MARKERS ASSISTED SELECTION FOR SALT TOLERANCE AMONG SOME COTTON (*Gossypium barbadense* L.) GENOTYPES.

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Salinity is one of the most limiting factors in cotton production with frequent occurrence in arid and semiarid regions. Due to continuous use of low quality irrigation water for agriculture purpose, about $5.7x10^6$ ha of arable land had been affected by salinity (Mujtaba *et al.*, 2003). It was evident that salt tolerance is a complex trait which is greatly affected by the environmental factors (Abdel-Tawab *et al*., 1997). Genetic approach appears more feasible and economical to deal with salinity. As well as, it is the way to produce crop cultivars suitable for the areas affected by salinity. Analysis of genetic diversity is the main prerequisite to improve any crop. Most of genetic diversity analysis studies in Egyptian cotton varieties have been carried out on the basis of morphological characteristics. Randomly amplified polymorphic DNA (RAPD) was used to analyze genetic relationships and genetic diversity (Williams *et al.*, 1990; Multani and Lyon, 1995). Technical simplicity and speed of RAPD methodology is a principal advantage (Gepts, 1993). RAPD analysis has been used for *Gossypium* (Abdel Tawab *et al*., 2001; Rana and Bhat, 2002). Markers-assisted selection (MAS) would enable the plant breeders to grasp the promising genotypes having the desired trait with more confidence in their merits, as selection will be based on genetic rather than phenotypic basis. This approach is fast, reliable and cost effective which can reduce the required time for cotton breeding programs. To start a breeding program on salinity tolerance, significant amount of genetic variability in the gene pool of cotton must be available. Previous studies of salinity tolerance in cotton are relatively few; Bhatti *et al.* (2006) and Azhar *et al.* (2007) suggested that different varieties of upland cotton responded differently to NaCl salinity.

This investigation aimed to evaluate the genotypic performance of ten Egyptian cotton (*Gossypium barbadense* L.) varieties under salt stress conditions based on vegetative, yield and yield component indices. These varieties compared with genetic distance estimated using RAPD markers to obtain reliable molecular markers for salt tolerance could help in breeding programs.

MATERIALS AND METHODS

Plant materials and growth conditions

Ten cotton genotypes i.e, Munofi, Ashmony, Giza 45, Giza 70, Giza 85, Gi-

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za 86, Giza 87, Giza 92, Giza 93 and Giza 94 were evaluated at Sakha Agricultural Research Station (normal condition), Agricultural Research Center (ARC) and El-Hamoul (salinity stress condition), Kafr El-Sheikh Gevornorate in 2016 and 2017 growing seasons.

A randomized complete blocks design with three replications was conducted. Each plot was represented by four rows 5 m long and 0.7 m wide. Seeds were planted on one side of the ridge at 30 cm hill spacing with three seeds per hill. Data were recorded on 6 individual guarded plants chosen at random from each plot.

The data were recorded for the studied traits; Position of the first fruiting node, no. of symbodial branches, plant height (cm), seed cotton yield /faddan (kg), lint yield/faddan (kg), boll weight (g), lint percentage., seed index (g), lint index (g), fiber length, uniformity ratio and micronaire reading.

The reduction ratio (RR) for each character was calculated for each genotype under investigation by formula of Dwivedi *et al.* (1990) as follows:

RR% = (Value of each trait under normal -Value of the same trait under stress)/(Value of the same trait under normal) X 100.

Statistical analysis

The data were subjected to the analysis of variance of all genotypes for each trait, separately. This analysis provides a test of significance between genotypes. After this step, multivariate technique was conducted using principal component analysis according to Hair *et al.* (1987). This analysis was calculated from a matrix based on correlation between the contributed characters for all genotypes. The principle components (PC) associated with all genotypes were expressed as Eigen value and each PC axis. The dissimilarity coefficients among cotton genotypes were estimated according to Johnson and Wichern (1988). Hierarchical clustering was then carried out using Ward's minimum variance methods, which minimize within cluster sum of squares across all partition. Results from principal components analysis and cluster analysis were presented in graphical and dendrogram presentations. These computations were performed using SPSS analysis program (1995).

DNA extraction

Total genomic DNA was extracted from seedlings by the easy extraction kit (EZ-10 Spin Column Genomic DNA Minipreps Kit, plant (BIOBASIC INC) followed by the quantification. Qualification of the extracted DNA was determined on 0.8% agarose gel stained with ethidium bromide.

RAPD analysis

RAPD analysis was used to characterize genetic variation of the studied genotypes. A set of twelve 10-mer random primers as shown in Table (1) was used for this analysis. PCR amplification reac-

tions were carried out in 25 µl reaction volume according to Williams *et al.* (1990).

