

COMBINING ABILITY AND GENETIC DIVERGENCE IN COTTON (*G. barbadense* L.)

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ABSTRACT: This experiment was conducted in order to estimate general and specific combining abilities effects and genetic divergence for yield and quality characters using the line x tester mating design. Seven lines and four testers along with their 28 crosses of (*Gossypium barbadense* L.) were evaluated for yield and fiber characters at Sakha Agric. Res. Stat. during 2018 growing season. Analysis of variance revealed significant differences among the genotypes, parents and crosses for all studied characters, indicating the presence of considerable amount of genetic variability among the evaluated genotypes. The variance due to parents versus crosses was also significant for most studied characters indicating that significant heterosis could be expected in crosses for these characters and comparison will be much relevant. The variance due to males and females were also significant for most studied characters and majority than the variance due to parents (lines and testers), these results indicated that the experimental materials possessed considerable variability and the two types of combining ability were involved in the genetic expression of these characters. However line vs. tester showed highly significant differences for most studied traits, showing the importance of both additive and non additive variance gene effects. Among the female parents (testers) Karshenky2 was the best combines for earliness index and micronaire reading. Giza 94 was the best general combines for earliness index , most yield and fiber characters. Giza45 and Giza 86 were predicted to be best general combines for fiber characters. While, Giza 93 has positive and significant general combining ability (GCA) for all the studied yield traits and fiber strength. The cross combinations Giza 86 x Giza 94 and Giza 93 x Giza 94 showed significant positive SCA values for boll weight, seed index and lint index. The dissimilarity coefficients among eleven cotton genotype corresponding to 55 possible comparisons showed that about 95% of the values were significant as Chi squares values. The eleven cotton parental genotypes evaluated in this study were grouped into five major clusters by using hierarchical clustering method on the basis of dissimilarity among parents and contribution of evaluated characters. The inter cluster distance was higher than the intra cluster indicating wide genetic divergent among the genotypes. The female parents Kar₂, Suvin, Giza89*_{p_{s6}} and Giza94 grouped at three wide clusters and divergent distance from each others. The extra-long varieties Giza 96, Giza 93and Giza 92 grouped at the same cluster and closely related with Giza 45 (cluster5) and divergent distance with the other groups. The male parents Giza 85, Giza90 and the female Kar₂ grouped at the same cluster (1) and characterized as a good combiner for earliness index. The Egyptian variety Giza94 and the Indian genotype Suvin formed unique two groups (clusters 2 and 4) and pose most genes which controlling general combining ability for yield traits. The 36 genotypes were grouped into 12 major clusters based on relative dissimilarity among genotypes. The distribution of parental genotypes and their F₁ heterozygous in dendrogram reflects a broad parallelism between divergence distance, general and specific combining ability. Parents for hybridization could be selected based on large inter cluster distance to isolate useful recombinants through segregates

Key words: Line x tester - combining ability – multivariate - genetic diversity- Cotton.

INTRODUCTION

Cotton breeders have managed to evolve early and high yielding with better fiber quality through different genetic manipulation and breeding practices, thus the information about different polygenic traits may assist the breeder in up grading the genetic makeup of the plant in particular direction. For this purpose, use of already existing genetic variability in breeding material and creation of new variability along with its genetic understanding, is of crucial importance in a breeding program. Thus, introducing new germplasm of cotton may be useful source for increasing the gene pool of cotton and will serve as a short term program to meet immediate national need (Busu et al. (1995).

Selection of the appropriate parents to be used in artificial crosses is one of the main decisions faced by plant breeder that will facilitate the exploitation of maximum genetic variability and production of superior recombinants genotypes. For this purpose, study of genetic diversity and genetic distance among parental genotypes. Breeders rely on genetic variation between parents to create unique gene combinations necessary for new superior cultivars. According to quantitative genetic theory, the genetic variance, and hence the probability of producing transgressive segregates, increase in proportion to the number of loci for which parents carry different alleles, (Esbroeck and Bowman, 1998). This diversity is essential to increase the chance of recovering superior genotypes. (El-Mansy et al., 2015).

All cotton breeders aim to develop cotton cultivars with good fiber quality and yield. Yield of cotton can be improved by improving characteristics that make genotype of cotton plant, such as; developmental characters (optimum

plant height, number of sympodial and monopodial branches, number of nodes or internodal length and earliness), economic characters (number of bolls per plant, boll weight, yield of seed cotton) and quality traits (lint percentage or ginning out turn, lint index, seed index, staple length, fiber strength and fiber fineness).

