THE RELATIVE IMPORTANCE OF CHARACTERS AFFECTING GENETIC DIVERGENCE IN COTTON

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ABSTRACT

Principal component analysis and herachical clustering analysis were used to study the genetic dissimilarity among nine cotton parents and 36 hybrids . Seventeen agronomic and growth as well as fiber characters were evaluated . Analysis of variance revealed significant differences for all studied characters indicated a considerable amount of genetic variability. The nine parents differ significantly in boll growth rate at two intervals of boll growth . The Russian variety $Kashenky_2$ and cross (G.89xpima S_6) showed the largest values on the first interval and decreased in boll maturation period. All cotton parents exhibited signifecant increases in fiber diameter during the first 30 days , of fiber development . The parents Giza 87, Monoufi and Kar_2 exhibited the smallest change in diameter and gave low value and transmitted across the progeny . By 30 days post anthesis the fiber diameter remained the same throughout. All genotypes started deposition on secondary wall by 20 days post anthesis. Simultaneous increase in fiber diameters and wall deposition between 20-30 days post anthesis indicate that the secondary cell wall of cotton fiber is not rigid and is capable of expansion. Significant deviation of regression coefficient from unity and from zero revealed the presence of epistasis and correlated genes distribution among the parents . Dominance and over dominance were operative in the inheritance of most characters and consequently estimation of h^2_{ns} were low for growth and yield characters and it were relatively moderate for fiber development characters. Principal component analysis revealed that the first five components accounted for about 75% of all total variation while, the first two components were significant and accounted for 46% of multivariate variance among genotypes and showing the highest joint eigen values . Fiber development characters i.e fiber diameter and deposition on secondary wall were the most important source of variation among genotypes with largest coefficients on the first PC axis. However, the second axis deals with most earliness characters i.e. boll growth rate , maturation period , first node and fiber length .

The nine parents were grouped into six major groups based on relative dissimilarity among them with significant differences among groups for most characters , the progeny produced from crossings

between two distantly related parents showed divergent distance and gave values surpassed their parents in most characters .

Keywords:multivariate-principal component-genetic divergence-cotton

INTRODUCTION

Genetic divergence among parents is considered an important factor for obtaining heterotic effects. This diversity is the best tool for breeding programs based on hybridization, because it generates parameters for identifying superior parents. This distance is essential to increase the chance of recovering superior genotypes . Cox et al, 1985, suggested crossing distantly related lines in an inbred improvement programe to maximize the number of segregating loci in the F2 and subsequent inbred generations..

Estimation of genetic diversity is an important step for any breeding programe, but not the last one. Another helpful issue to be evaluated is the relative importance of the characters. Though plant breeders, often measure several characters simultaneously in cotton development, then it is possible to estimate the genetic divergency by using multivariate method exist.

Multivariate technique could resolve several phenotypic measurements into fewer, more interpretable and more easily visualized dimensions such an analysis which used principal components (Hair et al., 1987) seemed to elucidate pattern of variation in agronomic attributes and to obtain the intial factor solution using eigen values. These values measure the explained varience associated with each variable and refer to its contribution to the whole divergence.

The efficacy of the genetic divergence as a criterion for choosing parents for crossing programmes has been reported by several workers (Sandhu and Boparai, 1997; Patil et al., 1999; El-Mansy, 2005; Gooda, 2007 and Abou El-Yazied et al, 2009). Morever, principal component analysis and factor analysis have analogous efficacy to determine the most suitable combinations and grouping the varied genotypes into varied groups. Seyam et al., 1984 used factor analysis in determining traits that could be selected for high yield. Abd El-Sayyed et al., 2000 and El-Mansy et al., 2008 used principal component and cluster analysis to create genetic variability in Egyptian cotton. On the other hand El-Lawndey et al., (2008) used multivariate technique to determine the relative contribution of characters of variation and grouping the genotypes into vaired

clusters. El-Mansy, 2009. selected some superior F3 families by using multivariate analysis.

Thus, the objectives of this research were to study the genetic divergence among nine parents and 36 crosses by using multivariate analysis on the basis of agronomic and physiological trials data to give graphical presentation of genotypes, and to select the most suitable combinations as well as, to investigate the relative importance of the evaluated characters .

MATERIAL AND METHODS

The experimental materials consisted of nine parents, three of them were foreign genotypes i.e pima S_6, Karshenky$_2$ and suvin and six Egyptian genotypes i.e Dandra, Monoufi, Giza 86, Giza 87, (Giza 89 X Pima S6) and Giza 92, and 36 F_1's generation resulting from all possible crosses excluding reciprocals between the nine parents. The nine parents and 36 F_1's were grown at Sakha Agric Res. Station in 2008 season.