Data analysis and phylogenetic tree construction

Separated bands were scored for RAPD-PCR technique based on the presence and absence of bands, generating a binary data matrix of 1 and 0 for each band presence. The obtained matrix for amplified DNA fragments was analyzed using the PAST program, version 1.90. The data matrix was used to calculate genetic similarity based on Jaccord`s similarity coefficients to establish genetic relationships among the genotypes under investigation based on unweighted pair group method of arithmetic averages (UPGMA).

RESULTS AND DISCUSSION

For successful breeding of cotton cultivars tolerant to soil salinity or water salinity conditions through conventional approach, basis information about the breeding materials must be available to the breeder. First, must present significant variability in the genotypic response to saline condition and secondary this available variation must be genetically controlled.

Under normal condition, significant interaction for any trait indicates the performance of this trait which differs from environment to environment. Thus, evaluation of these materials should be conducted under different environments (Falconer, 1981).

Impact of soil salinity on yield and fiber traits in cotton

Under saline condition, absolute yield and growth are usually the ultimate good indicator of salinity tolerance. Cotton yield is dependent on the production and retention of boll and both could be decreased under salt stress. The data revealed that increasing salt concentration in soil solution led to significantly decreasing in seed cotton yield and other yield related traits. This is primary due to the reduction in number of bolls and boll weight except for lint percentage which showed increasing values under saline condition. This would be due to saline condition increasing in immature seed and led to decreasing in seed weight as well as immature fiber.

Under saline condition (Table 2), plant height greatly reduced in range of 47% in genotype Giza 93 to 62% in Ashmony. Under saline soil condition, this led to reduce in number of fruiting branches ranged from 49-72% if compared with plants grown under normal condition. The fruiting branches are the fruiting bodies that put up with bolls for producing seed cotton yield. Similar results obtained by Dinakaran *et al.* (2012) were related with decreasing seed cotton yield under saline condition for about 22-50% as compared with normal condition. Giza 86 followed by Giza 94 cotton cultivars recorded high seed cotton yield under saline condition and these genotypes rec-

orded the minimum reduction in seed cotton yield under saline condition. On the other hand, the extra-long variety Giza 93 and Monoufy recorded high yield potential under normal condition but it was highly reduced under saline condition. The reduction in cotton yield under stress condition was generally due to reduction of fruiting branches, fewer flowers as well as increase in boll abortions and reduction of boll numbers, similar results were obtained by Karademir *et al.* (2011).

With regard to fiber length and length uniformity, all genotypes showed decrease fiber length and length uniformity under saline condition. The highest reduction ratio was recorded in Giza 45 variety followed by Giza 70, while the lowest reduction ratio was the lowest influenced for Giza 94 by saline condition.

The results indicated that cultivar Giza 86 was the most salt tolerant, where it showed the lowest rank value (37) over all the investigated traits. On the other hand, variety Giza 70 was the most sensitive one for salt stress where it showed the highest rank value (83) over all the investigated traits.

Genetic variation for salt tolerance in cotton genotypes

Genetic diversity of plants determines their potential for improved efficiency and hence their utility in breeding, which eventually may resulted in production. Under stress condition, the performance of genotypes may be changed, and the study of inter relationships among genotypes is very important for breeder. On the other hand, improvement of yield has been realized by hybridization among distantly related genotypes. Thus study of genetic divergence in cotton under stress condition revealed some interest features of differentiation and adaptability importance.

Multivariate technique (which using principal components analysis), simultaneously examined differences in morphological variables and indicated the relative contribution of each variable to genetic diversity. This analysis seemed to elucidate pattern of variation in agronomic attributes, which are of economic importance and to obtain initial factor solution using Eigen values, this value could measure the explained variance associated with each factor or variable (Hair *et al*., 1987). This approach is very helpful indicating which agronomic traits of crop contributing most to yield, subsequently these traits should be emphasized in breeding program (El-Mansy *et al*., 2014).

The first three principal components were significant ($P < 0.01$) and accounted for 84.6181among genotypes variance with Eigen values more than unity (Table 4). In this connection, El-Mansy *et al.* (2014) reported the important contribution of the first PCA in total variability in cotton.

Herein, in an analysis with thirteen variables 13 axes were existed. However, only those which exhibited high multivariate variations were considered. The first three PC were significant and accounted

most variations among genotypes. The first principal components accounted for maximum variability in the data with respect to succeeding components. PC1 explained for about 41.502% of the total variability among genotypes with the largest Eigen values 5.395 and dominated by a large loading from most yield and fiber traits, i.e., seed cotton yield, lint yield, boll weight, seed index, lint index, micronaire reading and susceptibility index. Most of these characters showed positive relation with yield.