Cotton breeder should combine these desirable components of yield and quality. Information about combining ability, gene action and heterosis are important in breeding programs superior cotton cultivars. Combining ability method is important in the breeding programme as it provide information's about the heritability of crossing parents involved in the production of hybrid cotton seeds. It provides a specific guide line to the plant breeder about the establishment of a unique breeding experiment for the evolution of spectacular cotton varieties (Shakeel et al., 2012).

The line x tester analysis is one of the most important statistic-genetic methods which provides available knowledge about general and specific combining abilities of parents (GCA) and crosses (SCA) (Usharani et al., 2016, Khokhar et al., 2018, Munir et al., 2018, Patil et al., 2018). Increasing diversity is therefore essential to genetic improvement efforts. Each of the three major approaches to increasing genetic diversity (mutagenesis, germplasm introgression, and transformation) has advantages and disadvantages. Interspecific germplasm introgression is particularly attractive in that it utilizes abroad germplasm base, can be targeted to one or more specific traits or genes or modulated to include thousands of genes or even entire genomes (Saha et al., 2004).

Therefore eleven cotton (*Gossypium barbadense* L.) genotypes were evaluated

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using line x tester analysis to determine the genetic potential of elite parental combinations having remarkable combining abilities of yield and quality traits. On the basis of genetic information controlling the potential traits forthcoming breeding strategies will be outlined. Determining the genetic potential of parents combining ability estimate also depict the type of gene action underlying the yield as well as the fiber quality traits of cotton. On the basis of genetic information controlling the potential traits forthcoming breeding strategies will be outlined. Also estimate the dissimilarity coefficients to classify cotton genotypes into different clusters. Quantification of divergence would be of help to develop better recombinants between groups and in choosing suitable genotypes for cotton breeding programs.

MATERIALS AND METHODS

This investigation was conducted at the Sakha Agriculture Research Station, ARC Egypt during 2017 and 2018 growing seasons. The experimental material consisted of eleven parents and their 28 hybrids. Twenty eight crosses were synthesized during 2017 season by utilizing four genotypes as female parents i.e. Kar.2, Suvin, G.89* Pima S₆ and G.94 with seven male lines viz., G.45, G.85, G.86, G.90, G.92, G.93 and G.96 in line x tester mating design to produce twenty eight F₁ crosses. The eleven parents and their 28 crosses were grown in randomized complete block design with three replications during 2018 growing season. Each plot was one row 4 m. length with distance between rows 0.70 m and distance between hills 0.30 m with two plants / hill. All the cultural managements were applied as recommended. At harvest the inner eight individual plants of the eleven parental cotton genotypes with their derived 28 hybrids were harvested from each row and ginned in order to, estimate six

agronomic traits boll weight (BW) in grams as the average weight of ten bolls per plant, seed cotton yield per plant (SCY) in grams, lint yield per plant (LY) in grams, lint percentage (L%), seed index (SI), lint index (LI) in grams and earliness index (EI). Also, three fiber quality traits i.e.; fiber length (FL), Pressely index (FS) and micronaire reading (Mic), were estimated at Cotton Technology Laboratory, Cotton Research Institute, Agricultural Research Center, Giza, Egypt.

Data were subjected to analysis of variance according to Gomez and Gomez, 1984 to determine significant differences among genotypes. The variation among parental cotton genotypes and their F₁ hybrids was partitioned into two sources of general combining ability (GCA) and specific combining ability (SCA) effects and calculated accordance with the procedure suggested by Kempthorne, 1957 and adopted by Singh and Chaudhary (1985).

Cluster analysis using multivariate analysis based on yield, its components and fiber quality traits using averaged linkage (within groups) was calculated as outlined by Johnson and Wichern 1998 to investigate genetic dissimilarity between eleven parental cotton genotypes and their F₁ hybrids. The dissimilarity coefficient and dendrogram were done by using SPSS software.

RESULTS AND DISCUSSION

Development of high yielding varieties with acceptable fiber quality properties is one of the important objectives in cotton breeding programs. Cotton is one of the few crops which are accessible to the development of genotypes as varieties and at the same time amenable for commercial exploitation of heterosis.

Analysis of variance for, yield and fiber characters are shown in Table (1). The data revealed significant differences among the genotypes, parents and crosses for all studied characters, indicating the presence of considerable amount of genetic variability among the evaluated genotypes. Such variation could be attributed to the varied genetic background. The variance due to parents versus crosses was also significant for most studied characters indicating that significant heterosis could be expected in crosses for these characters and comparison will be much relevant. In this regard Karademir and Gencer (2010), and Sultan *et al.*, (2018).

