Journal of Plant Production

Journal homepage & Available online at: www.jpp.journals.ekb.eg

Multivariate Analysis in Egyptian Cotton *Gossypium barbadense* L.

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ABSTRACT

Eleven parental cotton genotypes (*Gossypium barbadense* L.) and their 28F1hybrids were canvassed by Principal Components and Linkage Cluster analyses to identify the major characters which account for the variation in yield contributing traits. Analysis of variance revealed highly significant differences for genotypes, crosses, parents for all the studied traits. Parents vs. crosses were significant for most traits indicating the heterotic response. The first principal component contributed 41.9 %to the total variability and was mainly attributed to plant height, boll weight, seed cotton yield/plant, number of fruiting branches/plant, lint yield /plant, boll number and seed index. The second PCs contributed 16.7 % to the total variability and were mainly due to fiber fineness, length and uniformity ratio and showed positive loadings with most characters. The PC3 and PC4 contributed 9.1 % and 7.9 % of the total variability and were mainly attributed to pressely index, earliness index, vegetative branches and days to flowering. The 11cotton parental genotypes were grouped into four major clusters based on dissimilarity among them and sixteen contributed characters. The female parents (testers) Suvin, (Giza 88xOkre leaf), (Giza 85xOkre leaf) and 24202 were grouped into two wide clusters. The parental genotypes Giza 93 and (Giza 81xAustraly12) formed two wide clusters from the other parents and having wide dissimilarity coefficients compared with other parents. The 39 genotypes, 11 original parents and 28 F_1 crosses, were grouped into 13 major clusters relative to dissimilarity among them.

Keywords: Cotton, Multivariate analysis, Genetic diversity, cluster analysis

INTRODUCTION

Cotton, also known as "White Gold," is the world's most important renewable natural fiber crop. It is Egypt's mainstay and has played an important role in the world's economic, political and social development. To launch new varieties of Egyptian cotton (*Gossypium barbadense* L.), the breeding programme relies on the production of pure lines. The breeding program's main goal is to create new varieties with high yield capacity and high fiber quality characteristics El-Mansy (2014). Cotton breeders must look at genetic control and behaviour for factors that affect yield, its components, and fiber quality because cotton yield components may be connected or segregate independently.

Any crop improvement programme is built on genetic divergence. Because hybrids between lines of diverse origin generally show greater heterogeneity than those between closely related parents, understanding the variation in germplasm is an important and necessary aspect of starting any crop breeding programme. Genetic diversity is required for successful breeding in order to maximise improvement while minimising the inherent field genetic vulnerability. As a result, it is critical to create hybrids between genotypes of different origins rather than those involving closely related parents in order to maximise heterosis.

There are several ways to evaluate the amount of genetic variation that is accessible for crop improvement Mohammadi and Prasanna (2003). Pedigree analysis is one option, although parental coefficient alone hasn't been shown to be a reliable predictor of a cultivar's success in terms of growth VanEsbroeck and Bowman (1998).The use of molecular markers for genomic prediction in a variety of hybrid maize was only marginally successful, highlighting the importance of high-quality phenotypic data as a useful predictor of offspring performance Windhausen, *et al.*, (2012), reinforcing the previous finding about the importance of quality over quantity of diverse germplasm in plant improvement.

Cross breeding between different groups is widely accepted to increase genetic variance in the resulting progeny and allow selection to advance. Cluster analysis is one method for measuring genetic divergence in a population, and it has been used in cotton to select promising plants Abd El-Baky, (2006) and El Mansy (2015). This technique can predict genotypes with high index scores that fall into different groups to be crossed in order to produce the most variance for good combinations of characteristics. Khan *et al.*, (2007), and to distinguish cotton genotypes based on their interactions with biotic or abiotic stress. Aslam *et al.*, (2013).

Plant breeders typically use multivariate biometrical methods like principal component analysis (PCA), correlation analysis, and multidimensional scaling to investigate genetic variability among genotypes and the direct and indirect effects of characteristics Brown *et al.*, (1999). Keeping in view the above discussion regarding genetic diversity in cotton breeding, the present study was

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DOI: 10.21608/jpp.2022.180154.1200

executed to explore genetically divergent genotype with desirable correlated agronomic attributes.

Because environment has a large influence on these traits and the selection process, genetic diversity has been exploited through many morphological and agronomic characters for a successful hybridization programme Ahmad *et al.* (2012). Therefore, developing cotton types with high productivity should receive a lot of attention. Plant height, direct and indirect fruit bearing branches, boll weight, number of bolls per plant, seed index, and ginning out tern are all factors that affect cotton production, whether it be in terms of seed yield or lint. For the plant researcher to address the limitation of cotton yield, a thorough study of the crop's nature, degree of performance, and relationship of numerous agronomic variables with yield is important.

Thus, the objective of this investigation were 1) to study the genetic diversity among eleven parental cotton genotypes and their 28 F_1 cross combinations using multivariate analysis based on agronomic trails data to give graphical presentation of genotypes and 2) to select the most suitable combinations as well as to investigate the relative importance of the evaluated traits.

MATERIALS AND METHODS

The genetic materials used in the present study included eleven genotypes i.e., Giza 94, Giza 93, Giza 92, Giza96, (Giza 89 x Giza86), (Giza75 X P.H.P), (Australy 12 x G81), Suvin, (Giza88 X Okra leaf), (Giza85 x Okra leaf) and 24202. In 2013 season the single crosses between eleven parental genotypes were made by using the seven following genotypes i.e., Giza94, Giza93, Giza92, Giza96, Giza89 x Giza86, (Giza75 x P.H.P), (Australy 12 x G81) as lines (Females) and four remaining genotypes i.e., Suvin, (G88 x Okra leaf), (G85 x Okra leaf) and 24202 were used as testers (Males) to produce 28 F_l hybrids. In 2014 season, the 11 parents and their 28 F_1 hybrids were planted in a randomized complete blocks design with three replications. Each plot was represented by one row 4 m. long and 0.7 m. wide. Hills within rows were 0.35 m. apart allowing of 10 plants per plot. Hills were later thinned to two plants per hill. The recommended agricultural practices were applied at proper time.

