Genetic divergence among Egyptian cotton genotypes under water deficit conditions

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Genetic divergence among Egyptian cotton genotypes under water deficit conditions

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ABSTRACT

Background: water shortage is the greatest significant reason controlling crop yield that harmfully affects fruit production, boll shedding, lint yield and fiber properties quality in cotton plants. Objectives: this study was carried out at Sakha Agricultural Research Station, Kafr El-Sheikh, Agric. Res. Center, Egypt, during 2014 and 2015 growing seasons. A study was undertaken in cotton (*G. barbadense* L.) to detect the magnitude of genetic divergence among parental cotton genotypes and their F_1s cross combinations and to select most suitable combinations for tolerant water deficient. Results and conclusion: the data showed that the first eight main principal components with eigen value more than one are extracted from the complicated components, the total cumulative variance of these eight factors amount for about 85.28% of the total multivariate variance. Suggesting that these PCA scores might be used to summarize the original variables in any further analysis of the data. The female parent 10,229 formed wide cluster having wide divergent distance from the other groups. On the same trend, the extra-long varieties Giza 96 and Giza 45 formed unique groups, cluster number 8 and cluster 1 nearly related. Cluster number 7 and cluster 4 which consisted of two genotypes for each characterized by susstable to water deficit conditions. The cross combinations Giza 77 x Dandra, Giza 77 x Pima S6, Giza 96 x Australy and Minufy x Dandra grouped at the same cluster, however the cross combinations Giza 86 x Dandra and Giza 68 x 10,229 classified into two different clusters. The data revealed that the inter cluster distance was higher than the intra cluster, indicating wide genetic divergent among the studied genotypes. Principal components analysis is useful in identifying and most influential characters affecting genetic variation of population.

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1. Introduction

Water deficit is the most important factor limiting crop productivity that adversely affects fruit production, square and boll shedding, lint yield and fiber properties quality in cotton [1]. The demand for water deficit tolerant genotypes will be exacerbated as water resources and the funds to access them become more limited [2].

One of the important approaches cotton breeding to gave more tolerant about stress conditions is hybridization and subsequent selection. Thus, parents choice in the first step in breeding program through hybridization for effective evaluation and utilization of germplasm measure of extent of available genetic, is of almost important.

Genetic diversity among parents is considered an important factor for obtaining heterotic effect. Breeders rely on genetic variation between parents to create unique gene combinations necessary for new superior cultivars. This diversity is one of the restoring tools for breeding program based on hybridization, because it generate parameters

for identifying superior parents [3,4]. Another helpful issue to be evaluated is the relative importance of the characters. Though, plant breeders often measure several characters simultaneously in cotton development.

For successful cotton breeding program the presence of genetic diversity plays a vital role which is essential to meet the diversified goals of plant improvement, such as attempt to increase yield potential, quality, adaptation and tolerance to stress conditions. Developing high yielding cotton cultivars is an important objective of cotton breeding programs. Thus, information of the structure of divergence of cotton aids the breeder for in choosing the diverse parents for hybridization. Breeding high yielding cotton cultivars, which are an important strategy to sustain yield. Production draws the plant breeder's attention. Lint yield is the end product in cotton and is the integration of many traits that effect plant growth through the growing period. Each trait changes to a different extent and direction under the influence of environmental factors. Thus, statistical analysis of agronomic and physiological characters could be informative in cotton breeding program, so such characters are a reflection of gene effects. Therefore, this study aimed to detect the magnitude of genetic divergence among parental cotton

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genotypes and their F$_1$s crosses and to select the most suitable combinations for tolerant water stress conditions.

2. Material and methods

The present experiment was conducted at Sakha Agric. Res. Stat. Kafr El-Sheikh, Agric. Res. Center Egypt, during 2014 and 2015 growing seasons.

2.1. Genetic material and experimental design

Thirteen cotton genotypes used as parents in the present study (Table 1) and were crossed, in such away Line x Tester (9 × 4) mating design by using four parents as a Tester parents i.e. Dandra, Pima S$_6$, Australy and 10,229 and nine cotton genotypes as a Line parents i.e. Giza 45, Minufi, Giza 67, Giza 68, Giza 86, Giza 77, Giza 94, Giza 96 and Giza 69, in 2014 crop season to produce 36 F$_1$ hybrid seeds, and the original parents were also selfed.

In 2015 season the 36 F$_1$ hybrids and their parents were grown in a randomized complete block design (RCBD) with three replicates under two irrigated conditions. The first one is the normal irrigated 7 irrigations during the growing season and the second is the stress conditions, three irrigations only during the growing season. Each experimental plot consisted of one ridge, measuring five meters in length and 0.70 m in width, with plants spaced 30 cm within ridge. Two plants were left per hill at thinning time. Recommended cultural practices were applied for all the entries.

