92
Pima S <sub>6</sub>		5.711*	5.914*	3.877	4.084*	4.753*	4.459*	3.164	5.905*
Kar <sub>2</sub>			3.254	5.464*	5.898*	7.675*	3.723	6.651*	4.631*
Suv.				3.682	7.321*	7.562*	5.777*	6.106*	5.200*
Dandara					6.146*	6.456*	6.509*	4.240*	6.156*
Monoufi						1.936	5.058*	4.830*	4.638*
Giza 86							5.801*	4.643*	5.337*
Giza 87								6.034*	4.284*
PS <sub>6</sub> XG.89									7.248*

\* Significant at 0.05 level of probability

Genetic divergence based on Euclidean distances between the nine parental genotypes are presented in Figure 1. It is clear that the two Egyptian varieties Giza 86 and Monoufi formed a wide group having divergent distance from the other genotypes and both parents appeared to nearly related with coefficient 1.936

On the other side the divergent among Suven and kar<sub>2</sub> was not clearly pronounced since these genotypes appeared to be closely related with coefficient 3.254 among them. Dandra, pima S<sub>6</sub> and G.89X pima S<sub>6</sub> tended to be nearly related and formed single cluster .

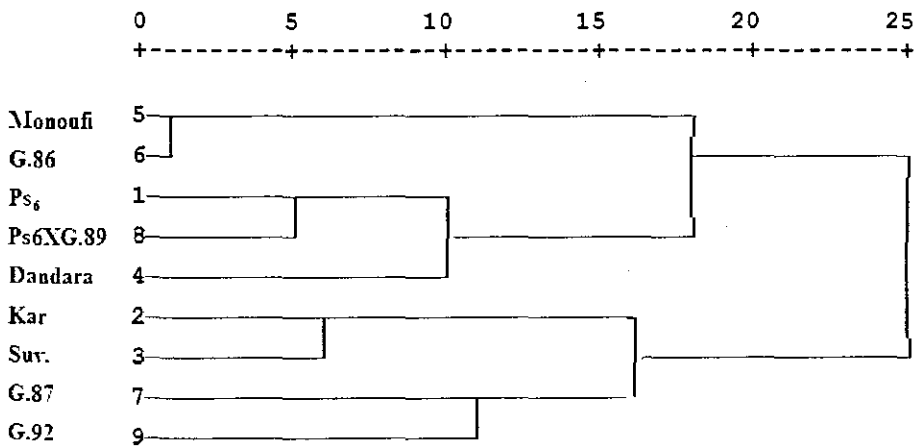


Figure : Dendrogram presentation of nine parental cotton genotypes

Distribution of parental genotypes in varied clusters are given in Table 8. The data revealed the existence of four major groups. Cluster I include three parents, Pima S<sub>6</sub>, dandra and G.89 x PimaS<sub>6</sub>. These parents exhibited significant GCA effect for yield characters.

**Table 8. Distribution of cotton parented genotypes into clusters**

Clusters	N. of genotypes	Representative genotypes
I	3	Pima <sub>s6</sub> , dandra, G.89 x P <sub>s6</sub>
II	2	Monouvi, Giza86
II	2	Suvin, Kar <sub>2</sub>
IV	1	Giza87
V	1	Giza92

Cluster II consists of two parental genotypes, Giza86 and Monoufi, these parents exhibited significant GCA for most yield and fiber characters. On the other side, Giza87 and Giza92 formed two clusters and nearly related these parents surpassed all parents in GCA for fiber characters but they were inferior for yield characters. Cluster III contain two genotypes and exhibited significant GCA effect for earliness index but inferior in the other yield and fiber characters, in this regard *Abo El-Yazed et al., (2009)*.

It is worth to note that the hybridization between the wide divergence clusters showed significant specific combining ability in most studied characters. In this trend (*Sandhu and Boparai, 1997*) reported that genetically diverse genotypes when used as parents in hybridization programme generate a wide rang of variability and provide transgressive segregants.

The results suggested the utilization of diverse Russian and American genotypes for hybridization programs , as a desirable parent , aimed to improve Egyptian cotton for more earliness .

Finally, the cotton breeder desire to increase genetic diversity among cotton cultivars, while at the same time maintaining the complex of desired agronomic and quality characters present in existing economic cultivar. Developing such a combination can be difficult, as the introgression of new genetic material in expected to disturb genetic complex responsible for desirable characters. The use of crosses among divergent cultivars could be a mean to achieve both ends.

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## الملخص العربي

### تقدير المكونات الوراثية والتباعد الوراثي في الهجن الدائرية للقطن

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أجرى هذا البحث بمحطة البحوث الزراعية بسخا خلال موسم ٢٠٠٦ ، ٢٠٠٧م وقد استخدم ٩ آباء من القطن متباعه وراثياً وهي بيما ٦ ، كارشنكي ٢ ، سيوفن ، دندرة ، منوفى ، جيزة ٨٦ ، جيزة ٨٧ ، جيزة ٨٩ × بيما ٦ ، جيزة ٩٢ .

وقد أجريت التهجينات الممكنة بنظام Half diallel ، وذلك لدراسة ميكانيكية التحكم في التباين الوراثي والأهمية النسبية لمكونات التباين الوراثي ، ودرجة التباعد الوراثي بين الآباء .

أوضح تحليل القدرة على التآلف معنوية كل من القدرة العامة والخاصة مما يدل على أهمية كل من التباين المضيف والغير مضيف في وراثة الصفات المدروسة .

أظهر تحليل الانحدار معنوية معامل الانحدار عند الـ Zero والواحد الصحيح لمعظم الصفات مما يدل على وجود تفاعل بين الجينات .

أظهرت درجة السيادة وجود سيادة فائقة لمعظم الصفات مما يدل على أهمية الفعل الجيني السيادة كما أن المساهمة العالية لقيمة  $H_1$  ،  $H_2$  أظهرت أهمية التفاعل بين الجينات " التفوق " .

أوضحت النتائج أن درجة التوريث بالمعنى الضيق تراوحت بين قيم منخفضة لصفات معامل التكبير ومحصول الشعير إلى قيم متوسطة إلى عالية لباقي الصفات .

كما أن قيم درجة التوريث العالية لصفات التيلة يمكن عن طريقها تحسين هذه الصفات في انتخاب النباتات الفردية المتوقعة .

أوضح تحليل التباعد الوراثي بين الآباء المستخدمة معنوية معامل عدم التشابه لأكثر من ٨٥% من القيم ، كما أوضح تحليل Euclidean distance أن الآباء المستخدمة في الدراسة تم توزيعها على خمس مجاميع كبيرة على أساس عدم التشابه النسبي بينها ؛ كما أظهرت النتائج أن التهجين بين الآباء في المجاميع المتباعدة نتج عنه معنوية القدرة الخاصة لمعظم الصفات تحت الدراسة .