Data were recorded on 10 guarded plants chosen at random from each plot in middle ridge for F_1 and their parents at flowering (flower.), First fruiting node (F.F.N.), Earliness index (E.I.), number of vegetative branches (monpodia)/plant (NoV.B./P.), number of fruiting branches (sympodia)/plant (No.F.B./P.) ,Plant height (PH), Seed cotton yield g /plant (S.C.Y./P. g), Lint cotton yield g /plant (L.C.Y./P. g) , Lint percentage (L. %), Boll weight g (B.W), Seed index g (S.I.), Number of bolls/plant (No.b./P.), Fiber fineness in Micronaire (F.F.), Fiber strength in Pressely (F.S.), Fiber length in millimeter (F.L) and Uniformity ratio (U.R. %) were estimated at Cotton Technology Laboratory, Cotton Research Institute, Agricultural Research Center, Giza, Egypt.

Biometrical analysis:

Data were analyzed using the analysis of variance in accordance with Gomez and Gomez, (1984) to determine significant differences among genotypes. Multivariate technique was used to assess the similarities among varied groups and to evaluate morphological parameters contributing to the variation in each genotype. For this purpose, principal components analysis was performed, on the correlation matrix of contributed characters for all genotypes. The principal components were expressed as Eigen value, latent root, and manifested in eigen vector for all studied traits in each principal components axis Hair *et al.* (1987).

The genetic diversity and distance as described were determined using a hierarchical clustering approach employing Ward's minimal variance method, which minimizes within-group sums of squares across all partitions Anderberg (1973) and developed by Johnson and Johnson and Wichern (1988). The Euclidean distance was computed and the results from clustering analysis are presented as dendrogram. All computations were performed using Minitab (version 15) and SPSS (version 19) computer procedures.

RESULTS AND DISCUSSION

The amount of information available to plant breeders about the target crop and traits influences the improvement of any breeding programme. Cotton breeders use various mating models to pass preferred alleles to the next offspring because hybridization is an important technique for inducing genetic variation. The plant materials used in this study include eleven *Gossypium barbadense* L. cotton genotypes. and their twenty eight cotton crosses. To identify genotype variation for both agronomic and fiber quality variables, analysis of variance was applied (Table 1). Significant differences for genotypes, crosses, parents, lines, and testers for all examined traits were found, demonstrating that these genotypes are highly variable. Such variations could be attributed to the varied genetic background. The variances due to lines and testers were also significant for all traits studied and higher than the variance due to interaction (L x T), indicating that the experimental materials possessed considerable variability and general and specific combining ability were involved in the genetic expression of such traits. While parents vs. crosses were significant for most traits indicating the heterotic response for such traits. Similar results were obtained by AL-Hibbiny, (2015) ; Sultan *et al.*, (2018) ; Mahrous, (2018) ; and Yehia and El-Hashash, (2019).

Mean performance

Data presented in (Table 2) showed wide range of performance among the parental genotypes for most traits. The mean performance was considered as the first important selection index in the choice of parents and the parents with high mean performance will result in superior hybrids. The parental tester 24202 showed desirable performance for most earliness traits followed by parental line (Giza75xP.H.P) and tester (Suvin**)** showing the lowest values of flowering dates and decreasing the first fruiting node with acceptable values of earliness index. While the tester (G88 x Okra leaf) and (Giza85 x Okra leaf) gave the highest earliness index values and surpassed all parents for this traits, for yield and yield components traits, the parental line (Australy12xG81) gave the highest mean values for most yield traits but it showed some sort of

lateness. However, the parental tester 24202 showed high desirable values of most yield traits with earlier in maturity. On the other side the parental tester (G88xOkra leaf) and (Giza85xOkra leaf) gave the inferior performance of all yield traits followed by Giza 93. The Egyptian Variety Giza 93 surpassed all parental genotypes lint percentage and seed index with some sort of earliness and acceptable fiber traits. The extra long variety Giza 93 surpassed all parents for all fiber quality traits followed by Giza 96 and (Austraily12xG81). Generally, No parental lines or testers surpassed for all studied traits, but in most or some traits, for this purpose the parental line Giza 96 gave desirable performance for most traits followed by the tester 24202.

Table 1. Mean squares of the studied growth, earliness, yield and fiber traits

S.O.V	d.f	Flowering	F.F.N	E.I	No.V.B.P	No.F.B.P	P.H	No.B.P	B.W	S.C.Y	L.Y	L%	S.I	F.F	F.S	F.L	U.R
Rep.	2	2823**	1122**	59135**	1054**	9220**	402237**	325	345**	744560**	189141**	3348**	889**	094**	492**	8241**	4330**
Genotypes	38	1368**	117**	15837**	091**	688**	71370**	26192**	028**	452230**	69947**	1255**	115**	021**	015**	315**	256**
parent	10	848**	268**	19131**	079**	1732**	16728**	40226**	069**	840170**	142800**	1561**	288**	044**	0068	790**	374**
crosses	27	908**	065**	10331**	098**	327**	38493**	16787**	013**	273500**	37148**	1169**	055**	013**	018**	147**	214**
parent vs crosses	1	18990**	020	131554**	00035	011	011	139794**	017*	138530**	208259**	504**	00024	0044	027*	098	214*
Lines	6	20100**	050**	7151**	114**	168	593	26703**	007	261640**	50720**	2399**	095**	039**	019**	231**	166**
Testers	3	079	241**	49410**	341**	1888**	281270**	33553**	076**	1055200**	135723**	1093**	158**	023**	020*	1045*	7041**
Lines x Testers	18	649**	040**	4878**	052**	120	8880*	10687**	005	147180**	17234**	771**	025	0033**	017*	126**	149**
Error	76	027	012	442	0146	076	4343	912	003	527	1084	063	015	0014	0056	034	043

*** and ** significant at 5% and 1% levels of probability, respectively.**

Table 2. The Mean performances of eleven parents and the F_1crosses for earliness, growth, yield and fiber traits in line X testers' hybrids of cotton.