2.2. Studied traits

The following observations were recorded on six individual guarded plants during the grown season.

Ten leaves were taken randomly from plants (fourth upper leaf) of each replicate from lines x testers experiment at 120 days after sowing to determine total water content (%), free water (%), bound water (%), leaf water deficit (%), relative water content (%), Osmotic pressure (bar), chlorophyll A (mg/g dwt), chlorophyll B (mg/g dwt), carotenoids (mg/g dwt), leaf area (cm^2), proline content (mg/g fwt). Also number of fruiting branches, Plant height (cm), Position of first fruiting node (F.F. N), Boll maturation period (B.M.P), Relative growth rate (R.G.R) of boll weight (mg/g/day), Earliness index, Seed cotton yield per plant in grams (S.C.Y), Lint yield per plant in grams (L.Y), Boll weight in grams (B.W), Lint percentage (L.P %), Seed index in grams (S.I), Lint index in grams (L.I), Fiber fineness (F.F), Fiber strength (F.S), Fiber length (F.L), Uniformity ratio (UR), Tolerance index (TOL), Mean productivity (M.P.), Harmonic mean (HARM), Stress susceptibility index (S.S.I.), Geometric mean productivity (G.M.P.), Stress tolerance index (S.T.I.),

Relative drought index (R.D.I.), Yield index (YI), Yield stability index (YSI) and Drought resistance index (D.I.) were also studied during the grown season. All these computations were performed by using SPSS and Minitab computer programs.

2.3. Statistical and genetical analysis

Multivariate technique were used to assess the similarities among varied genotypes and to evaluate morphological parameters contributing to the total variation for this purpose, principal components analysis were calculated from a matrix based on correlation between the contributed characters for all genotypes. The principal components were expressed as eigen values, latent roots and manifested in eigen vector for all studied characters in each principal component axis [5].

2.3.1. Cluster analysis

This procedures was carried out using herachical clustering procedure using wards minimum variance method, which minimize within group sum of squares across all partitioning, was applied to determine the genetic divergence and distances. The procedure used method performing a disjoint cluster analysis on the basis of Euclidean distances as outlined by [6,7] and developed by [8]. The Euclidean distances were computed and the results from clustering analysis are presented as dendograms. All these computations were performed using SPSS and Minitab computer procedures.

3. Results and discussion

Multivariate technique using principal components analysis (PCA) simultaneously examines differences in morphological variables and indicates the relative contribution of each variable in genetic divergence. This analysis seemed to elucidate patterns of economic importance and to obtain the initial factor solution using eigen values. This value could measure the explained variance associated with each factor, variable [5,9]. This approach is very helpful indicating which traits of crop contributing to product or phenotypic or/and yield.

In order to know which type of agronomic characters of the cotton genotypes would attention high yielding over water deficit conditions (PCA) was performed in (Table 2). The scree plot of the PCA (Fig. 1) show that the first eight eigen values correspond to the whole percentage of the variance in the database site. The first eight main principal components with eigen value more than one are extracted from the complicated components, the total cumulative variance of these eight factors amount for about 85.28% of the total multivariate variance. Suggesting that these PCA scores might be used to summarize the original variables in any further analysis of the data. In this respect, [4,10]

Table 1
Origin source, a brief description and characteristics of thirteen cotton genotypes used as parents in the present study.

Genotypes	Abbrev.	Origin	Characteristics
Giza 45	G.45	Egypt (Giza 28 x Giza 7)	Late in maturation and extra long staple.
Minufy	G. 36	Egypt (Giza 12 x Sakha 3)	Extra long staple.
Giza 67	G. 67	Egypt (Giza 53b x Giza 30)	Long staple, high yielding.
Giza 68	G. 68	Egypt (Giza 36 x Giza 56)	Extra long stable.
Giza 86	G. 86	Egypt (Giza 75 x Giza 81)	Commercial variety, late in maturity, high yield with high lint percentage and long staple with strong lint.
Giza 77	G. 77	Egypt (Giza 70 x Giza 68)	Extra long stable.
Giza 94	G. 94	Egypt (Giza 86 × 10,229)	Long staple, high yield, high fiber properties and early in maturity.
Giza 96	G. 96	Egypt (Giza 84 x (Giza 70 x Giza 51b) x S62	Extra long staple, as a new variety high yield with high lint percentage.
Giza 69	G. 69	Egypt (Giza 51a x Giza 30)	Long staple with high lint percentage
Dandra	G. 31	Egypt Giza 3	Long staple and tolerance high temperature.
Pima s6	Ps6	American Egyptian genotype (5934-23- 2- 6) x (5903-98- 4-4)	Long staple, high lint yield, high lint percentage and early in maturity.
Australy	Aust 13	Australian variety	Long staple, high yield
10,229	10,229	Russian variety (introduced genotype)	Long staple, earlier in mature with high lint yield and high lint percentage.