Fiber length and length uniformity decreased under saline condition. In the second PC axis plants with high fiber length and length uniformity with decreased in the first fruiting node influenced by a reduced lint percentage and other yield potential with decrease in fiber fineness, since fiber length and lint percentage were the largest coefficients in the second PC axis (Table 3). Then when there was a decrease in fiber yield, there is also an increase in its fiber length and length uniformity. The uniformity of length is very important trait for the consumer market of cotton, since the higher index and the lower the loss in spinning processes. El-Mansy *et al.* (2012) reported that the first canonical function accounted for 64.6% of the total variability and was affected largely by fiber quality characters. The rest axis accounted about 10.91% of the total variability and domintialy affected by sympodial branches. Shaker *et al.* (2016) found that the first three PCA whose Eigen values were greater than unity significantly and accounted for about 90.3% of the total variability.

According to Chahal and Gosal (2002), traits have the highest absolute values closer to one within the given PC can influence the clustering more than variables that have lower absolute value closer to zero. Thus differentiation of genotypes into different clusters was referred to the relatively high contribution of few characters rather than small contribution from the other characters. The positive or negative loading showed the presence of positive or negative correlation trend between the components and the variables. Thus some characters may have great importance than other, since each character was important source of variation in one axis. Generally, the results reflect the importance of yield and component characters in the total variability. In the same time, fiber quality characters were more important genotypes under saline condition. Thus increasing of yield potential is a prime goal for cotton breeders. Progress in yield results from the progressive accumulation of genes conferring high yield or elimination of the unfavorable genes through the breeding program.

Heirachical clustering analysis

The cluster analysis provided more accurate grouping information for breeding materials used in accordance with pedigree (Nizamani *et al.*, 2017). The relationship between these genotypes depends on the all studied traits (Euclidean) in this study.

This procedure which uses disjoint cluster analysis on the basis of Euclidean distance was applied to illustrate relative genetic distance and genetic divergence within a given germplasm. The Euclidean dissimilarity coefficients between the ten cotton genotypes were significant as Chi-square values in most cases except for Giza 85 and Ashmony, Giza 92 and Giza 45. These coefficients ranged from 6.679 between Giza 92 and Giza 87 to 43.096 between Munofi and Giza 94 (Table 4).

The wide range of genetic distance among cotton genotypes may reflect the presence of wide range of genetic variability among them. Under saline condition, the ten cotton genotypes were grouped into six major clusters on the basis of dissimilarity among genotypes and relative contribution of evaluated characters (Fig. 1) indicating the presence of considerable amount of genetic variability among the materials.

It is clear that the extra-long staple genotype Giza 93 formed wide cluster (cluster 5) having divergent distance from the other groups. However the extra-long varieties Giza 87, Giza 92 and Monofi grouped at the same cluster (4). The old variety which being considered the common parent for all Egyptian varieties; Ashmony formed unique cluster (6) and nearly related with cluster number (2) which consisted of two genotypes Giza 70 and Giza 85 and such varieties characterized as sensitive to salt tolerance. On the other side, the extra-long stable variety Giza 45 grouped with the new variety Giza 94 in the same cluster (cluster 1) and nearly related with Giza 86 which formed unique cluster (3). Nizamani *et al.* (2017) classified 15 cotton genotypes into four different clusters based on eight yield and fiber characters. The wide genetic divergence among the genotypes may be due the adaptation of such genotypes to environmental conditions.

The inter-cluster distance between represented the index of genetic diversity among clusters (Table 5). The maximum inter cluster distance 45.625 was noticed between cluster 3 and cluster 5 this was true since cluster 3 consisted of one genotype Giza 86 which characterized by most tolerance to stress conditions and cluster 5 contained one genotype Giza 93 and high sensitive to stress conditions, followed by clusters 3 and 6, cluster 1 and cluster 6, revealing the magnitude of genetic divergence between these clusters. Inter crossing the genotypes from these clusters might result in a wide array of variability making selection of efficiency (Haritha and Ahamed, 2013). The lowest inter cluster distance was recorded between cluster 2 and cluster 4 (12.637) and clusters 1 and 3 (13.231) (Fig. 1), showing narrow genetic distance among these clusters. The genotypes belonging to these clusters were relatively closer to each other as compared with genotypes from the other clusters. In this regard El-Mansy *et al*. (2012) classified 28 cotton genotypes into 11 clusters and the Egyptian old genotype Ashmony formed unique cluster having divergent distance from the all genotypes. The cluster mean for each of 13 evaluated charac-

ters under saline condition were presented in Table (6). The data revealed that cluster 3 showed the highest seed cotton yield Kent/Fed as well as either yield attributed characters, with acceptable fiber characters, this cluster contained one genotype Giza 86 which characterized by high susceptibility index for saline condition. However, cluster number 5 gave the lowest yield values and high sensitivity to stress condition with best values for fiber quality characters. Cotton breeder desire is to increase genetic diversity among new cultivars, at the same time maintaining the complex of desired agronomic and quality characters present in existing commercial varieties.