The experimental design was randomized complete block design with three replications. Each entry was planted in a single row plot with intra and enter row distances of 30 and 70 cm respectively. Standard cultural practices were followed throught the growing seasons. Data were recorded on 15 guarded plants basis for each entry for 17 agronomic, morphological and growth characters as well as fiber characters i.e relative growth rate of boll at two growing stages 10-20 and 20-30 days after anthesis , (RGR/B) plant growth rate at 60-90 and 90-120 days from sowing (two stage) (RGR/P), root – shoot allometric coefficient (K) at 60, 90 and 120 days seed cotton yield/plant (SCY), fiber diameters (D) at 10, 20 and 30 days from anthesis as well as fiber deposition (DOS) at 20 and 30 days, fiber length (FL) and earliness characters as first frusting node (F.N) and boll maturation period (B.M.P).

Statistical procedure :

Data recorded were subjected to two methods of statistical analysis. Initially, analysis of variance was conducted to test the differences among various genotypes. As long as, the data of the traits (RGR / B, RGR / P, root shoot allomatry, diameter and deposition) were taken at different stages, the analysis of variance were conducted separately for each stage of each trait. The diallel analysis was used to evaluate characters that had significant variation among the parents. Simple additive and dominance model approaches of Hayman, 1954;

Jinks , 1954 and Singh and Chaudhary, 1999 were allowed for genetic analysis.

After this step, the dissimilarity among cotton genotypes was estimated by using multivariate analysis (Johnson and Wichern, 1988). Therefore hierarchical clustering procedure using Ward's minimum variance methods, which minimize within cluster sum of square across all partitions was applied to determine genetic divergence and distance. This procedure used a method performing a disjoint cluster analysis on the basis on Euclidean distance as described by Hair et al, 1987. the dendrogram is constructed on Euclidean distance basis. On order to study the relative importance of the studied characters towards genetic divergence, principal component analysis was performed according to Hair et al, 1987. This analysis was calculated from a matrix based on correlation between the contributed characters for all genotypes. The principal components associated with all genotypes were expressed as eigen values and manifested in eigen vector for all the studied characters in each principal component axis. The genotypes were also grouped as diagram on principal component axis. All these computations were performed using SPSS 1995 and Minitap computer procedure.

RESULTS AND DISCUSSION

Results of the analysis of variance indicated significant differences at the two levels of probability for all the studied characters. The significance of (F) test indicated that, the parents were diverse for all characters under study and presence of considerable amount of genetic variability between them. While, parents vs crosses were significant for most studied characters indicating the heterotic response for these characters (Table 1).

Table 1. Analysis of variance of the studied cotton genotypes for all the studied characters .

S.ov	d.f	RGR/B			RGR/p		Root Shoot Allo . (k)			SCY
		RGR/B	10-20	20-30	60-90	90-120	60	90	120	
Replication	2	4.839E-07	0.0022	3.738E-05	0.00012	9.279E-05	0.0006	0.0009	5.18E-05	11187.6
Genotypes	44	2.839E-05**	0.0005**	0.0009**	0.0108**	0.00012**	0.0085**	0.0021**	0.00192**	2142.54**
Parents	8	0.00003**	0.000325**	0.00063**	0.0007**	0.00019**	0.0192**	0.0036**	0.0026**	692.875
Crosses	35	0.000016**	0.0005**	0.00015**	0.00015**	0.00010**	0.0056**	0.00136**	0.0017**	1492.8857
PvsC	1	0.000003**	0.000005	0.0283**	0.00001**	0.00042**	0.0215**	0.0138*	0.00233**	36477.8**
Eroor	88	7.529E-07	8.879E-05	9.533E-05	0.0045	6.7E-05	0.0012	0.00032	0.00025	1419.55

S.ov	d.f	Diameter			Deposition		F.L	F.N	B.M.P
		10	20	30	20	30			
Replication	2	0.0259	0.00125	0.0071	0.0025	0.00024	0.1836	0.0222	10.2889
Genotypes	44	4.0031**	4.0186**	3.9647**	0.7158**	0.6868**	4.8497**	3.9712**	49.4636**
Parents	8	3.4399**	4.7125**	5.4039**	1.13325**	1.02933**	11.2389**	2.625**	31.2593**
Crosses	35	3.9320**	3.8657**	3.6715**	0.06406**	0.6281**	3.3528**	4.2548**	54.2629**
PvsC	1	10.9967**	1.8217**	2.7122**	0.0067**	0.0005	4.6268**	4.8163**	27.126
Eroor	88	0.0085	0.0047	0.0055	0.0008	0.0042	0.3577	0.2040	14.5540

*, ** Significant at 0.05 and 0.01 levels of probability respectively

The mean values of relative growth rate of boll and plant as well as root-shoot allometric coefficient illustrated in Table2. Data revealed that the nine parents were approximately differented in growth rate. These different behaviours were clear at the two intervals of boll development and crop maturity. The Russian genotype Karshenky$_2$ and the Egyptian genotype (Promising cross), G.89 x Ps$_6$, were similar behaviour in the first interval but varied in the second interval. This behaviour was transmited to the progeny involved the two parents.