Table 2

Principal components analysis of cotton genotypes under water deficit conditions.

Characters	Components								Extraction
	1	2	3	4	5	6	7	8	
Total water content (%)	−0.533	0.823	0.050	−0.077	0.062	0.021	-−0.020	0	**0.974**
Free water (%)	−0.637	0.534	0.419	−0.092	0.026	−0.115	0.114	0.008	**0.902**
Bound water (%)	−0.492	0.835	−0.013	−0.072	0.066	0.042	−0.042	−0.001	**0.952**
Leaf water deficit (%)	0.232	0.515	−0.584	−0.007	0.023	0.129	−0.435	0.004	**0.866**
Relative water content (%)	−0.586	0.751	0.167	−0.117	0.024	−0.030	0.088	−0.018	**0.960**
Osmotic pressure (bar)	0.254	0.517	−0.569	0.027	0.020	0.125	−0.461	0.048	**0.888**
Chlorophyll A (mg / g dwt)	−0.640	0.576	0.420	−0.093	−0.015	−0.082	0.098	0.021	**0.943**
Chlorophyll B (mg / g dwt)	−0.574	0.521	0.424	−0.022	−0.016	−0.143	−0.070	0.075	**0.812**
Carotenoides (mg / g dwt)	−0.618	0.686	0.251	−0.047	0.077	0.032	0.091	0.041	**0.934**
Proline (mg / g fwt)	0.410	−0.875	0.069	0.034	−0.079	−0.061	0.107	−0.009	**0.962**
Seed cotton yield / plant (g)	0.803	0.520	0.021	0.201	−0.029	−0.086	0.109	0.002	**0.976**
Lint percentage (%)	0.020	−0.269	0.503	0.379	0.346	0.403	−0.077	−0.120	**0.771**
Boll weight (g)	−0.054	0.078	0.286	0.191	0.507	0.170	−0.282	0.016	**0.493**
Lint yield / plant (g)	0.791	0.429	0.185	0.324	0.072	0.051	0.085	−0.037	**0.965**
Seed index (g)	−0.134	0.091	0.233	0.022	−0.366	0.618	0.305	0.001	**0.689**
Lint index (g)	−0.041	−0.143	0.531	0.316	0.061	0.708	0.113	−0.095	**0.930**
Earliness (%)	−0.007	−0.049	−0.058	−0.288	−0.139	0.433	−0.106	0.436	**0.496**
Leaf area index (cm^2)	−0.555	0.814	0.095	−0.085	0.049	−0.003	0.005	−0.001	**0.988**
Uniformity ratio (%)	0.086	−0.086	−0.052	−0.261	0.742	−0.236	0.178	−0.137	**0.743**
Fiber length	0.314	−0.197	0.007	0.150	0.674	0.223	0.159	0.067	**0.695**
Fiber strength (pressley)	−0.041	0.068	−0.490	−0.466	0.120	0.133	0.098	−0.545	**0.802**
Fiber fineness (micronaire)	−0.053	−0.016	0.174	0.558	−0.056	−0.051	−0.537	0.277	**0.715**
Relative growth rate 1	−0.044	0.147	−0.476	−0.302	−0.332	0.299	0.318	−0.001	**0.642**
Relative growth rate 2	0.065	−0.203	0.422	−0.071	−0.232	0.146	−0.330	−0.233	**0.466**
Position of first fruiting node	0.206	−0.248	0.092	−0.121	0.137	−0.184	0.373	0.636	**0.723**
Plant height (cm)	−0.259	0.200	−0.670	−0.053	0.158	0.263	0.107	0.164	**0.691**
N. of fruiting branches	−0.112	0.299	−0.636	−0.089	0.308	0.329	0.011	0.187	**0.752**
Tolerance index	−0.593	−0.043	−0.344	0.677	−0.060	−0.058	0.147	−0.035	**0.961**
Mean productivity	0.548	0.551	−0.149	0.557	−0.071	−0.059	0.177	−0.044	**0.977**
Harmonic mean	0.652	0.569	−0.091	0.445	−0.062	−0.050	0.150	−0.040	**0.986**
Stress susceptibility index	−0.789	−0.286	−0.261	0.455	−0.004	−0.039	0.064	−0.035	**0.986**
Geometric mean productivity	0.604	0.563	−0.119	0.501	−0.067	−0.054	0.163	−0.042	**0.983**
Stress tolerance index	0.789	0.285	0.262	−0.455	0.004	0.039	−0.064	0.035	**0.986**
Yield index	0.785	0.548	0.006	0.240	−0.042	−0.031	0.106	−0.028	**0.990**
Yield stability index	0.789	0.285	0.262	−0.455	0.004	0.039	−0.064	0.035	**0.986**
Relative drought index	0.789	0.286	0.261	−0.456	0.004	0.039	−0.064	0.034	**0.986**
Drought index	0.867	0.458	0.128	−0.046	−0.010	−0.003	0.041	−0.008	**0.982**
Eigen value	**9.822**	**7.908**	**4.005**	**3.410**	**1.910**	**1.817**	**1.527**	**1.155**	–
% of variance	**26.55**	**21.37**	**10.83**	**9.22**	**5.16**	**4.91**	**4.13**	**3.12**	–
Comulative %	**26.55**	**47.92**	**58.75**	**67.96**	**73.12**	**78.04**	**82.16**	**85.28**	–