The variance due to males and females were also significant for most studied characters and majority than the variance due to parents (lines and testers), these results indicated that the experimental materials possessed considerable variability and the two types of combining ability were involved in the genetic expression of these characters. The testers contributed a major share to the genetic variance in respect to most yield characters, while the contribution of lines was maximum for most fiber and earliness characters. However line vs. tester showed highly significant differences for most studied traits, showing the importance of both additive and non additive variance gene effects. The same results for different cotton crosses belonging to *Gossypium*

barbadense L., obtained by AL-Hibbiny, (2015), Mahrous, (2018);, Sultan *et al.*, (2018) and Yehia and El-Hashash, (2019).

The ultimate to choice parents for any breeding program is generally based on phenotypic performance of their F₁s. However; GCA and SCA effects were more informative than phenotypic performance, since it also revealed the type of gene action, which could help plant breeder to choose the most suitable breeding strategies. The estimates of general combining ability effects of the parents for all character under study are given in Table (2) The results showed that among the female parents(testers) Karshenky2 was the best combines for earliness index and micronaire reading. However it was the poorest one for yield and yield components traits. On contrast Giza 94 was the best general combines for earliness index, most yield and fiber characters. The Indian genotype, Suvin, recorded desirable GCA effect for almost yield traits. Among the male (lines) parents Giza 45 and Giza 86 were predicted to be best general combines for fiber characters. While, Giza 93 has positive and significant general combining ability (GCA) for all the studied yield traits and fiber strength, so the Egyptian cotton breeders define Giza 86 as a good combiner for cotton yield traits and its components. Among the male parents Giza 90 was the best combiner and recorded significant positive GCA effect values for boll weight and earliness index.

Table 1. Mean squares of yield and yield components and fiber quality characters .

Source	d.f.	BW	SCY/P	Lcy/p	L.P.%	S.I.	L.I.	E.I.	Mic.	F.S.	FL
Replications	2	0.001	181.056	19.94	1.203	2.793	0.728	2.172	0.095	0.059	0.677
Genotypes	38	0.242**	331.112**	65.064**	10.864**	1.334**	1.570**	327.215**	0.611**	0.933**	7.545**
Parents	10	0.276**	410.777**	82.615**	19.358**	2.134**	3.011**	471.470**	0.781**	1.570**	12.326**
Crosses	27	0.234**	241.920**	45.66**	6.727**	1.052**	0.952**	270.438**	0.557**	0.657**	5.730**
Par.vs.crosses	1	0.136	1942.618**	413.297**	37.616**	0.965	3.846**	417.631**	0.382	2.013**	8.737**
Lines	6	0.299**	205.008**	54.217**	13.874**	0.856	1.222**	818.253**	1.328**	1.274**	19.644**
Testers	3	1.214**	1178.241**	212.784**	18.470**	3.072**	4.035**	442.637**	0.929**	0.954**	3.847**
Lines x testers	18	0.049	98.171	14.963	2.388**	0.780**	0.349**	59.134**	0.238**	0.402**	1.405**
Error	76	0.023	53.018	6.62	0.493	0.245	0.090	13.012	0.041	0.148	0.461

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

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Table 2. Predicted general combining abilities effects for testers and lines with respect to yield and fiber characters.