On the other hand, Giza 86 as well as Giza 87 and Monoufi showed the same trend in the first interval of boll development but varied in the second interval and both varieties Giza 86 and 87 showed Lateness in boll maturation period .

RGR of dry boll weight showed upward trend with time tell end of the first interval of development (10-20) days, owing to increasing of the metabolic products translocated to boll as time proceeded. However, it showed downward trend at the late interval of development owing to maturation of boll and fiber.

It is interesting to mention that, the genotypes which possessed high RGR of boll in the first interval exhibit low RGR in the second interval of boll development. These genotypes showed reduction in boll maturation period. These results indicated that, these genotypes differed in time of ball weight accumulation and time of boll maturation as well as period of fiber elongation and period of fiber thickening, which agreed with Eid and Abdel-Rahman, 1986 and Khedr, 1998.

Table 2. Mean performance of nine cotton parents for all the studied characters

Characters / parameters	P1 (Pimas$_6$)	P2 (Kars)	P3 (Suvin)	P4 (Dandra)	P5 (Monoufi)	P6 (Giza86)	P7 (Giza87)	P8 (G89xp56)	P9 (Giza92)	LSD (0.05)
RGR/B	0.026	0.023	0.023	0.021	0.026	0.027	0.024	0.020	0.023	0.0014
RGR/B 10-20d	0.0191	0.0228	0.210	0.209	0.195	0.198	0.198	0.223	0.210	0.0153
RGR/B 20-30d	0.072	0.023	0.056	0.038	0.037	0.056	0.060	0.037	0.038	0.0158
RGR/p 60-90d	0.042	0.043	0.076	0.017	0.046	0.056	0.052	0.049	0.049	0.109
RGR/p 90-120d	0.017	0.012	0.010	0.033	0.017	0.009	0.007	0.020	0.010	0.013
Root /Shoat Allometery 60d.	0.032	0.102	0.074	0.095	0.010	0.030	0.009	0.0180	0.043	0.056
Root /Shoat Allometery 90d.	0.393	0.341	0.277	0.338	0.332	0.396	0.347	0.343	0.348	0.029
Root /Shoat Allometery 120d.	0.377	0.370	0.327	0.353	0.385	0.438	0.364	0.375	0.376	0.026
Seed cotton yield	182.747	131.70	157.671	153. 5	157.671	221.967	153.500	166.067	223.000	61.220
Fiber development										
Diameter 10	18.350	16.067	16.947	16.440	16.777	16.853	14.353	17.160	17.123	0.149
Diameter 20	18.40	16.600	18.873	17.143	16.890	17.533	14.380	17.237	17.223	0.111
Diameter 30	18.670	16.767	19.377	17.270	16.950	18.053	14.503	17.290	17.300	0.121
Deposition 20d	5.353	4.773	5.363	5.060	4.943	4.930	4.000	5.033	5.033	0.045
Deposition 30d	6.017	5.227	6.763	5.753	5.480	5.633	4.600	5.600	5.400	0.105
Fiber length	33.570	33.300	30.667	30.067	34.567	34.367	36.233	32.433	34.867	0.972
First node	7.5	6.000	7.5	7.00	8.000	8.00	9.000	6.50	7.00	0.733
Boll maturation period	52.33	43.67	50.00	52.33	48.67	53.33	54.00	48.30	49.00	6.198

As regard to plant growth rate, the parental genotypes Giza 86 and suvin exhibited high values of plant growth rate at the first

interval as compared with other parents but, showed lower values in the second interval. However the crosses which contain the Russian variety Karsheny$_2$ or suvin gave high value of maturity in the second interval. This is due to these genotypes were began development and terminated earlier as compared with other genotypes. These results were in agreement with those of Ali et al, 2009.

The allometric coefficient (K) is an index of balance of growth between root and shoot components of the plant integrated over a period of time. It is evident that, root shoot allometery was low at the first stage owing to shoot growth and then drifted slowly upward with time but diminished by flowering stage at 90 days. Most genotypes were differed significantly at the first stage.(Khedr, 2002)

Fiber diameter (D) was measured at three intervals of bool development, while deposition (DOS) was determine at 20 and 30 days of boll development only. Fiber diameter is the only variable that directly affected primater and it is regulated by biological mechanisms that control expansion characteristic of the cell wall and establish cell diameter . All cotton parents and crosses exhibited significant increases in maximum diameter and thus, perimeter during the first 30 days of boll development. These results were in agreement with those of Bradow et al, 1996.

All parent genotypes exhibited had approximately similar final diameter except, three parents i.e Giza 87, Monoufi and Karshinky$_2$ which exhibited low diameter and thus showed better micronair values. The initial diameter of Giza 87 was smaller than other genotypes and this parent exhibited smallest change in diameter compared with other genotypes. On the other side, the parental genotype suvin showed the largest changes in fiber diameter followed by Pima S_6 and Giza 86. By 30 days post anthesis the genotypic diameter remained the same throughout.