reported that the important contribution of the first PC in the total variability while studying different characters.

The principal components analysis had grouped the estimated cotton variables into eight main components. The relative magnitude of the eigen coefficients of each character related to the first eight PC axis from the components analysis might provide an interpretation for each component axis. Though no clear guidelines existed to determine the significance of the trait coefficient, one rule of the thumb is to trait coefficients >0.5 as having a large enough effect to be considered importance [5,9]. The sign of the eigen coefficient is being irrelevant and in fact arbitrary. Each character was an important source of variation in at least one principal components axis. So, each PC axis was given equal weight in the multivariate analysis. Thus, some characters may have great importance in determining plant phenotypes than other [5].

According to [11], characters with largest absolute values closer to unity within the first principal components influence the clustering more than those with lower absolute values closer to zero. Therefore, in the present study differentiation of the genotypes into different groups was because of relatively high contribution of few characters rather than small contribution of specific few characters [4,12].

The first principal component explained about 26.55% of the total variance among all genotypes with the largest eigen value 9.82 and it was related to seed cotton yield, lint yield and had positive loading with drought tolerant indices. Increased yield potential in this group was negatively corrected with increased of some physiological and water relations characters. In this connection, [13] reported that the first four PCs with eigen values more than one contributed about 64.8% of the total variability. PC$_1$ and PC$_3$ related with good yield characters.

The second PC exhibited positive effect for all water relations and biochemical characters. Thus, in this axes, increasing of water relations characters with increase in chlorophyll A, B and carotenoids content under drought or stress conditions contributed to the increase of seed cotton yield. Thus, the higher PC$_2$ score for genotypes, the higher values for the above characters. The third axis accounted for 10.83% of the total variability deals with fiber quality characters which showed negative loading. The other rest axis accounted for about 25% of the total multivariate variation deals with different group characters. In this respect, [14] applied multivariate technique by using PCA in cotton and reported that the first three PCAs with eigen values more than unity explained for about 90% of the total variance, yield and yield components characters were the most contribution on the first two axis. It is great important to note that under water stress condition some characters may have great importance in determining plant phenotype than other, since each character was an important source of variation in one axis.