Testers	BW	SCY/P	Lcy/p	L.P.%	S.I.	L.I.	E.I.	Mic	FS	FL
Kar.2	-0.3132**	-10.776 **	-4.6955**	-1.0205**	-0.5717**	-0.5996**	3.0167**	-0.2798**	-0.2274**	-0.1964
Suvin	0.172**	6.5596 **	2.2521**	-0.1462	0.2236**	0.0923	-1.6976**	0.2298**	-0.1226**	-0.025
G.89 * P ₅₆	-0.0632**	2.489**	0.8388**	-0.0857	0.1469	0.0542	-5.6786**	0.0393	0.1107	-0.3821**
G.94	0.2044**	1.7268	1.6045**	1.2524**	0.2012**	0.4532	4.3595**	0.0107	0.2393**	0.6036**
Differences	0.0464	2.2471	0.794	0.2167	0.1528	0.0927	1.1132	0.0628	0.1189	0.2095
Lines										
G.45	-0.0408	0.0751	-1.3012**	-1.691**	0.3021**	-0.2619**	-3.5333**	-0.3429**	0.3214**	1.6488**
G.85	0.0192	-5.0199**	-1.6462**	0.2424	0.1263	0.1264**	8.2**	-0.3262**	-0.2369**	-1.5012**
G.86	-0.2875**	-4.2299**	-2.057**	-0.5726**	-0.2537**	-0.2861**	-5.375**	-0.3595**	0.2131**	1.0655**
G.90	0.2258**	0.8551	0.9438	0.8365**	-0.3654**	-0.0211	15.092**	0.2738**	-0.6036**	-1.7595**
G.92	-0.0175	2.5435	1.0313	0.154	-0.0954	-0.0236	-3.375**	0.1905**	-0.0536	0.7655**
G.93	0.1158**	7.1026**	3.9571**	1.619**	0.3338**	0.6423**	-4.8833**	0.4238**	0.1881**	-0.1762
G.96	-0.015	-1.3265	-0.9279	-0.5885**	-0.0479	-0.1761**	-6.125**	0.1405**	0.1714**	-0.0429
Differences	0.0614	2.9726	1.0504	0.2867	0.2021	0.1226	1.4727	0.0831	0.1572	0.2771

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

Since general combining ability reflects parental performance and it is the results of additive gene effects and additive x additive interaction gene effects. In few of this, significance of GCA for the studied characters shows the importance of additive gene effect for these characters. Thus breeder may utilize the good general combiner genotypes in specific breeding programs for improvement the performance of Egyptian cotton. Similar results were obtained by Ashokumar (2010), Karademir and Gencer (2010). However Azhar and Naeem (2008) and EL-Mansy *et al*, (2014) suggested that parents having good GCA for the yield and its components characters are expected to yield good hybrids and this suggestion appeared to be true in the present study.

On the basis of specific combining ability (SCA) effects (Table 3) revealed that most of the combinations having significant SCA effects were related to genetically diverse parents and most combinations which had good specific combining ability were having one or two parents of their good x good or good x

poor general combining ability. The important aim for cotton breeding program is to obtain a cross combination with high values for all yield components. On the basic of SCA effect, the cross combination G.90 x G.89* P₅₆ was the best combination for earliness index followed by the combinations G.93 x G.94 and G.86 x Kar.2 . Such crosses which included one good and one poor general combiner could produce desirable transgressive sergeants if fixable gene complex (additive) in good combiners and complementary epistatic effect in poor combiners acted in the same direction to maximize the desirable attributes. Similar conclusion was reported by El – Mansy *et al.*, (2014). For yield characters, no cross combinations gave desirable SCA values for all yield characters. The cross combinations Giza 86 x Giza 94 and Giza 93 x Giza 94 showed significant positive SCA values for boll weight, seed index and lint index. The cross combination Giza 45 x Suvin followed by Giza85 x Giza94 observed highest positive significant SCA effects for seed cotton and lint yield characters. For lint percentage, seven crosses

register positive and significant SCA effects.

No cross combinations were surpassed for all fiber quality characters. The cross G.86 x G.89* P_{S6} and G.96 x Suvin recorded significant desirable values for fiber strength and fiber length. The results of SCA effects showed that the best specific combinations were not always obtained from parents with good and positive general combining ability effects. This finding is inconsistent with reported by Basal *et al.* (2009), Shakeel *et al.*, (2012) and Shaker *et al.*, (2016).

It is interested to note that, the significant estimated and positive

general and specific combining ability effects indicated the epistasis and / or dominance effects for F1 hybrid in cotton could be important to a certain extent. The presence of signification general and specific combining ability in F1 generation is a consequence of fluctuations in additive and dominance relationship respectively among the parents. (Basbag *et al.*, 2007). Also, the results revealed that a higher GCA doesn't necessarily confer a higher SCA and that the GCA and SCA were independent of one another , this finding similar to the obtained by Basal *et al.*, (2009) and Khan *et al.*, (2010).

Table (3). Specific combining ability effects of 28 F₁ crosses for yield, yield components and fiber quality.