It is worth to mention that most variabilities in wall diameter among parents transmitted to the progency. For example the hybrids which involved Giza 87 and or Karshencky$_2$ as well as Monoufi as a common parent showed lower values of wall diameter as compared with other hybrids.

Prior to 20 days post anthesis fibers exhibited no detectable deposition of secondary wall. The lake of detectable wall brief ringence coincides with the synthesis of primary cell wall (Seagull, 1998). Between 20-30 days post anthesis fibers from all genotypes exhibited a dramatic increase in Dos, indicating deposition of highly

ordered arrays of cellulose microfibrils in the secondary cell wall. The parental genotypes as well as hybrids exhibited differently significant deposition rate. Both pima S_6, suvin, dandra and Giza 86 exhibited a rapid rate of wall development as indicated by the relative increase of Dos means. Both Giza 87 and Monoufi showed similar and slower changes in deposition of secondary wall with time.

In all genotypes fiber diameter significantly increased between 10-20 days post anthesis (Table2) a period when the cell wall exhibited significant increases in deposition. The observed increases in secondary wall deposition coincide with higher rate of wall synthesis and dry weight accumulation in fiber (Ryser 1985). The development of secondary cell wall by deposition does not appear to alter changes in fiber diameter since most genotypes exhibited significant increase in well depositions between 20-30 days post anthesis yet continued to increase in cell diameter similar results were obtained by Seagull et al., 2000.

Fiber length differed significantly among genotypes. The parental genotypes Giza 87 and Monoufi showed high mean values for fiber length followed by Giza92 and Giza 86 . Also the hybrids which contained Giza 87 or Giza 92 as a common parents showed high value for fiber length .

Generally, growth and development of cotton fiber are consisted of two phases, period of fiber elongation, concluded development in fiber length and diameter and period of fiber thickening. The genetic control of fiber elongation and wall diameter not necessary coupled with that of fiber thickening and both phases might not be necessarily controlled by the same genetic factors. Therefore, it is possible to changes either of them without appreciably changing the other.

In order to test the adequacy of additive dominance model to the data set, joint regression analysis was carried out. The regression coefficients were significantly deviated from unity for most characters, which indicated, non additive variation included epistasis or multiple allelism and correlated genes distribution among the parents. Therefore, the data did not fulfill the diallel assumptions, hence, additive dominance model was partially inadequate (Table 3).

The additive component (D) and the dominance components (H_1 and H_2) were significant for all characters, with some exception, indicating the importance of additive and non additive gene effects in the genetic control of these characters. Moreover, values of H_2 were relatively small than those of H_1, indicating that the positive and negative alleles, at the loci of the traits in question, are not equal in proportion to the parents. While the dominance gene effects were

large in magnitudes than the additive one for all characters except for fiber length, showing that dominance ratio were more than unity and suggesting some sort of over dominance gene effect in the genetic control of these characters (Table 3). Similar results were obtained by El-Mansy, 2005.

The positive values of the F component for most characters indicated on excess of dominant alleles were present in the parents. While it was negative for seed cotton yield and boll maturation period indicated an excess of recessive alleles.

Estimates of h^2 were found to be significant and positive for root-shoot allomatric at 60, 90 days, seed cotton yield, diameter at 10 days and fiber length indicating, the prevalence positive genes controlling these characters and suggesting unidirectional dominance genes. The other characters showed ambidrictional dominance (Table 3).

The ratio of $H_2/4H_1$ estimated the frequency of negative versus positive alleles at loci exhibiting dominance, it was 0.158 to 0.258 being almost less or and equal to maximum value of 0.25. This suggest equal distribution of the genes among parents. High ratio of KD/KR for most characters confirming the existence of more dominance than recessive genes in the parents.

The estimation of additive and dominance components of genetic variation appeared to be biased by epistasis to an unknown extent. The presence of epistasis lead to kind of discrepancy in the relative importance of components of genetic variation.

Heritability values in narrow sense were low for growth characters. This due to low additive effects. While it was relatively high to moderate for fiber characters. According to Hayman, 1957 epistasis can decrease or increase degree of dominance, which also have affected on heritability estimates (Murtaza, 2005).

Table3: Test of regression coefficient of covariance (Wr) on variance (Vr), estimates of genetic parameters and heritability for all the studied characters