Since, the first and second PC axes explained the major contribution of all variability among genotypes (47.9%) of total variability and most influenced by yield with tolerance indices, water relations and biochemical characters. In the same time, fiber quality characters were more important for crop differentiation. Thus, increased yield potential
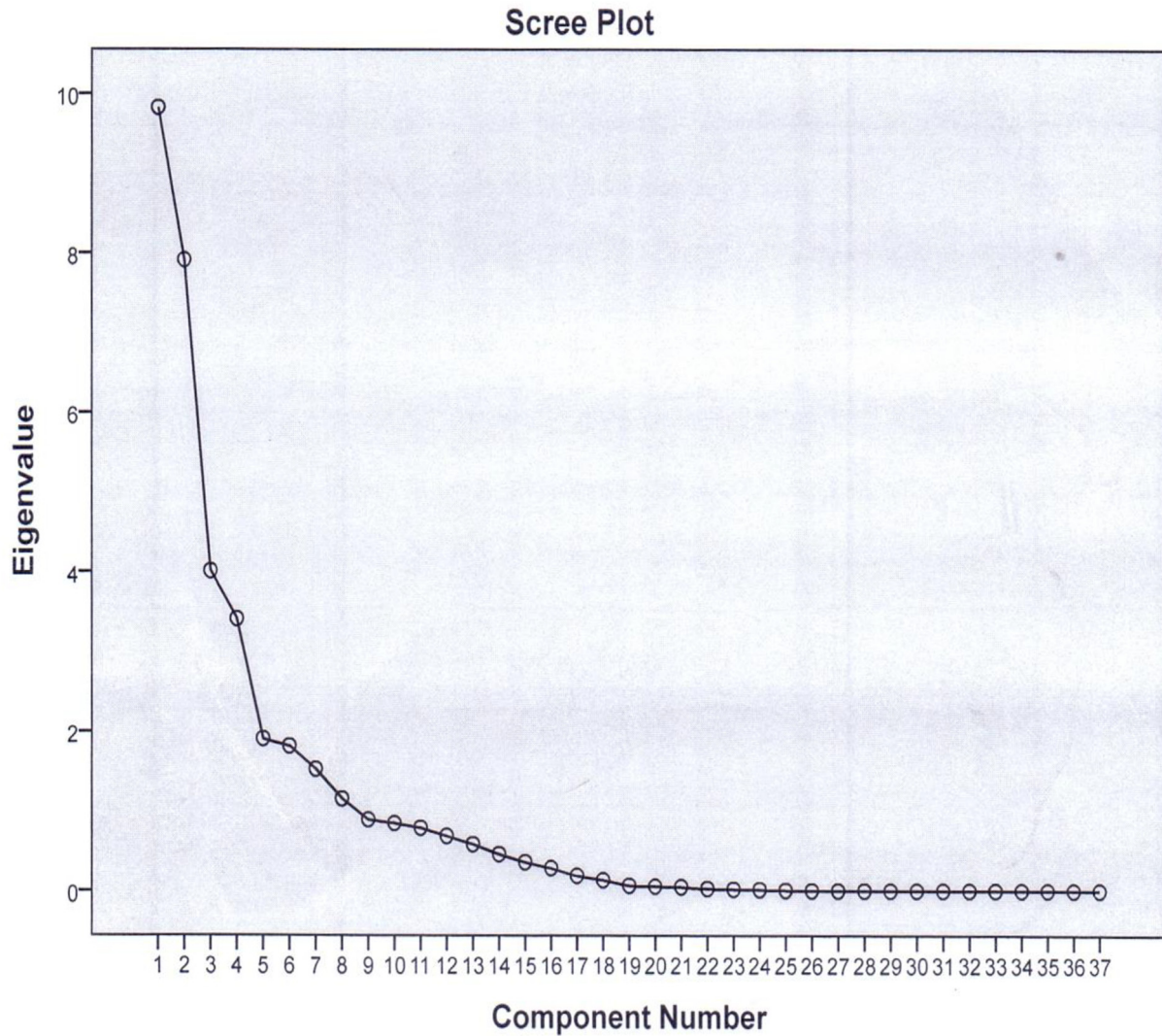
Scree Plot

Fig. 1. Scree Plot of the 37 characters contributed towards genetic divergence among cotton genotypes under water deficit conditions.

is an important goal for cotton breeder. Progress in yield potential results from the progressive accumulation of genes conferring higher yield or elimination of unfavorable genes through the breeding process. The present investigation revealed that under water deficit conditions

relative water content, chlorophyll and carotenoids content, as well as proline accumulation on leave tissues had strong relation with yield in the second and first axis, suggesting that we need more for emphasis on such characters for increasing tolerance for water deficit and to

Table 3
Dissimilarity coefficients among parental cotton genotypes in matrix form.