Genotypes	Flower	F.F.N	E.I	No.V.B.P	No. F.B.P	P.H	No. B.P	B.W	S.C.Y	L.Y	L%	S.I
Giza 94	66.33	5.67	60.60	3.07	17.67	154.33	44.68	3.47	154.96	63.67	41.07	11.96
Giza 93	67.33	6.13	50.04	2.42	18.00	151.00	29.07	3.45	100.44	34.13	33.85	10.75
Giza 92	66.33	6.20	57.58	3.60	19.53	160.33	45.42	3.91	176.42	64.28	36.41	10.75
Giza 96	67.00	7.07	60.16	3.47	18.13	158.00	46.47	3.63	166.83	67.06	40.20	10.75
Giza 89xGiza 86	64.67	6.20	61.48	3.40	18.53	154.00	49.33	3.71	180.13	65.92	36.57	10.61
Giza75 x P.H.P	65.67	5.67	53.79	3.07	17.87	151.67	45.59	3.57	162.08	61.08	37.68	11.57
Austerely12 x Giza81	67.00	7.00	51.54	3.07	18.87	177.00	57.45	3.77	215.83	85.93	39.79	11.69
Suvin	65.00	5.67	65.83	3.07	18.60	156.33	47.60	3.72	177.21	71.27	40.20	9.20
Giza88 x okra leaf	70.67	8.73	75.13	4.53	11.77	96.67	22.35	2.35	52.55	19.27	36.67	8.83
Giza85x okra leaf	68.67	6.83	71.80	3.25	13.67	107.00	23.35	2.73	63.82	23.49	36.80	9.94
24202	67.00	5.53	65.92	3.33	18.60	151.00	50.00	3.77	188.76	75.91	40.19	10.38
Suvin x G.94	62.67	6.47	60.86	2.67	18.47	158.00	57.65	3.69	212.03	86.23	40.64	11.04
Suven x G.93	64.67	7.07	60.25	3.20	18.27	167.33	46.94	3.65	170.87	59.67	34.87	11.04
Suvin x G.92	66.33	6.60	62.31	3.03	19.13*	162.33	47.91	3.83	182.07	64.97	35.60	10.88
Suvin x G.96	64.00	6.40	57.33	2.53	18.13	156.33	44.69	3.63	162.11	65.14	40.14	10.24
Suvin x (G.89 x G.86)	64.33	5.80	70.29	3.42	18.17	159.33	53.33	3.63	193.67	73.27	37.74	10.99
Suvin x (G.75 x P.H.P)	63.33	5.67	60.00	3.27	17.67	154.33	51.74	3.53	182.95	71.22	38.86	10.50
Suvin x (AUS 12 x G.81)	64.00	6.20	67.94	2.42	18.00	157.00	52.53	3.60	188.65	65.97	34.93	10.50
(G.88 x OKraleaf) X G.94	60.00	6.47	68.91	3.40	16.73	142.33	48.50	3.35	162.46	65.39	40.24	11.10
(G.88 x Okra leaf) X G.93	60.67	6.60	66.94	3.80	17.00	136.67	38.65	3.40	131.23	49.20	37.45	10.39
(G.88 x Okra leaf) X G.92	67.33	6.47	70.72	3.82	16.67	139.00	48.80	3.33	162.58	63.02	38.71	10.20
(G.88 x Okra leaf) X G.96	65.00	6.93	65.04	3.15	17.40	144.00	37.77	3.48	131.99	52.19	39.47	9.52
(G.88 x Okra leaf) X (G.89 x G.86)	66.00	7.13	67.34	4.80	15.87	132.00	52.05	3.17	164.75	65.63	39.82	10.49
(G.88 x Okra leaf) X (G.75 x P.H.P)	64.67	6.93	74.43	4.87	16.93	133.67	46.71	3.39	158.16	60.45	38.13	10.08
(G.88 x Okra leaf) X (AUS 12 x G.81)	66.00	6.80	82.51	3.33	16.40	131.00	43.40	3.28	142.66	57.37	40.16	9.82
(G.85 x Okra leaf) X G.94	62.00	6.00	73.68	2.93	16.67	137.67	47.44	3.33	158.38	63.86	40.14	10.88
(G.85 x Okra leaf) X G.93	62.00	6.13	76.86	3.03	16.60	132.00	36.57	3.32	121.57	47.49	39.06	9.98
(G.85 x Okra leaf) X G.92	64.67	6.60	80.16	3.40	16.13	133.67	47.29	3.23	151.82	58.47	38.48	10.64
(G.85 x Okra leaf) X G.96	64.67	7.00	72.51	3.75	16.20	138.00	44.75	3.21	143.79	57.78	40.08	10.01
(G.85 x Okra leaf) X (G.89 x G.86)	65.00	6.33	72.38	3.60	16.33	137.67	54.95	3.27	179.55	70.89	39.45	10.74
(G.85 x Okra leaf) X (G.75 x P.H.P)	65.33	5.60	69.22	2.93	17.47	141.67	46.22	3.49	161.99	65.69	40.44	10.49
(G.85 x Okra leaf) X (AUS 12 x G.81)	63.67	6.67	73.22	2.93	16.47	141.33	59.58	3.29	196.28	69.01	35.07	10.66
24202 X G.94	64.00	5.60	66.47	2.80	17.13	144.00	46.88	3.43	160.33	65.35	40.70	10.77
24202 X G.93	62.67	5.80	69.32	2.87	19.53	165.00	48.40	3.91	189.29	70.00	36.90	10.89
24202 X G.92	65.33	6.07	68.19	3.47	19.27	160.00	54.08	3.85	206.56	71.86	34.73	10.85
24202 X G.96	66.33	6.33	67.61	3.70	17.93	157.33	51.41	3.59	184.57	74.58	40.30	10.37
24202 X (G.89 x G.86)	62.00	5.93	66.63	3.53	16.73	147.67	62.96	3.35	210.53	84.55	40.04	10.75
24202 X (G.75 x P.H.P)	63.00	6.00	64.33	2.80	18.70	155.33	72.06	3.74	269.45	102.33	37.93	11.30
24202 X AUS 12 x G.81	63.67	5.80	68.49	3.20	18.67	153.67	46.09	3.73	172.02	69.68	40.46	10.97
L.S.D.0.05	0.84	0.56	3.42	0.62	1.42	10.71	4.91	0.28	11.80	5.35	0.97	0.63