Developing such a combination can be difficult, as the introgression of new genetic material is expected to disturb genetic complex responsible for desirable traits. The use of crossing among divergent cultivars could be a means to achieve both ends. However more extensive molecular data are needed in order to interpret the best general conclusion about the relation between cotton genotypes and tolerance to stress conditions.

Polymorphism analysis as detected by RAPD-PCR analysis

Data showed in Table (7) summarize that 109 bands were generated from all RAPD primer pairs. Seventy five out of them were polymorphic and representing 80% of the total generated bands with an average of 6.25 polymorphic bands per primer. Considerable genetic variation among the ten cotton genotypes was shown. The number of amplicons/primer ranged from 5 (OPB-10, OPC-05) to 13 (OPF-14). The primers OPA-01 and OPB-07 gave the highest percentage of the polymorphic bands (100%), while primer OPB-10 produced the lowest percentage of polymorphic bands (40%). Furthermore RAPD analysis was able to reveal genetic variation among cotton genotypes. Primer OPA-11 showed two unique bands, in Giza-94 with molecular sizes of 610 and 550 bp (Fig. 2). These bands could be used as molecular marker for salinity tolerance as clearly shown by the vegetative and yield traits for this variety (Table 2 and 6). El-Mansy *et al.* (2012) found that 44 out of 52 microsatellite markers were polymorphic and accounting for 84.6% of the total number of generated bands with an average of 7.3 polymorphic bands per primer.

Genetic relationship among cotton genotypes

Based on RAPD data analysis, the similarity matrices among the 10 varieties ranged from 0.738 to 0.94. The highest similarity value revealed was between Giza-92 and Giza-70 (0.94), while the lowest similarity value was between Giza-94 and Giza-93. The genetic distance coefficients, among the studied genotypes based on the RAPD fragments, were used to construct a dendrogram (Fig. 3).

The dendrogram separated all genotypes into two main groups where Giza-86 was placed in one group while all other genotypes were placed in the second one. This distribution is clearly agreed with the

performance of Giza 86 as the best genotype comparing with others according to vegetative traits studied and yield and its attributes (Tables 2 and 6). The second group was separated into two main clusters. First cluster included Munofi, Giza 85, Giza-45 and Ashmoni genotypes distributed on three subclusters. Most of these genotypes presented high values for yield and seed index parameter according to data shown in Tables (3 and 7). Second cluster included Giza-87, Giza-93 genotypes in one subcluster and Giza-94, Giza-70 and Giza-92 in another subcluster. The two genotypes showed good values for the technological traits.

The use of RAPDs for comparative purposes relies on the assumption that similarity of fragment size is a dependable indicator of homology (Rieseberg, 1996). Abdel Ghany and Zaki (2003) clearly demonstrated the powerful potential for using RAPD markers in cotton improvement, where it has been successfully used in identification and differentiation among cotton cultivars under investigation. Many investigators developed different markers for different characters using bulked segregate RAPD analysis which partially agreed with our results (Wu *et al*., 2001; Abdel-Tawab *et al*., 2001; El-Kadi *et al*., 2006).

Finally, results from morphological measurements and RAPD markers are complementary for each other in studying and understanding the genetic control of salt tolerance in plant population, and both gave essential information for understanding genetic divergence of Egyptian cotton germplasm. This will provide a useful guide for conserving elite cotton genotypes and developing future cotton breeding programs.

SUMMERY

Ten Egyptian cotton genotypes were evaluated at normal and saline soil conditions for yield and fiber properties through two years. The data revealed that increasing salt concentration in soil solution leads to significantly decreasing in seed cotton yield and other yield related characters except for lint percentage which showed increasing values under saline condition. Under saline condition, plant height was greatly reduced in high for about 37-52%, followed by reduction in number of fruiting sympodia of about 49-72% as compared with normal condition. Therefore, the reductions in cotton yield under stress condition, in generally, due to reduction in boll production primarily because of fewer flowers and less boll number due to increased boll abortions. Among the cotton genotypes, Giza 86 followed by Giza 94 recorded high seed cotton yield under both conditions and these genotypes recorded the minimum reduction in seed cotton yield under saline condition. The first three principal components PC were significant ($p< 0.01$) and accounted for 84.62 among genotypes variance with Eigen values more than unity. The first principal components accounted for maximum variability in the data with respect to succeeding components. PC1 explained for about 41.502%

of the total variability amongst genotypes with the largest Eigen values 5.395 and dominated by a large loading for most yield and fiber characters i.e., seed cotton yield, lint yield, boll weight, seed index, lint index, micronaire reading and susceptibility index. In the second PC axis, plants with high fiber length and length uniformity with decreased in first node influenced by a reduced in lint percentage and other yield potential with decreased fiber fineness. The rest axis accounted about 10.91% of the total variability and domintialy affected by sympodial branches. Under saline condition the ten cotton genotypes were grouped into six major clusters on the basis of dissimilarity among genotypes and relative contribution of evaluated characters. The data revealed that cluster 3 showed the highest seed cotton yield (K/Fed) and either yield attributed characters with acceptable fiber properties. This cluster contained one genotype, Giza 86, and characterized by high susceptibility index for saline condition.