| Case	Euclidean distance												
	Giza 45	Minufy	Giza 67	Giza 68	Giza 86	Giza 77	Giza 94	Giza 96	Giza 69	Dandra	PimaS$_6$	Australly	10,229
Giza 45	–	31.920	41.598	28.583	19.367	22.772	30.681	44.696	24.633	20.215	17.120	24.285	74.562
Minufy		–	53.134	33.007	22.875	27.570	17.701	21.588	24.341	38.684	16.108	36.477	93.337
Giza 67			–	37.248	40.980	39.954	57.703	67.479	44.649	44.633	46.401	48.949	70.126
Giza 68				–	19.658	23.444	32.637	48.833	15.725	29.423	28.240	19.224	72.399
Giza 86					–	10.030	27.917	41.182	11.357	18.816	15.016	20.849	72.714
Giza 77						–	33.851	45.820	14.101	17.521	19.606	25.572	67.843
Giza 94							–	20.653	26.887	41.399	19.132	34.381	96.974
Giza 96								–	42.159	55.679	30.076	52.193	111.561
Giza 69									–	22.155	20.007	17.343	72.526
Dandra										–	27.592	20.775	58.550
PimaS$_6$											–	28.789	84.384
Australly												–	67.938
10,229													–
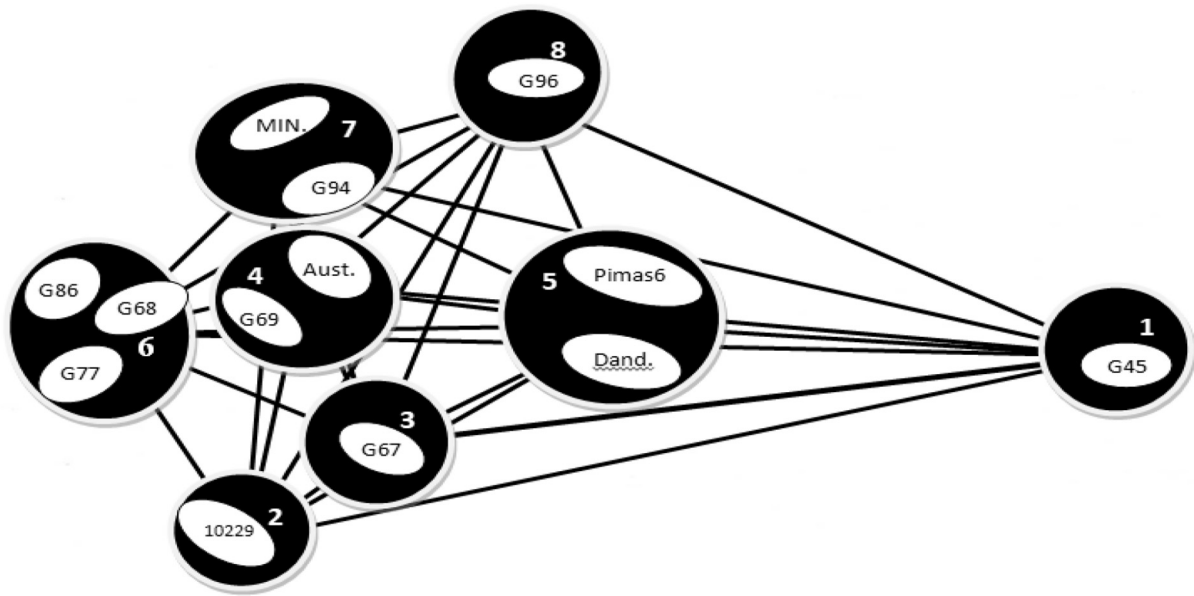
Fig. 2. Dendrogram presentation of 13 cotton genotypes under water stress condition.

Table 4
Inter and intra cluster distance among eight clusters.

Cluster	Distances between final cluster centers							
	1	2	3	4	5	6	7	8
1	0.00	79.163	43.226	22.810	25.219	16.961	22.245	37.120
2		0.00	70.126	72.035	67.938	65.990	94.760	111.561
3			0.00	40.356	48.949	40.882	54.755	67.479
4				7.86	16.534	17.038	26.970	44.935
5					9.56	20.545	34.322	52.193
6						8.100	30.114	47.052
7							8.56	19.182
8								0.00

increase yield in cotton. It is worth to examine the possibility of utilizing such characters to increase the efficiency of selection for these traits as well as the other characters which closely related to seed cotton yield. In this purpose [15] applied multivariate technique in F_3 in cotton and selected some families possess desired yield and fiber quality characters. In this connection, [12,14–17] reported similar results.

It is interest to mention that principal components analysis is useful in identifying the genetic variation and the most influential characters affecting genetic variation in population. PC loading of agronomic characters of the populations indicates the magnitude of such variation. [4,15] noticed that PCA may allow the plant breeder more flexibility in finding the number of plants to be evaluated and use multivariate method by first determining the combination of traits that constitute an ideal plant. By plotting the PCAs that are considered to be important, plant close to the ideal type would be selected.

Hierarchical cluster analysis highlights the nature of relationship between any type of samples described by any type of descriptors. It could serve a basis of selection of parental type that could result into superior hybrids [18]. This procedure using disjoint cluster analysis on the basis of Euclidean distance was applied to illustrate relative genetic distance and genetic diversity within a given germplasm base. Physiological, biochemical and morphological characters have been successfully used for estimation of genetic diversity under water stress conditions, since they provide a simple way of quantifying genetic variation [4,17].

The dissimilarity coefficients among 13 parental cotton genotypes corresponding to 78 possible comparisons are presented in Table 3. The data revealed that all the dissimilarity coefficients were significant as Chi-Square values, except among parents Giza 86, Giza 77 and Giza 68. These coefficients were ranged from 10.03 between the parents Giza 86 and Giza 77 to 111.56 between parents Giza 96 and Giza 10,229. The wide range of genetic distance among the parental genotypes may reflect the presence of wide range of genetic variation among them and an opportunity to improve the genetic basis of cotton by implementing crossing.