Table.2 cont

Genotypes	F.F	F.S	F.L	U.R
Giza 94	4.30	9.60	33.13	84.67
Giza 93	3.20	9.33	36.50	85.90
Giza 92	3.83	9.70	33.20	84.47
Giza 96	4.10	9.63	34.60	85.20
Giza 89xGiza 86	4.10	9.70	33.20	84.90
Giza75 x P.H.P	4.40	9.66	34.33	84.83
Austerely12 x Giza81	4.70	9.87	32.23	83.63
Suvin	4.20	9.90	30.53	83.37
Giza88 x okra leaf	3.87	9.57	32.43	83.90
Giza85x okra leaf	3.90	9.60	31.33	81.70
24202	4.17	9.63	33.50	84.53
Suvin x G.94	4.23	9.43	32.87	84.77
Suven x G.93	3.80	9.50	34.93	85.80
Suvin x G.92	3.77	10.00	32.90	85.40
Suvin x G.96	4.10	9.57	33.67	85.27
Suvin x (G.89 x G.86)	4.10	9.90	32.00	84.03
Suvin x (G.75 x P.H.P)	4.10	9.90	33.00	84.03
Suvin x (AUS 12 x G.81)	4.43	9.60	32.47	83.83
(G.88 x OKraleaf) X G.94	4.17	10.07	33.07	84.93
(G.88 x Okra leaf) X G.93	3.70	9.80	34.33	84.73
(G.88 x Okra leaf) X G.92	3.87	9.83	33.20	82.43
(G.88 x Okra leaf) X G.96	3.83	9.73	33.87	85.03
(G.88 x Okra leaf) X (G.89 x G.86)	4.13	9.97	33.50	84.47
(G.88 x Okra leaf) X (G.75 x P.H.P)	3.93	10.13	33.57	84.37
(G.88 x Okra leaf) X (AUS 12 x G.81)	4.23	9.80	34.00	83.90
(G.85 x Okra leaf) X G.94	4.00	9.33	32.70	82.87
(G.85 x Okra leaf) X G.93	3.60	10.07	33.17	83.97
(G.85 x Okra leaf) X G.92	3.60	9.53	34.17	83.63
(G.85 x Okra leaf) X G.96	3.93	10.03	33.63	84.63
(G.85 x Okra leaf) X (G.89 x G.86)	4.03	9.90	32.73	84.20
(G.85 x Okra leaf) X (G.75 x P.H.P)	4.07	9.70	33.63	84.03
(G.85 x Okra leaf) X (AUS 12 x G.81)	4.10	9.53	33.20	84.70
24202 X G.94	4.17	9.73	34.07	84.93
24202 X G.93	3.83	9.57	34.10	86.17
24202 X G.92	4.10	9.83	34.23	84.93
24202 X G.96	4.30	9.43	32.17	85.03
24202 X (G.89 x G.86)	4.20	9.47	32.57	85.10
24202 X (G.75 x P.H.P)	4.20	10.27	33.70	85.87
24202 X AUS 12 x G.81	4.20	9.67	33.37	85.23
L.S.D.0.05	0.19	0.38	0.95	1.07

It is worth noting that the ultimate choice of parents in breeding program is usually based on the performance of the parents and their offspring. GCA and SCA, on the other hand, are more informative than performance because they reveal the type of gene effects that help breeders devise breeding and selection strategies.

The results revealed significant differences among F_1 crosses for all studied traits which reflected the differences among the original parents (table 2). Some F_1 crosses showed superiority than the original parents for all studied traits. Generally, the back crosses to the Indian genotype Suvin showed decreasing days to flowering and first fruiting node followed by back crosses to 24202 which surpassed all genotypes in node number of first branch. However, the combinations containing the testers (G88xOkra leaf) and (Giza85xOkra leaf) surpassed all genotypes for earliness index. For yield and yield component traits the cross combinations (Suvin x G94) followed by 24202 x (G89 x G86) and 24202 x (Giza75 x P.H.P) exhibited best means for all yield traits. In the same time the cross combinations contained the Indian tester's Suvin and/or 24202 as common parent gave the best means for most yield and earliness's traits. While the cross combinations possessed the Egyptian varieties Giza 93 and Giza 92 gave the best mean values for most fiber traits. Generally, the previous results indicated superiority of some F_1 combinations with respect to their corresponding parents. The results showed that heterotic effects could emerge highly in point for studied traits in such crosses. These results may reflect apparent genetic architecture of the Indian genotypes Suvin and 24202 as well as the Egyptian varieties Giza 94, Giza 93 and Giza 92 which might posses much potential to improve yield and quality, respectively.

Genetic divergence among cotton genotypes

A graphical assessment of genetic variety and intriguing features of differentiation and adaptability were discovered by studies of genetic divergence in cotton. This analysis could be beneficial supplementary information to examine the interconnections of genotype El- Mansy *et al* ., (2015) . Morphological traits have been successfully used for estimation of genetic diversity and cultivar development because they provide a simple method for measuring genetic variation.