Seventy five out of 109 bands were polymorphic and representing 80% of the total generated bands with an average of 6.25 polymorphic bands per primer, showing considerable genetic variation among the ten cotton genotypes. Based on RAPD data analysis, the similarity matrix among the 10 varieties ranged from 0.738 to 0.94. The highest similarity value revealed was between Giza-92 and Giza-70 (0.94), while the lowest similarity value was shown between Giza-94 and Giza-93. The dendrogram separated all genotypes into two main groups where Giza-86 was placed in one group and all other genotypes were placed in the second one. This distribution clearly agreed with the performance of Giza 86 as the best genotype comparing with others according to vegetative traits studied and yield and its attributes. Results from morphological measurements and RAPD markers are complementary for each other in studying and understanding the genetic control of saline tolerance in plant population, and both gave essential information for understanding genetic divergence of Egyptian cotton germplasm.

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Table (1): The used primer codes and their sequences.

Primer code	Sequence 5’ 3’	Primer code	Sequence 5’ 3’
OPA-05	AGG GGT CTT G	OPB-07	GGT GAC GCA G
OPA-11	CAA TCG CCG T	OPC-05	GAT GAC CGC C
OPB-10	CTG CTG GGA C	OPF-14	TGC TGC AGG T
OPC-02	GTG AGG CGT C	OPL-03	CCA GCA GCT T
OPD-07	TTG GCA CGG G	OPA-04	AAT CGG GCT G
OPA-01	CAG GCC CTT C	OPA-10	GTG ATC GCA G

Table (2): Mean performance of the ten cotton genotypes for 13 traits over two years under salinity and normal conditions.

Genotypes	Position of the first fruiting node				Symbodial branches				Plant height (cm)			
	Normal	Salinity	Reduction%	R	Normal	Salinity	Reduction%	R	Normal	Salinity	Reduction%	R
Giza 45	9.17	8.53	7.00	3	20.42	12.42	39.20**	5	164.17	74.17	54.80**	5
Giza 70	8.33	10.40	-24.20**	8	18.08	8.92	50.70**	10	138.08	67.42	51.20**	3
Giza 87	8.75	9.58	-9.50	7	19.75	11.33	42.60**	7	159.42	64.50	59.50**	8
Giza 92	7.58	9.50	-25.30**	9	18.25	11.25	38.40**	4	141.08	69.67	50.60**	2
Giza 93	8.00	10.3	-28.10**	10	14.75	11.42	22.60**	1	146.67	76.50	47.80**	1
Giza 85	7.83	8.00	-2.20	6	19.58	9.75	50.20**	9	141.67	62.75	55.70**	6
Giza 94	6.67	6.58	1.30	5	15.83	11.50	27.40**	2	156.67	61.58	60.70**	9
Giza 86	8.58	8.25	3.80	4	16.33	10.83	33.70**	3	155.00	71.42	53.90**	4
Ashmony	7.42	5.83	21.40*	2	18.17	9.33	48.70**	8	168.33	62.58	62.80**	10
Munofi	6.42	4.75	26.00*	1	17.33	10.00	42.30**	6	146.25	60.00	59.00**	7
LSD 0.05	0.63	0.59	1.23		1.09	0.68	2.56		7.58	2.95	10.48	
LSD 0.01	0.91	0.85	1.76		1.58	0.98	3.65		10.94	4.25	14.92	
Genotypes	Seed cotton yield /faddan (kg)				Lint yield/faddan (kg)				Boll weight (g)			
	Normal	Salinity	Reduction%	R	Normal	Salinity	Reduction%	R	Normal	Salinity	Reduction%	R
Giza 45	7.25	4.12	43.20**	3	7.77	4.86	37.50**	1	2.73	2.18	20.10*	4
Giza 70	6.95	2.11	69.60**	7	7.92	2.42	69.40**	8	2.85	2.24	21.40**	6
Giza 87	8.72	3.93	54.90**	4	9.63	4.48	53.50**	4	2.67	2.47	7.50	1
Giza 92	9.80	4.15	57.70**	5	11.55	4.89	57.70**	5	3.12	2.60	16.70*	3
Giza 93	10.05	2.06	79.50**	9	11.23	2.49	77.80**	9	2.72	2.05	24.60**	8
Giza 85	9.23	2.75	70.20**	8	11.30	3.49	69.10**	7	2.87	2.22	22.60**	7
Giza 94	11.88	7.37	38.00**	1	15.05	9.33	38.00**	3	3.38	2.24	33.70**	10
Giza 86	8.85	5.22	41.00**	2	10.95	6.84	37.50**	2	3.13	2.48	20.80**	5
Ashmony	10.00	3.79	62.10**	6	11.73	4.78	59.20**	6	2.87	2.54	11.50	2
Munofi	11.38	2.33	79.50**	10	13.23	2.90	78.10**	10	2.80	1.93	31.10**	9
LSD 0.05	0.61	0.34	1.28		0.80	0.43	1.63		0.15	0.26	0.41	
LSD 0.01	0.88	0.49	1.83		1.16	0.62	2.33		0.22	0.38	0.59	