The thirteen cotton parental genotypes evaluated in this study were grouped into eight major clusters by using hierarchical clustering

Table 5
Intra cluster distance between 11 clusters.

|	1	2	3	4	5	6	7	8	9	10	11
1	–	64.572	33.851	128.946	67.953	117.856	74.844	75.808	100.292	104.622	54.401
2		–	67.022	177.271	129.243	68.063	39.831	125.166	141.939	154.991	29.077
3			–	111.193	85.812	101.027	75.294	59.057	77.010	91.951	70.691
4				–	113.086	194.169	177.604	54.019	38.323	43.464	179.235
5					–	182.294	136.017	75.566	104.024	87.628	114.547
6						–	70.119	151.213	155.913	178.450	96.108
7							–	128.352	142.612	150.237	54.972
8								–	29.555	40.575	125.939
9									–	43.376	146.897
10										–	155.874
11											–
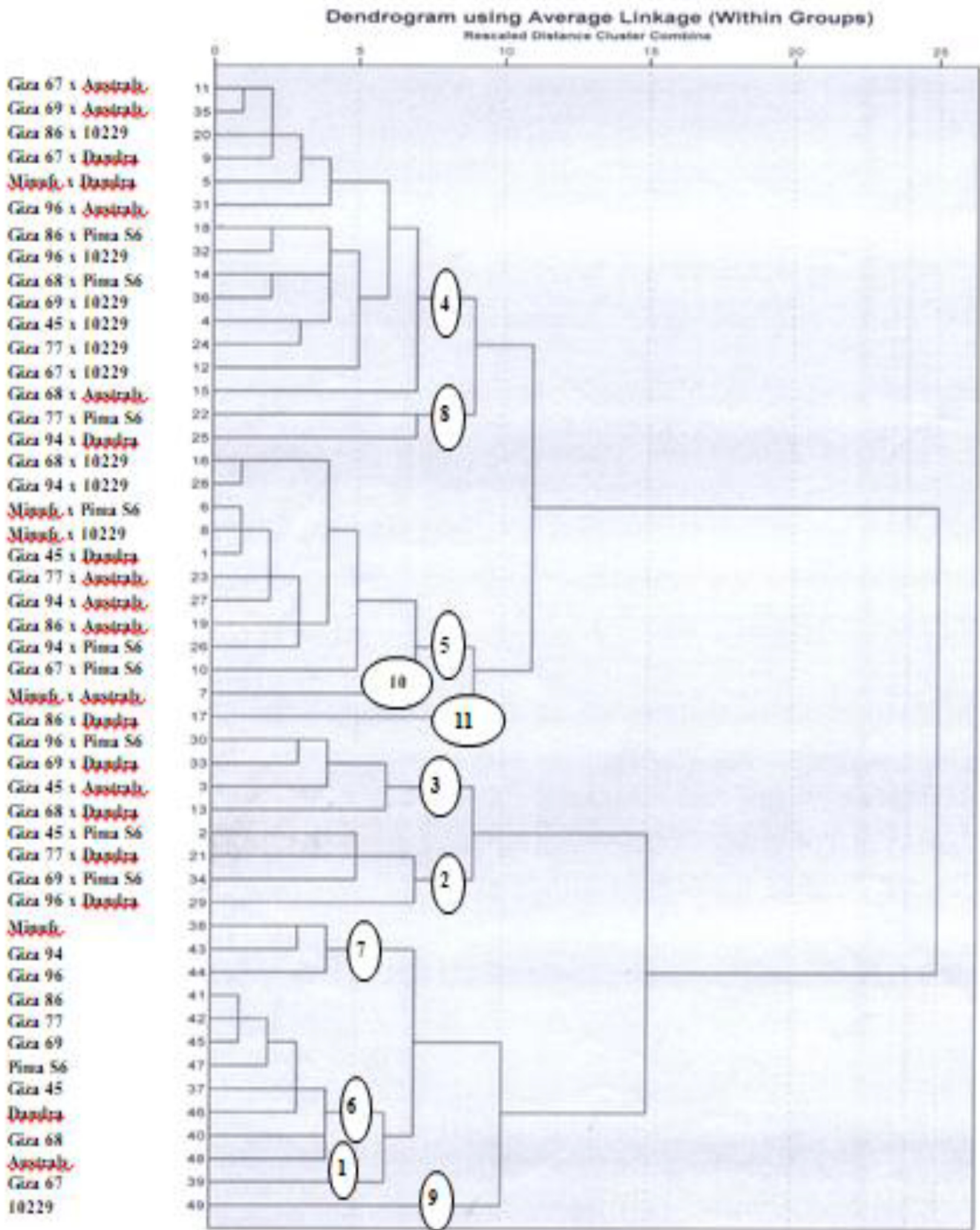
Fig. 3. Results of hierarchical cluster analysis based on dissimilarity coefficients between 49 cotton genotypes under water deficit conditions.