Developing Cotton varieties with desirable traits require a thorough knowledge about the existing genetic variability, the more of genetic diversity parents, the greater the chances of obtaining higher heterotic expression in F_1 and broad spectrum of variability in segregating population Abdel-Monaem *et al.*, (2020).

Multivariate analysis:

The multivariate approach utilizing (PCA). This PCA technique uses Eigen values to determine the initial factor solution and seems to reveal patterns of economic importance. The explained variation associated with each factor, variable, according to Hair *et al.* (1987) and Brown

(1991). This method is highly useful for identifying the agronomic qualities of a crop that contribute most to production; as a result, breeding programs should place emphasis on these traits.

Results from the principal component analysis for morphological and fiber quality traits are presented in Table (3). In an analysis with sixteen variables 16 axes were exited however only those which exhibited high multivariate variation were considered. Eigen values and variances associated with each principal axis were extracted by principal component analysis. Four out of the sixteen principal components (PC) extracted had Eigen values greater than one and altogether explained 75.6% of the total variation among the 39 cotton genotypes Suggesting that these principal components analysis analysis scores may be used to summarize the original variables in any further analysis of the data. In this respect Nazir *et al.,* (2013) and EL-Mansy *et al.,* (2014) reported that the significant contribution of the first PC in the total variance while studying different traits. Eigen vectors of Principal Components for 16 Characters in 39 cotton genotypes are presented in Table 3.

Table 3. Principal components analysis of sixteen variables of cotton genotypes.

Variables	Principal components			
	Factor 1	Factor 2	Factor 3	Factor 4
Flower	0.44	0.16	-0.39	0.651
P.H	-0.912	0.209	-0.107	0.17
F.F.N	0.641	0.014	0.226	0.519
NO.V.B	0.447	-0.334	0.478	0.453
No.F.B	-0.897	0.143	-0.009	0.04
B.W	-0.901	0.188	0.001	0.042
S.C.Y	-898	-0.302	0.151	0.11
L.Y	-876	-0.412	0.97	0.066
L%	-0.92	-0.592	-0.155	-0.207
E.I	0.329	-0.482	0.507	-0.389
NO.B/P	-0.788	-0.435	0.212	0.077
S.I	-0.705	0.138	-0.076	0.45
F.F	-0.445	-0.61	-0.365	0.279
F.S	-0.07	-0.432	0.574	0.164
F.L	-0.1	0.729	0.412	-0.053
U.R	-0.508	0.501	0.434	0.98
Eigen value	6.7087	2.6755	1.4502	1.2668
% Variance	0.419	0.167	0.091	0.079
Cumulative	41.9	58.6	67.6	75.6

The PCA grouped the estimated cotton variable into four principal components. The relative magnitude of each character's Eigen coefficients in relation to the first eight PC axes from the components analysis could provide an explanation for each component axis. Though there were no clear guidelines for determining the significance of the trait coefficient, one rule of thumb is to consider trait coefficients greater than 0.5 to have a large enough effect to be considered significant Hair *et al.,* (1987) and Brown (1991).

The Eigen coefficient's sign is actually and arbitrarily chosen. As a result, each PC axis received the same weight in the multivariate analysis. When determining plant phenotypic features, some traits could be more significant than others Hair *et al.,* (1987).

According to Chahal and Gosal (2002), Identified main components' features with the biggest absolute values closer to unity had an impact on clustering more than those with smaller absolute values closer to zero. Therefore, rather than a small contribution from a small number of features, the differentiation of the genotypes into separate groups in the current study was caused by a relatively significant contribution from a small number of characters. EL-Mansy *et al.,* (2014) and Dawwam *et al.,* (2016). Principal component (PC1) contributed 41.9%, to the total variability. The variation in principal component 1 was mainly attributed to plant height, boll weight, seed cotton yield/plant, number of fruiting branches/plant, lint yield /plant, boll number and seed index and were negative loadings. Thus, this axis deals with most yield contributed characters. On the other side, PC1 was correlated with poor fiber quality characters. On these axes increasing in yield characters were correlated with decreasing in earliness characters. The second PCs contributed 16.7% to the total variability and was depicted mainly in, Fiber fineness, fiber length and uniformity ratio and showed positive loadings with most characters. The PC3 contributed 9.1% to the total variability and was mainly attributed to Pressely index, earliness index and vegetative branches. Principal component 4 contributed 7.9% to the total variability and was mainly attributed to days to flowering. Saleh (2013) stated that PC1 had higher coefficient for lint yield/p, seed cotton yield/p, micronaire reading, lint index, lint percentage, boll weight and seed index and Negative loading with earliness index and leakage %. . Likewise, Shakeel *et al.,* (2015) stated revealed approximately 64.8% of the overall multivariate variation was contributed by the first four PCs with Eigen values greater than unity., PC1 and PC3 were associated with good productivity traits , however PC2 Isolated the genotypes with desired yield components.

Generally, the results reflect the importance of yield, yield attributed and fiber quality characters in the total variability among the genotype. Increased of yield potential is an important goal for plant breeders. At the same time fiber quality maintenance is considered the main goal of cotton breeder, which has a major impact on yield potential and its value. Progress in yield potential results from the progressive accumulation of genes conferring higher yield or elimination of the unfavorable genes through the breeding progress EL- Mansy *et al.,* (2015).

The present study revealed that boll weight, seed index, lint index and lint percentage as well as micronaire reading had strong association with yield suggesting the need of more emphasis on these components for increasing the yield in cotton Dawwam *et al.,* (2016). From the present study, the principal component analysis may allow the plant breeder more flexibility in finding the number of plants to be evaluated and could use the multivariate method by first identifying the combinations of traits that make up an ideal plant type Dawwam *et al.,* (2016), Shaker et al. (2016) and Nizamani et al. (2017).