Characters / parameters	Regression coefficient(b)	T value		Genetic components					
		b=0	b=1	D	F	H1	H2	h2	E
Boll growth rate0-10	0.311±0.322	0.968*	2.141*	5.05E-06	3.22E-06	3.46E-05*	2.96E-05*	7.78E-08	2.49E-07
10-20 day	0.421±0.328	1.285*	1.765*	6.313E-05	-2.201E-05	0.0004*	0.0004*	-1.682E-05	4.517E-05
20-30 day	0.021±0.206	0.104	4.752*	0.0002*	0.0002	0.0011*	0.0009*	-1.118E-05	3.136E-05
Crop growth rate 60-90 day	0.940±0.249	3.769*	0.242	0.0002*	0.0003*	0.0003*	0.0002*	-6.8E-06	1.724E-05
90-120 day	0.632±0.260	2.431*	1.413*	4.155E-05*	9.48E-05*	0.0002*	9.99E-05	5.31E-05	2.26E-05
Root-Shoat allo. 60 day	0.932±0.247	3.777*	0.274	0.006*	0.007*	0.009*	0.006*	0.003*	0.0004
90 day	0.524±0.400	1.309*	1.189*	0.0011*	0.0013*	0.0022*	0.0016*	0.002*	0.0001*
120 day	0.550±0.362	1.518*	1.243*	0.0008*	0.0011*	0.0026*	0.0021*	0.0003	8.13E-05
Seed cotton yield	0.327±0.089	3.641*	7.492*	0.0000	-3.44074	1489.228*	1442.552*	5121.827*	545.538*
Diameter 10 day	0.340±0.359	0.947*	1.841*	1.144*	0.653	4.390*	3.397*	1.608*	0.003
Diameter 20 day	0.308±0.343	0.899*	2.018*	1.569*	0.783	3.900*	3.588*	0.554	0.002
Diameter 30 day	0.510±0.340	1.499*	1.440*	1.799*	0.981	3.633*	3.292*	0.396	0.002
Dos 20 day	0.499±0.344	1.453*	1.458*	0.378*	0.304*	0.736*	0.621*	0.0002	0.0003
Dos 30 day	0.348±0.231	1.504*	2.817*	0.342*	0.239	0.684*	0.609*	-0.0005	0.0013
Fiber length	0.711±0.236	3.010*	1.220*	3.628*	1.981*	2.068*	1.639*	1.362*	0.118*
First node	-0.017±0.280	-0.061	3.628*	0.808	0.929	-5.429*	4.777*	0.678	0.0667
Boll maturation period	0.125±0.073	1.719*	12.017	5.600	-10.290	28.225	24.482	2.063	4.820*

*, ** Significant at 0.05 and 0.01 levels of probability respectively.

Continue Table3:

Characters / parameters	√H1/D	H2/4H1	KD/KR	Yr/(Wr+Vr)	H^2_n
Boll growth rate0-10	2.619	0.214	1.278	0.093	30.93
10-20 day	2.574	0.254	0.873	-0.046	20.48
20-30 day	2.519	0.205	1.651	-0.150	23.58
Crop growth rate 60-90 day	1.180	0.158	3.714	0.701	20.15
90-120 day	1.944	0.159	3.844	0.232	3.81
Root- Shoat allo. 60 day	1.216	0.166	2.907	0.945	33.00
90 day	1.402	0.183	2.476	-0.105	26.67
120 day	1.821	0.197	2.287	-0.060	15.44
Seed cotton yield		0.258	0.653	-0.362	0.00
Diameter 10 day	1.959	0.224	1.341	-0.610	32.36
Diameter 20 day	1.576	0.230	1.376	-0.625	37.94
Diameter 30 day	1.421	0.226	1.475	-0.556	41.28
Dos 20 day	1.396	0.211	1.810	0.540	37.69
Dos 30 day	1.415	0.222	1.659	0.209	36.63
Fiber length	0.755	0.198	2.133	-0.271	66.30
First node	2.591	0.220	1.570	0.156	17.42
Boll maturation period	2.245	0.217	0.419	0.143	47.29

*, ** Significant at 0.05 and 0.01 levels of probability respectively.

Multivariate technique using principal component analysis simultaneously examines differences in morphological variables and indicates the relative contribution of each variable in genetic divergence. Multivariate procedures based on morphological and fiber development characters have been used in the assessment of genetic divergence in cotton (El-Mansy, 2009) principal component analysis seemed to elucidate patterns of variation in agronomic attributes which are of economic importance and give enitial factor solution using eigen values. These values could measure the explained varience associated with each variable (Hair et al., 1987).

The first five principal component were significant and accounted for about 75% of the total variance of all characters. While the first two principal component axies accounted for about 46% of the multivariate variation among genotypes showing the highest joint eigen values 5.084 and 2.784 respectively (Table 4). Thus it is possible to include the corresponding amount of variance in a two dimensional plot of the components. Each genotype is plotted at it is principal component score on each axis. (Brown, 1991).

Table 4 : principal component (PC) analysis of characters associated with 45 cotton genotypes showing eigen values and proportion variation associated with the first five PC axes and eigen vector of characters .