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

Table (2): Cont'.

Genotypes	Lint percentage%				Seed index (g)				Lint index (g)			
	Normal	Salinity	Reduction%	R	Normal	Salinity	Reduction%	R	Normal	Salinity	Reduction%	R
Giza 45	33.33	35.7	-7.1	3	10.67	8.83	17.24**	5	5.40	6.10	-13.00	1
Giza 70	37.67	37.6	0.3	9	10.18	7.80	23.38**	9	6.17	4.93	20.10**	10
Giza 87	34.18	35.9	-5.1	5	9.83	9.02	8.24	1	5.12	5.07	1.00	3
Giza 92	37.75	37.9	-0.5	7	10.10	8.78	13.07**	3	6.12	5.52	9.80	6
Giza 93	35.17	35.0	0.6	10	10.25	8.22	19.80**	7	5.57	4.98	10.60	7
Giza 85	39.17	41.3	-5.5	4	9.87	8.43	14.59**	4	6.40	6.43	-0.50	2
Giza 94	41.33	41.3	0.0	8	11.48	9.10	20.73**	8	8.08	6.73	16.70**	8
Giza 86	40.03	41.5	-3.7	6	10.38	9.12	12.14*	2	6.95	6.73	3.20	5
Ashmony	37.63	41.3	-9.8**	2	11.40	9.38	17.72**	6	6.90	6.80	1.40	4
Munofi	36.63	41.3	-12.8**	1	11.42	7.48	34.50**	10	6.67	5.37	19.50**	9
LSD 0.05	0.62	0.52	2.24		0.31	0.61	0.83		0.33	0.49	0.79	
LSD 0.01	0.90	0.74	3.19		0.45	0.88	1.18		0.47	0.71	1.12	

Genotypes	Fiber length				Uniformity ratio				Micronaire reading				Rank
	Normal	Salinity	Reduction%	R	Normal	Salinity	Reduction%	R	Normal	Salinity	Reduction%	R	
Giza 45	35.67	32.30	9.40**	10	84.15	82.67	1.80*	2	3.40	3.35	1.50	10	42
Giza 70	35.93	33.00	8.20**	9	87.13	85.27	2.10	4	4.47	3.77	15.70**	4	83
Giza 87	36.60	34.60	5.40**	6	84.93	84.07	1.00	1	3.77	3.28	13.00**	6	47
Giza 92	33.90	33.00	2.70	3	87.73	85.83	2.20	5	3.87	3.68	4.90	8	52
Giza 93	36.38	34.40	5.50**	7	88.20	85.57	3.00*	8	3.23	3.12	3.40	9	65
Giza 85	31.50	29.60	6.10**	8	85.35	81.62	4.40**	9	4.45	3.27	26.50**	2	70
Giza 94	33.97	33.50	1.40	2	87.08	84.78	2.60*	7	4.78	4.10	14.20**	5	63
Giza 86	32.80	32.50	1.10	1	86.85	85.18	1.90	3	4.75	4.20	11.60**	7	37
Ashmony	31.57	30.40	3.70*	4	85.13	83.13	2.30	6	4.55	3.58	21.30**	3	56
Munofi	31.43	29.90	4.80**	5	85.37	78.57	8.00**	10	4.38	3.17	27.60**	1	78
LSD 0.05	0.35	0.47	0.96		1.00	1.76	2.26		0.17	0.15	0.33		
LSD 0.01	0.51	0.67	1.37		1.45	2.54	3.22		0.25	0.22	0.47		

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

Table (3): Principle components (PC) analysis under saline condition associated with the ten cotton genotypes.