It's noteworthy to note that detecting genetic variation and the factors that have the greatest influence on genetic variation in populations may both be done using the principle components analysis. The amount of this variation is indicated by the populations' agronomic traits' principal component loading. By concentrating emphasis on those specific features that are important for adaptation, breeders would benefit from knowing about genetic variance of traits between genotypes. By first identifying the set of traits that make up an ideal plant, by plotting the PCAs that important, and by planting plants close to the PCAs that are considered to be important, EL- Mansy et al. (2014) and EL- Mansy

(2015) observed that using the multivariate technique and PCA may give the plant breeder more choice in determining the number of plants to be analysed.

Cluster Analysis

In cluster analysis, related descriptions are mathematically grouped into the same cluster according to patterns of correlations between genotypes and hierarchical mutual exclusion grouping Aremu, (2005). Cluster analysis has four methods namely unweighted paired group method using cancroids (UPGMA). UPAMC provide more accurate grouping information on breeding materials used in accordance with pedigrees and calculated results found most consistent with known heterotic groups than the other clusters .

Among parents genotypes

The cluster analysis sequestrates parental cotton genotypes into varied clusters which exhibit high homogeneity within a cluster and high heterogeneity between clusters.

The data matrix of the dissimilarity coefficients on the basic of Euclidean distance are presented in Table (4).The dissimilarity coefficients among eleven corresponding cotton genotypes to 55 possible comparisons showed that about 90% of the values were significant as Chi squares values. These coefficients were ranged from 9.55 between the parents Giza 92 and (Giza 89xGiza 86) and (Giza 89xGiza86) x Suvin to 198.6 between the parental line (Giza 81xAustraly) and (Giza 88xOkra leaf). The wide range of genetic distance between the genotypes may reflect the presence of wide range of genetic variation among them. Similar results were obtained by Nizamani *et al.* (2017) and Abdel-Monaem *et al.*, (2020).

Table 4. Dissimilarity coefficients among parental cotton genotype

Genotypes	1	2	3	4	5	6	7	8	9	10	11
G.94	0	65.4	23.1	13.3	26.2	11.2	70.5	24.7	128.8	113.1	36.9
G.93		0.0	84.4	77.4	89.1	69.6	132.5	89.4	79.0	63.0	101.4
G.92			0.0	11.5	9.5	17.7	50.0	12.9	149.5	133.9	21.9
G.96				0.0	15.0	12.3	57.6	13.8	141.4	125.9	25.7
G.89 x G.86					0.0	20.8	48.9	9.5	150.8	135.6	14.9
G.75 x P.H.P						0.0	65.6	23.1	133.6	118.0	33.3
Austerely x G.81							0.0	49.5	198.6	183.1	42.2
Suvin								0.0	150.5	135.1	14.3
G 88 x Okra									0.0	16.9	160.2
G 85 x Okra										0.0	145.2
24202											0.0

Cluster analysis sequestrated eleven parental genotypes of cotton into four major groups based on dissimilarity among them and sixteen contributed characters as shown in Figure (1).

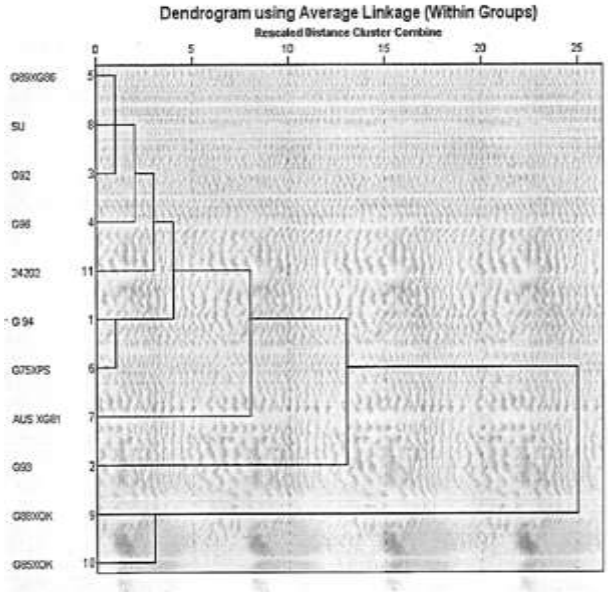

fig. 1. Dendrogram presentation of the studied parental cotton genotypes.

It's clear that male parents (testers) i.e., Suvin, (Giza 88 x Okre leaf), (Giza 85 x Okre leaf) and 24202 were grouped into two wide clusters. These parents varied in general combining ability for most characters on the other side, the parental lines Giza 93 and (Giza81 x Australy) formed two wide clusters from the other parents and having wide dissimilarity coefficients compared with other parents (Table 5). However, the rest female parents were grouped into the same group and showed clearly pronounced since the five genotypes appeared to be closely related and located in the same cluster. In this manner Abdel Salam *et al.*, (2010) grouped nine parents cotton into six major clusters, the Egyptian cultivars formed unique group and wide divergence from the other parents. EL-Mansy *et al.* (2014) grouped 12 parental cotton genotypes into six clusters, using hierarchical clustering analysis on basis of dissimilarity among the parents and contribution of evaluated characters. Giza 86, Giza 87 and the Russian genotype Kar_2 formed wide different clusters with the good combiner for yield, fiber and earliness characters, respectively.