Eigenvalue	5.0840	2.7839	1.9232	1.6520	1.2267
Proportion	0.299	0.164	0.113	0.097	0.072
Cumulative %	29.9	46.3	57.6	67.3	74.5
Eigen vector					
Variable	PC_1	PC_2	PC_3	PC_4	PC_5
AGR/B	0.128	-0.457	0.203	-0.134	-0.330
RGR_1/B	-0.108	0.479	-0.108	0.143	0.203
RGR_2/B	0.012	-0.066	-0.423	-0.043	0.423
RGR/P_1	0.191	-0.190	-0.531	-0.050	-0.202
RGR/P_2	-0.136	0.115	0.313	0.335	-0.170
K60	-0.054	0.146	0.515	-0.301	0.328
K90	0.007	-0.317	0.219	0.432	0.275
K120	0.240	-0.191	0.102	0.217	0.214
SCT	0.018	-0.002	0.080	-0.552	0.258
D1	0.403	0.089	0.050	-0.116	- 0.020
D2	0.423	0.087	0.088	-0.041	0.011
D3	0.426	0.078	0.103	-0.018	0.015
DOS 1	0.414	0.102	0.046	0.055	0.073
DOS 2	0.392	0.161	-0.031	0.096	0.008
F.N	-0.020	0.347	-0.168	0.042	0.115
FL	-0.080	-0.325	-0.046	-0.304	0.276
BMP	0.047	-0.356	-0.066	0.306	0.259

Each character was an important source of variations in at least one PC axis because each of PC axes was given equal weight in the multivariate analysis. Each character contributed to the information used to group genotypes, however some characters may have greater importance in determing plant phenotypes than others.

Fiber development characters i.e. stages of diameter and deposition were a primary source of variation with the largest coefficient in the first PC axis respectively. Hence the higher PC1 score for genotypes, the higher values for the above characters, thus this axis deals with fiber development characters.

Regarding to PC2, the earliness characters such as boll growth rate, first node and boll maturation period, with fiber length exhibited highest score on this axis (Table 4) and (Figure1). However the other rest PC axes deals with growth characters and yield.

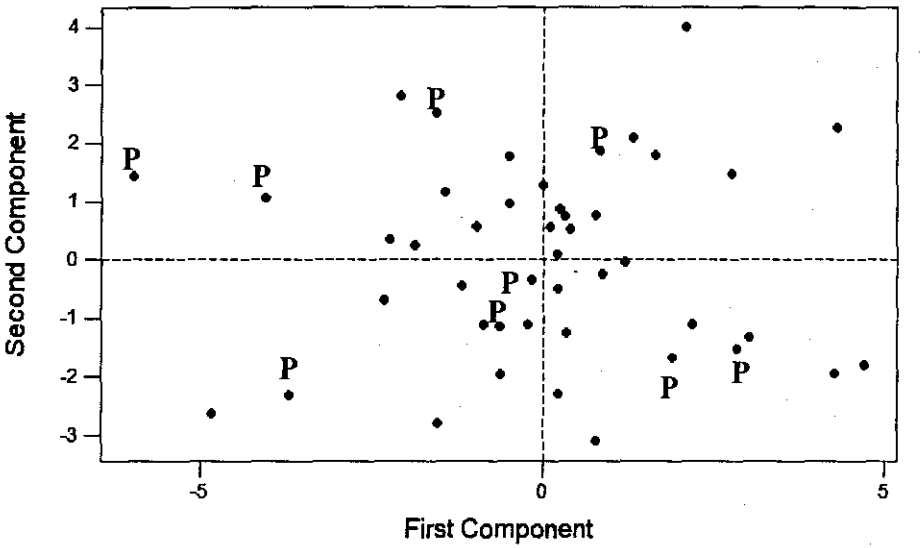

Figure 1 . Representation of 45 cotton genotypes of the first two PC axes of principal componant analysis

Each component score is a linear combination of the characters, similar to an index, such that the maximal amount of variance is shown in the first PC and second amount on the second PC, etc. The two dimensional distance between genotypes might reflect a summary of differences based on all characters measured to the extent that the first two PC axes are effective in capturing the combined variance of most characters. (Fig. 1). Therefore, the first two PC axes were used to plotting the studied parental genotypes and F_1 hybrids (Fig. 2) . In this connection You et al., (1998) and El-Lawenday et al, 2008.

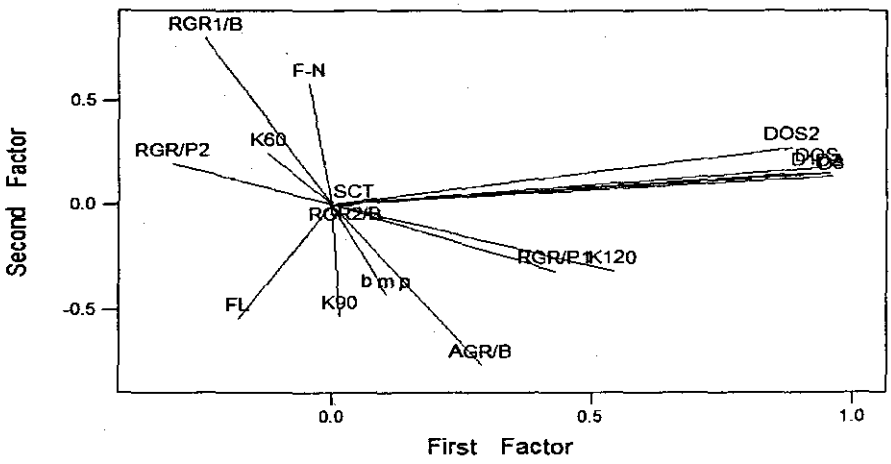

Figure 2 . loading plot of the 17 characters contributed twardes genetic divrgence