Variable	PC1	PC2	PC3
Eigen value	5.395	4.187	1.418
proportion	41.502	32.206	10.910
Cumulative	41.502	73.708	84.618
Eigen vector			
	1	2	3
Position of the first fruiting node	-0.121	0.897	0.292
Symbodial branches	0.377	0.538	-0.721
Plant height (cm)	-0.023	0.798	-0.110
Seed cotton yield /faddan (kg)	0.948	-0.070	-0.220
Lint yield/faddan (kg.)	0.947	-0.127	-0.203
Boll weight (g)	0.613	0.162	0.574
Lint percentage%	0.319	-0.885	0.192
Seed index (g)	0.849	0.093	0.058
Lint index (g)	0.713	-0.546	-0.041
Fiber length	0.237	0.869	-0.053
Uniformity ratio	0.448	0.739	0.420
Micronaire reading	0.794	-0.054	0.350
Fiber strength	0.921	0.121	-0.198

Table (4): Euclidean distances among the ten cotton genotypes as chi-square values.

Genotypes	G. 70	G. 92	G. 87	G. 93	G. 85	G. 86	G. 94	Ashmouny	Monofy
	Euclidean Distance								
G. 45	28.124	15.631	15.811	36.837	30.292	7.812	16.089	23.385	40.110
G. 70		15.779	12.974	13.927	8.485	29.911	34.013	11.926	15.917
G. 92			6.679	27.544	17.540	17.051	19.376	11.134	27.176
G. 87				23.364	16.025	17.345	22.510	10.705	26.047
G. 93					19.114	39.849	45.625	24.428	20.367
G. 85						31.108	33.614	8.867	10.779
G. 86							11.036	23.299	41.251
G. 94								25.167	43.096
Ashmouny									18.583

Table (5): Intra and inter cluster distance.

Cluster	1	2	3	4	5	6
1	3.91	27.00	13.23	15.65	38.17	40.50
2		6.41	30.67	12.64	18.78	14.34
3			0.00	20.73	45.63	43.10
4				3.34	25.32	26.41
5					0.00	20.37
6						0.00

Table (6): Cluster means of the contributed characters.

Traits	Clusters					
	1	2	3	4	5	6
Position of the first fruiting node	8.53	10.35	6.58	9.50	10.25	4.75
No. of symbodial branches	12.40	8.92	11.50	11.25	11.42	10.00
Plant height (cm)	74.20	67.42	61.58	69.67	76.50	60.00
Seed cotton yield /faddan (kg)	4.12	2.11	7.37	4.15	2.06	2.33
Lint yield/faddan (kg.)	4.86	2.42	9.33	4.89	2.49	2.90
Boll weight (g)	2.18	2.24	2.24	2.60	2.05	1.93
Lint percentage%	35.70	37.57	41.33	37.92	34.97	41.33
Seed index (g)	8.83	7.80	9.10	8.78	8.22	7.48
Lint index (g)	6.10	4.93	6.73	5.52	4.98	5.37
Fiber length	32.30	33.00	33.50	32.98	34.38	29.92
Uniformity ratio	82.70	85.27	84.78	85.83	85.57	78.57
Micronaire reading	3.35	3.77	4.10	3.68	3.12	3.17
Fiber strength	56.90	30.29	62.02	42.33	20.50	20.48

Table (7): Number of amplified DNA fragments and polymorphic % of studied genotypes investigated with twelve RAPD primers.

Primer code	Range of fragment size(bp)	Total No. of fragments	Monomorphic fragments	Polymorphic fragment	Unique fragments	Polymorphism%
OPA-05	180- 2200	10	0	8	0	80.00%
OPA-11	550- 2242	9	3	4	2	44.40%
OPB-10	188- 1719	5	3	2	0	40.00%
OPC-02	200- 2150	10	4	6	0	60.00%
OPD-07	265- 2461	6	3	3	0	50.00%
OPA-01	323- 1681	11	0	11	0	100.00%
OPB-07	137- 810	10	0	10	0	100.00%
OPC-05	294- 1316	5	2	3	0	60.00%
OPF-14	490- 3012	13	7	6	1	46.15%
OPL-03	380- 2420	9	3	6	1	66.66%
OPA-04	319- 1680	11	2	9	0	81.81%
OPA-10	197- 2100	10	3	7	0	70.00%
Total	137- 3012	109	30	75	4	68.80%
Average		9.08	2.5	6.25	0.33	