Distribution of parental cotton genotypes into different clusters are given in Figure (1). The clustering pattern based on Euclidean distance of the ten parents revealed the existence of four major groups, cluster I include two genotypes (Giza 88 x Okre leaf) and (Giza 85 x Okre leaf) and widely divergent distance from the other genotypes. These genotypes exhibited the inferior general combining values for all yield characters. Cluster II consisted of one parental genotype, as line parent (Giza 93) These genotype characterized as a good combiner for fiber characters, but inferior in yield characters. Cluster 3 consisted of 7 genotypes (five females and two males) with the lowest dissimilarity coefficients. Two males genotypes (Suvin and 24202) were grouped together with a narrow genetic base. These genotypes described as good general combiners for most studied yield traits but showed inferior fiber quality values. The rest females parents : Giza 94, Giza 92, Giza 96, Giza 89 x Giza 86 and (Giza 81 x Austerely12) were grouped at the same cluster with narrow genetic distance. In this trend, El-Mansy, (2014), Abd El-

Moghny *et al.,* (2015) used phenotypic performance to classified cotton genotypes into different clusters.

It is anticipated that genotypes concentrated within the same group (intra-cluster) will have a higher genetic similarity than genotypes clustered within separate groups (inter-cluster) (Table 5). These findings showed that 11 parental cotton genotypes were genetically very distant from one another. The highest inter-cluster distance was observed between clusters 1and 4 followed by clusters 1and 3. While, the lowest genetic distance occurred between clusters 3 and 4 followed by clusters 1 and 2. Therefore, hybridization between groups is more beneficial than crossbriding within clusters to increase genetic variation and obtain more transgressive sergeants in early generations. The same results were obtained by Abd El-Moghny *et al.,* (2015) ; El - Mansy *et al.,* (2020) and Machado *et al.,* (2002) It has been noted that selecting parents is a crucial step in obtaining the optimum combinations. The parents' mean performance as parents and their F1s was greater than average, in addition to having larger genetic divergence. Aside from being more informative than mean performance numbers, GCA and SCA affects Abd El-Salam *et al.* (2010) and El-Mansy *et al.,* (2014).

Table 5. Inter and intra cluster distance between the seven clusters.

cluster	1	2	3	4
1	8.425	70.946	136.965	190.815
2		0	82.144	132.461
3			12.2	54.116
4				0

Among parental genotypes and their F1 progenies

The thirty-nine genotype, 11 parents and 28 F_1 hybrids, were grouped into thirteen major clusters based on relative dissimilarity among the genotype and the studied contributed characters as shown in Figure 2. However, the eleven parents were aggregate in six major dusters. The F_1 hybrids differed significantly from each other and most F_1 Combinations were grouped into different cluster and wide from parent Fig (2). Divergence distance and principal component analysis, as well as general and specific combining abilities, are broadly paralleled in the relative distribution of 11 parents and their F_1 heterozygous in the dendogram. According to expectations based on the close affinity between the parents and their F1 progenies, the distribution patterns of the F_1 heterozygous were more or less influenced by their parents Abd-El Salam *et al.,* (2010) and El - Mansy *et al.,* (2014).

The data revealed the existence of 13 major groups. Cluster 11 was the largest and consisted of eight cross combinations and it can be divided into two sub clusters. Cluster 5 consisted of 7 genotypes (4 F_1 hybrids and 3 parents) this cluster was closely related with cluster 6 which contains four genotypes, three of them parental lines and one F_1 combination. The F_1 combinations 24202 X (G.75 x P.H.P), (G.85 x Okra leaf) X (AUS x G.81) and 24202 X G.92 formed unique groups (clusters 3, 13 and 10) and divergent from the original parents and other clusters. The rest F_1 combinations were aggregate in different clusters.

It is important to note that crossing distantly related parents may give best crosses which surpassed their parents in most characters and should produce higher genetic variability in segregation generation rather than crossing between closely related parents El - Mansy *et al* ., (2014).

Data in Table (6) illustrated the inter cluster distance. The inter cluster distances were higher than the intra - cluster distance indicating wide genetic diversity among the genotypes. The highest inter cluster distance (238.027) was observed between cluster 3 and 9 followed by cluster 7 and 9(190.815) and cluster 2 and 3(187.970) inducting wider genetic divergence between these clusters.

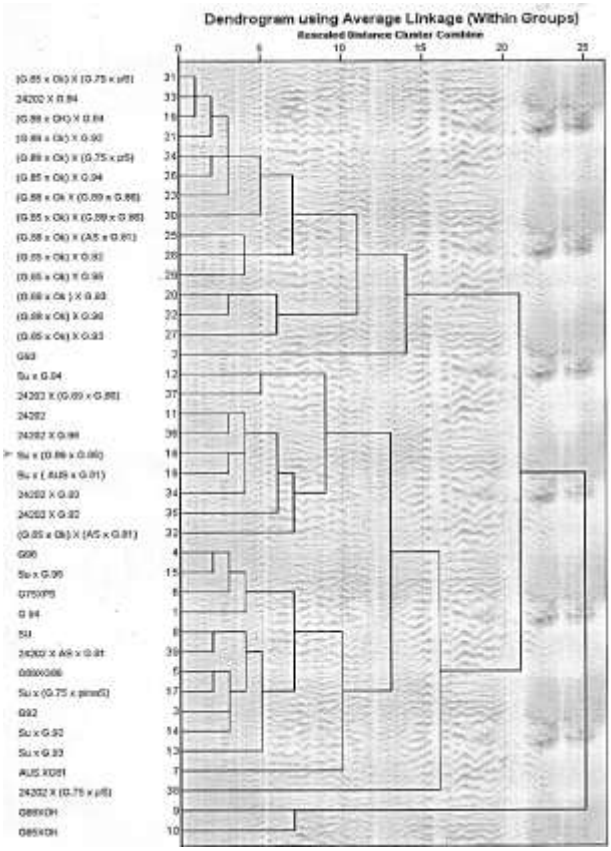

Fig. 2. Distribution of the 39 cotton genotypes based on cluster analysis.