The nine parents were grouped into six major cluster according to hierarchical clustering analysis based on the relative dissimilarity among the parental genotypes and 17 agronomic and growth characters (Fig. 3). The Egyptian variety G87 formed unique group and wide divergence from the other parents. The same trend was found with Karshenky$_2$ and the promising cross (Giza 89 x Pima 56), which formed divergent group. While the parental genotypes Giza 86 and Pima S_6 plotted in same cluster and characterized by large fiber diameter with high deposition.

1= pima s_6

2= kar$_2$

3= suvin

4= dandra

5= monoufi

6= Giza 86

7= Giza 87

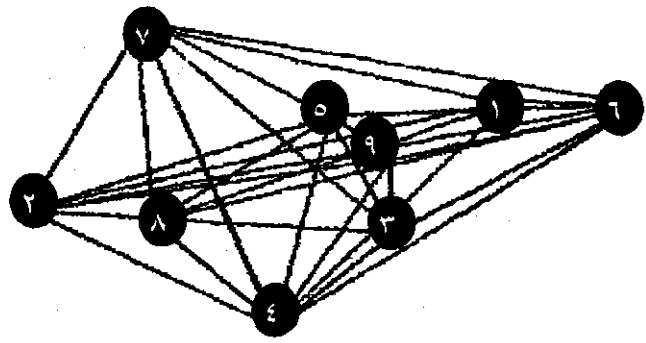

Figure 3 : dendrogrem presentation of 9 cotton parents based on dissimilarity coefficients

Machado et al (2002) chose parents which have greatest genetic divergence in order to obtain the best combination. However, not only genetic divergence might be used to choose parents for crossing but also their performance. Based on relative dissimiarity among genotypes. The 45 genotypes (9 parents and 36 F_1 hybrids) were grouped at nine major clusters (Fig. 4).

Clusters 3, 4 and 8 contained most genotypes which characterized by more earliness and low fiber diameter as well as low deposition. Contrarily of this trend cluster 2 consistsed of most genotypes which characterized by high seed cotton yield with high RGR/P and highest fiber length with highest values for diameter and deposition.

Cluster 5 consisted of three genotypes characterized with best fiber development characters and fiber length. This cluster contained Giza 87 as a common parent with two hybrids Giza 87 x Pima and Giza 87 x Giza 86.

The relative distribution of nine cotton parental genotypes and their 36 F_1 heterozygous in dendrogrames and scattar plots $axis_1$ and $axis_2$ Figures 3 and 4 reflects a broad parallelism between divergence distances and principal component analysis. The distribution pattern of the F_1 heterozygous was more or less influenced by their parents as expected on the basic of close affinity between the parents and their F_1 progenies.

It is interesting to note that from Figure 4 most of F_1 hybrids which possesses more earliness characters were segregating around the parental genotypes $Karshencky_2$ and Giza 89 x Pima S_6. This result suggested that these parents might involve dominant genes controlling those characters and contributing to the genetic divergence. In the reveres trend Giza 86 and Pima S6 aggregate most genotypes which characterized by lateness in maturity with high lint yield and more diameter as well as wall deposition.

It is evident to note that crossing of distantly related parents may give best hybrids which surpassed their parents in most characters and should produce higher variances for most characters in segregating generation rather than crossing between closed related parents which agree with Suinaga et al, 2005.

From a plant breeding principal component analysis is useful in identifying and the most influential characters affecting genetic variation of plant population. The loading of morphological and agronomic characters of an individual genotypes indicate the magnitude of genetic variation. Cluster analysis could efficiently

describe the characteristics of groups of genotypes and principal component analysis give a special representation of each mode.

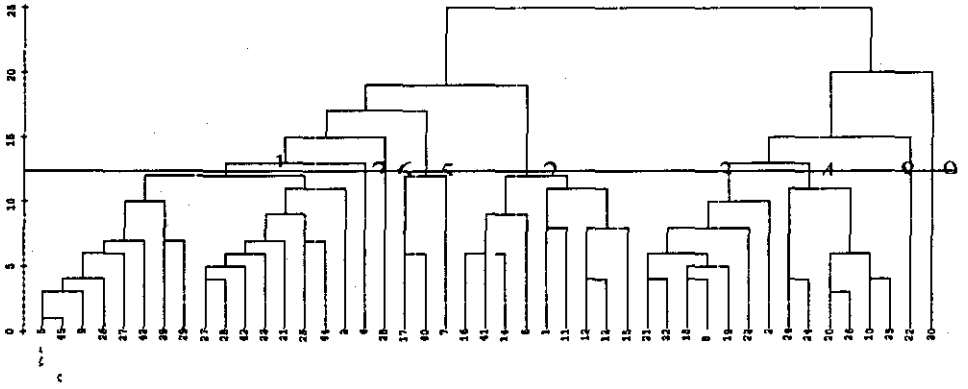

Figure 4 . Results of hierarchical cluster analysis based on dissimilarity coefficients between the 45 cotton genotypes .