method on the basis of dissimilarity among parents and contribution of evaluated characters, as shown in Fig. 2. It is clear that four parents out of 13 parents formed unique groups and divergent distance from the other parents. The female parent 10,229 formed wide cluster having wide divergent distance from the other groups. On the same trend, the extra-long varieties Giza 96 and Giza 45 formed unique groups, cluster number 8 and cluster 1 nearly related. Cluster number 7 and cluster 4 which consisted of two genotypes for each characterized by suitable to water deficit conditions. Cluster number 6 consisted of three parental lines Giza 68, Giza 86 and Giza 77, the genotypes in this cluster characterized as tolerant water deficit. The female parent Dandra and Pima S_6 formed cluster number 5 and characterized by somewhat tolerant to water stress. The Egyptian ancient variety Giza 67 formed one cluster 3 and characterized by tolerance to water deficit and high yield potentials.

Genotypes grouped in the same cluster (intra cluster) are expected to be genetically more similar than genotypes grouped in different clusters (inter cluster). The data in Table 4 revealed that the inter cluster distance was higher than the intra cluster, indicating wide genetic divergent among the studied genotypes (Fig. 2). The highest inter cluster distance was observed between clusters 2 and 8 (111.561) followed by clusters 2 and 7 (94.760), indicating wider genetic divergence between the genotypes in these clusters. On the other side, clusters number 4 and 5, as well as clusters 4 and 6 were nearly related. [19] noticed that in order to obtain the best combination choose parents which have greatest genetic divergence, however not only the genetic divergence might be used to choose parents for crossing but also the performance of parents and their F_1s. In addition, GCA and SCA effects are more informative than performance values [4,20].

It is well recognized that greater genetic distance between clusters, the wide genetic divergence would be between the genotypes. Thus, highly divergent genotypes would produce abroad spectrum of segregation in the subsequent generations enabling further selection and improving [21].

The genotypes formed cluster 6 showed the lowest intra cluster distance which might nearly related, however the maximum intra cluster distance was observed in cluster 2 followed by cluster 7. It is evident to note that genotypes within the clusters with high degree of diversity would produce more desirable breeding materials for achieving maximum genetic advance.

The 49 cotton genotypes, 13 parents and 36 F_1 combinations were grouped into 11 major clusters based on relative dissimilarity among genotypes (Figure, 3). The distribution of parental genotypes and their F_1 heterozygous in dendrogram reflects a broad parallelism between divergence distance, general and specific combining abilities. The distribution pattern of F_1 heterozygous was more or less influenced by their parents as expected on the basis of close affinity between the parents and their F_1 progenies. Similar results were obtained by [14]. Data illustrated in Fig. 3 revealed that the parental genotypes were grouped into four major clusters, while F_1 combinations grouped into 7 major clusters and wide divergent from parents. The cross combinations Giza 77 x Dandra, Giza 77 x Pima S6, Giza 96 x Australy and Minufy x Dandra grouped at the same cluster and characterized by significant SCA for most water relations and physiological characters, however the cross combinations Giza 86 x Dandra and Giza 68 x 10,229 showed the best values of SCA for seed cotton and lint yield over two conditions and classified into two different clusters.

From the previous results, it is evident to note that crossing of distantly related parents within a major cluster should produce higher variance for quantitatively inherited characters in segregating populations than crossing between closely related parents, which agree with [3,4].

The maximum intra cluster distance (Table 5) were observed between cluster 4 and cluster 6 followed by cluster 5 and 6 and cluster 4 and 7. Both of clusters 7 and 6 consisted one of parental genotypes and having divergent distance from other parents and F_1 combinations. On the other side, clusters 2 and 11 followed by clusters 8, 9 and 4, 9

were nearly related, showing minimum inter cluster distances. [4,14,20] found that the F_1 hybrids and their parents were grouped into different clusters. However, [17] classified 15 cotton genotypes into four different clusters based on eight yield and fiber characters.

Cotton breeder desire to increase genetic diversity among new cultivars, while, at the same time, maintaining the complex of desired characters present in the existing popular cultivars. Developing such a combination can be difficult as the introgression of new genetic material is expected to disturb genetic complexes responsible for desired traits. The use of crosses between divergent cultivars could be a mean to achieve both ends.

4. Conclusion

Generally, the results of principal components analysis and clustering analysis appeared to be in complete accordance. Principal components analysis is useful in identifying the most influential characters affecting genetic variation of population. Thus, plant breeder would have useful information which would enable him to identify which traits would be selected to achieve high yielding potential. However, cluster analysis could efficiently describe the characteristics of group of genotypes in different clusters. The application of both analyses seemed to look reasonably straight forward.

Declaration of Competing Interest

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