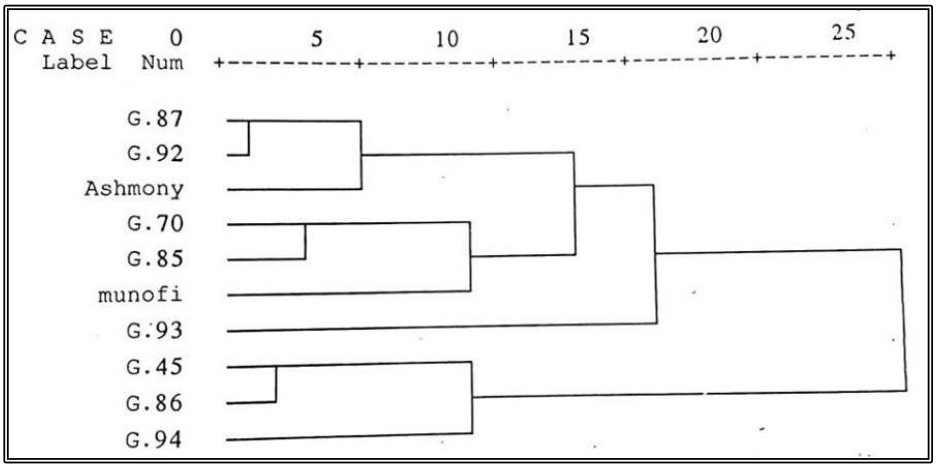

Fig. (1): Cluster analysis for ten genotypes under saline condition.

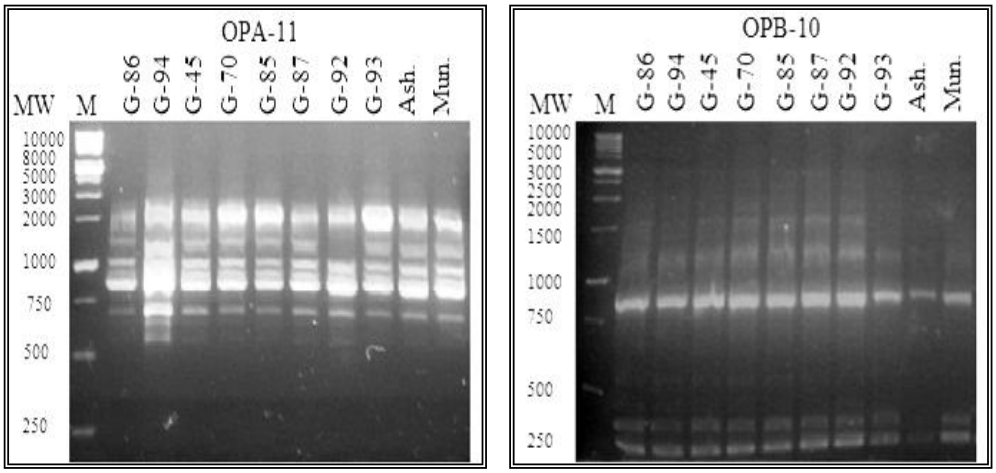

Fig. (2): Banding profiles of studied genotypes for RAPD, using the random primers OPA 11 and OPB-10.

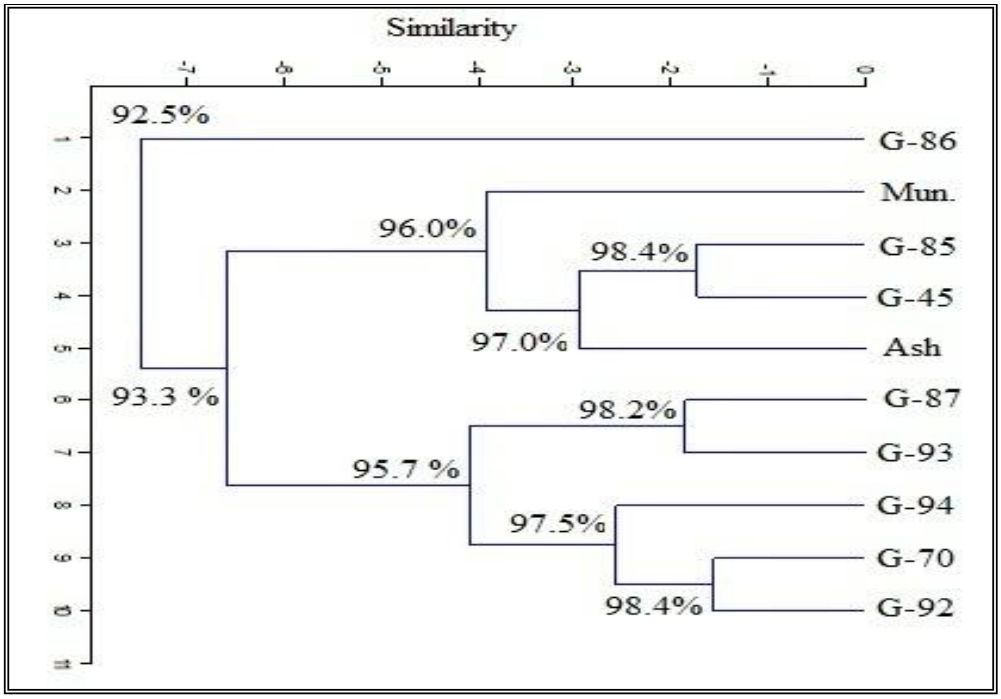

Fig. (3): The Dendrogram of genetic distances among all tested genotypes based on band polymorphisms generated by RAPD-PCR primers.