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الملخص العربى

الأهمية النسبية للصفات المؤثرة فى التباعد الوراثى فى القطن

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يهدف هذا البحث لدراسة الاختلافات الوراثية بين الآباء والجيل الأول لصفات معدل النمو النسبى للوزة والنبات وكذلك صفات تطور التيلة مثل القطر والترسيب فى مراحل مختلفة من نمو اللوزة والنبات وكذلك عمر اللوزة والتوازن بين نمو الجذر والساق فى مراحل مختلفة من عمر النبات .

كما استخدم تكنيك التحليل المتعدد Multivariate analysis باستعمال تحليل المكونات الأساسية principal componant analysis وتحليل التباعد الوراثى genetic divergence على أساس عدم التشابه النسبى بين المجموعات وذلك لدراسة الأهمية النسبية للصفات المختلفة ومدى مساهمتها فى التباين الوراثى وكذلك أهميتها فى التباعد الوراثى وفصل التراكيب الوراثية المختلفة قى مجاميع مختلفة .

- أظهرت النتائج وجود اختلافات معنوية لكل الصفات مما يدل على وجود كمية كبيرة من الاختلافات الوراثية ؛ كما أعطت الآباء كارشنكى٢ والهجين المبشر جـ٨٩ × بيما س٦ أعلى قيم لمعدل النمو النسبى للوزة فى الفترة الأولى كما أظهرت اختزال فى عمر اللوزة .
- أظهرت كل الآباء المستخدمة اختلافات معنوية للزيادة فى قطر الشعرة خلال الـ٣٠يوما الأولى من نمو الشعرة ؛ أعطت الآباء جـ٨٧، منوفى وكارشنكى٢ أقل قيم لقطر الشعرة كما أعطت أقل تغيرات فى قطر الشعرة كما إنتقلت هذه الصفات للنسل الناتج منها .
- جميع التراكيب الوراثية بدأت فى عملية الترسيب للجدار الثانوى بعد عمر ٢٠ يوم تقريباً من الإحضاب ؛ كما إن زيادة الترسيب ونمو القطر فى الفترة من ٢٠–٣٠ يوم من الإخصاب تدل على أن الجدار الثانوى قابل للزيادة وليس ثابت .
- يشير انحراف قيم معامل الإنحدار معنوياً عن الوحدة لمعظم لصفات إلى وجود تأثيرات راجعة للتفاعل بين الجينات والتى تحكم هذه الصفات .
- كان الفعل الجينى السيادى وكذلك السيادة الفائقة الأكثر أهمية فى وراثة جميع الصفات ماعدا صفة طول التيلة وينعكس ذلك على قيم درجة التوريث بالمعنى الضيق حيث كانت منخفضة لمعظم صفات

النمو والمحصول فى حين كانت تقترب من المتوسطة لصفات نمو وتطور التيلة.

- أظهر تحليل المكونات الأساسية أن الخمسة مكونات الأولى كانت تحصر حوالى ٧٥% من التباين الكلى فى العشيرة بينما أعطى المكونات الأول والثانى ٤٦%من التباين الكلى حيث أظهر قيماً عالية من التباين المرتبط Eigen Value ٥,٠٨، ٢,٨ على التوالى .
- كانت صفات نمو وتطور التيلة (القطر والترسيب) الأكثر أهمية فى التباين بين التراكيب الوراثية على المحور الأول .First axis بينما تعامل المحور الثانى مع صفات التبكير " معدل نمو اللوزة " ، ارتفاع أول عقدة ، عمر اللوزة ، وصفة طول التيلة .
- باستخدام تحليل المجموعات المتباعدة Herarchical clustering analysis تم توزيع التراكيب الأبوية ٩ آباء إلى ستة مجموعات على أساس عدم التشابه النسبى بينهما مع وجود معنوية بين هذه المجموعات لمعظم الصفات .

أظهر النسل الناتج من التهجين بين آباء متباعدة درجة كبيرة من عدم التشابه النسبى والتباعد الوراثى كما أعطى قيماً تفوق قيم آبائها لمعظم الصفات .

وعلى هذا فإن المربى يمكن استخدام تحليل المكونات الأساسية PCA لوصف معظم الصفات التى تؤثر فى التباين الوارثى فى العشائر النباتية كما يستخدم تحليل التباعد الوراثى لتوزيع التراكيب الوراثية ومعرفة العلاقة الوراثية بينها.