Table 6. Inter cluster distance among 13 clusters

cluster	2	3	4	5	6	7	8	9	10	11	12	13
1	41.4	155.7	25.6	57.3	45.0	106.3	68.2	85.4	86.2	41.2	94.6	74.3
2		188.0	65.7	87.3	72.4	132.5	99.7	70.9	117.2	77.9	127.1	109.5
3			133.2	101.5	116.3	63.4	89.5	238.0	72.5	115.0	61.9	83.1
4				40.5	33.8	88.7	48.8	106.1	65.9	19.5	73.2	51.2
5					15.7	49.5	12.6	142.2	30.9	23.8	40.9	29.7
6						62.0	28.0	129.4	46.1	22.2	55.3	42.6
7							40.6	190.8	30.0	70.1	28.1	49.6
8								152.9	19.4	30.8	29.2	21.4
9									170.4	124.1	178.1	155.9
10										48.2	19.0	23.0
11											54.3	34.4
12												27.3

It is well recognized that greater the distance between clusters wide the genetic diversity would be among the genotypes. Inter - crossing between these clusters might resulting in wide array of variability making selection effective Haritha and Ahmed., (2013). The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregates of high magnitude of heterosis. The lowest inter cluster distances were observed between clusters 5 and 8 (112.973) followed by clusters 5 and 6 and clusters 8, 10 suggesting a close relationship between members of them and narrow genetic divergence among the genotypes. Since the magnitude of heterosis largely depends on degree of genetic diversity among parents and hence, selection of parents from these clusters should be avoid for combination breeding Naik *et al.*, (2016).

Finally, the hierarchical cluster analysis and principal component analysis confirmed the findings of each other. PCA is useful in identifying the most influential characters influencing genetic variation in population. However, cluster analysis could efficiently describe the characteristics of group of genotypes in different groups.

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الملخص

تم فحص 11 تركيبا أبويا من القطن المصري و28 تركيبا هجينيا ناتجة من التهجين بينها بطريقة السلالة × الكشاف باستخدام تحليل المكونات الأساسية وتحليل المجموعات المتباعدة لوصف الصفات المؤثرة في التباين الوراثي. تم دراسة صفات التزهير، موقع أول عقدة ثمرية معامل التبكير، عدد الأفرع الخضرية للنبات، عدد الأفرع الثمرية للنبات، ارتفاع النبات، محصول القطن الزهر للنبات، محصول الشعر للنبات، معدل الحليج، وزن اللوزة، معامل البذرة، عدد اللوز على النبات، نعومة التيلة بالميكرونير، المتانة بالبرسلي، طول التيلة، دليل الانتظام. 1- أظهر تحليل التباين وجود اختلافات معنوية لكل الصفات تحت الدراسة لكل من التراكيب الوراثية والآباء والهجن مما يدل على وجود قدر كافي من الاختلافات الوراثية وكانت الاختلافات الراجعة لكل من السلالة والكشاف معنوية لكل الصفات تحت الدراسة وكانت تمثل الجزء الأكبر من التباين بالمقارنة بتباين التفاعل مما يدل على أن هذه التراكيب الوراثية على قدر من التباين لكل من القدرة العامة والخاصة. 2- كان التباين الراجع للتفاعل بين الاباء والهجن معنويا لمعظم الصفات محل الدراسة مما يدل على وجود التأثيرات الهجينية لهذه الصفات.3- كانت الأربع مكونات الأولى من التباين الكلى معنويا مع وجود قيم التباين المرتبط أكبر من الواحد الصحيح وتمثل حوالى 75.6 % من التباين الكلى بين التراكيب الوراثية. 4- يمثل المحور الأول من التباين مقدار 41.9 % من قيمة التباين الكلى وكان أكثر تأثراً بصفات ارتفاع النبات، وزن اللوزة، محصول القطن الزهر للنبات، محصول الشعر للنبات، عدد الأفرع الثمرية للنبات، عدد اللوز للنبات ومعامل البذرة.5- على المحور الأول من التباين فإن النباتات التى تتميز بزيادة الصفات المحصولية ترتبط عكسيا مع صفات التبكير حيث إن التراكيب الوراثية مرتفعة المحصول كانت متأخرة في النضج. 6- يمثل المحور الثانى من التباين قيمة 16.7 % من التباين الكلى وكان أكثر تأثراً بصفات جودة التيلة . 7- بينما يمثل المحور الثالث والرابع ما قيمته 9.1 % - 7.9 % من قيمة التباين الكلى وكان أكثر تأثراً بمعامل البرسلى – معامل التبكير – تاريخ التزهير وعدد الأفرع الخضرية. 8- تم توزيع الأحد عشر تركيبا أبويا في أربع مجموعات رئيسية كبيرة على أساس التباين النسبى بينها وأهمية الصفات المساهمة في التباين. 9- تم توزيع الكشافات في مجموعتين متباعدتين مع اختلافها في القدرة العامة على التآلف لمعظم الصفات. 10- مثلت التراكيب جيزة 93 – جيزة 81 × استرالى 12 فى مجموعتين متباعدتين عن جميع الأباء حيث تمتلك أكبر معامل لعدم التشابه عن الآباء الأخرى.11- كانت أكبر مسافة بين التجميع رقم (1) والتجميع رقم (4) متبوعا بالمسافة بين التجميع رقم (1) ورقم (3) بينما كانت اقل مسافة بين التجميع رقم (3) ورقم (4) مما يدل على أن التزاوج بين التراكيب الوراثية في المجموعات المتباعدة تعطى قوة هجين.12- تم توزيع 39 تركيبا وراثيا (11 أب و 28 هجين) في 13 مجموعة كبيرة على اساس عدم التباين النسبى والاهمية النسبية للصفات المساهمة.13- في النهاية فإن نتائج كل من تحليل المكونات الاساسية والمجموعات المتباعدة تؤكد بعضها البعض حيث إن تحليل المكونات الأساسية مفيد جدا في وصف الصفات المساهمة في التباين الوراثى للعشيرة بينما تحليل التباين الوراثى أكثر فاعلية لوصف التراكيب الوراثية في المجموعات المتباعدة