Crosses	BW	SCY/P	Lcy/p	L.P.%	S.I.	L.I.	E.I	Mic	FS	FL
G.45 x Kar.2	0.07655	-2.5394	-0.8445	-0.1929	0.34833	0.17714	-1.8	0.00476	-0.031	1.013**
G.85 x Kar.2	0.05988	-3.2144	-2.143**	-1.393**	0.26417	-0.1879	1.00	0.05476	0.3941**	-0.1702
G.86 x Kar.2	-0.0601	-3.4444	-0.9254	0.44548	0.11417	0.18131	5.2417**	-0.0119	-0.2226	0.09643
G.90 x Kar.2	-0.0635	2.70393	1.37714	0.7363**	0.1425	0.2663**	-7.892**	-0.0786	-0.0726	-0.779**
G.92 x Kar.2	0.06988	5.22894	2.1363**	0.38548	-0.2775	-0.0679	2.84167	0.00476	0.14405	0.02976
G.93 x Kar.2	0.05321	4.8331	2.227**	0.8205**	-0.523**	-0.1604	-1.4167	0.1381	0.00238	-0.895**
G.96 x Kar.2	-0.136**	-3.5677	-1.8279	-0.802	-0.0683	-0.2087	2.025	-0.1119	-0.2143	0.7048**
G.45 x Suvin	-0.1487**	14.32**	5.0312**	-0.0438	-0.2502	-0.1648	3.0476**	-0.7048	0.631**	0.1417
G.85 x Suvin	-0.0054	-2.7363	-1.0171	0.02952	0.6389**	0.3936**	2.347	0.312**	-0.344**	0.25833
G.86 x Suvin	-0.032	2.3136	-0.3196	-1.496**	-0.454**	-0.637**	-1.4441	0.07857	-0.461**	-0.942**
G.90 x Suvin	0.18464**	-0.6246	0.58952	0.8454**	-0.843**	-0.302**	-3.244**	0.245**	0.08929	0.050
G.92 x Suvin	0.03131	-6.27**	-2.548**	-0.3488	0.16726	0.0069	-0.8107	0.02857	-0.2607	-0.2417
G.93 x Suvin	-0.1654**	-5.6655	-2.471**	-0.5205	0.38143	0.09107	-1.6691	-0.0048	-0.2024	0.06667
G.96 x Suvin	0.13548**	-1.3396	0.73452	1.5337**	0.35976	0.6127**	1.772	0.04524	0.5476**	0.6667**
G.45 x G.89*P _{S6}	0.02655	-3.3742	-1.6421	-0.588**	0.1231	-0.08	1.1619	0.2524**	-0.2024	-0.2345
G.85 x G.89* P _{S6}	-0.0401	-1.2692	-0.0771	0.6396**	0.10893	0.24167	-0.0048	0.10238	-0.2441	-0.5179
G.86 x G.89* P _{S6}	-0.0335	-2.9992	-0.4463	0.8441**	-0.2611	0.05083	-0.4631	0.03571	0.4059**	0.6156**
G.90 x G.89* P _{S6}	0.13321**	0.3425	-0.2971	-0.579**	0.5873**	0.2225	9.0036**	-0.131	-0.2441	0.17381
G.92 x G.89* P _{S6}	-0.0568	0.28417	0.18869	0.11738	0.06726	0.07833	-2.6298	-0.248**	0.4059**	0.14881
G.93 x G.89* P _{S6}	0.08988	2.50167	1.02619	-0.0143	-0.405**	-0.254**	-4.688**	0.08571	0.13095	0.09048
G.96 x G.89* P _{S6}	-0.1193	4.51417	1.24786	-0.4201	-0.2202	-0.259**	-2.3798	-0.0976	-0.2524	-0.2762
G.45 x G.94	0.0456	-8.409**	-2.545**	0.8243**	-0.2211	0.06762	-2.4095	0.4476**	-0.398**	-0.920**
G.85 x G.94	-0.0144	7.22**	3.237**	0.7243**	-1.012**	-0.447**	-3.343**	-0.469**	0.19405	0.42976
G.86 x G.94	0.1256**	4.12988	1.69131	0.20595	0.6013**	0.405**	-3.335**	-0.1024	0.27738	0.22976
G.90 x G.94	-0.2544**	-2.4218	-1.6695	-1.003**	0.11298	-0.1866	2.13214	-0.0357	0.22738	0.5548**
G.92 x G.94	-0.0444	0.75655	0.22298	-0.1541	0.043	-0.0174	0.59881	0.2143**	-0.2893	0.0631
G.93 x G.94	0.2226**	-1.6693	-0.7829	-0.2857	0.547**	0.3235**	7.774**	-0.219**	0.06905	0.738**
G.96 x G.94	0.11976	0.39321	-0.1545	-0.3116	-0.0712	-0.1449	-1.4179	0.16429	-0.081	-1.0952
CD	0.1227	5.9452	2.1008	0.5733	0.4043	0.2452	2.9453	0.1662	0.3145	0.5542

Genetic divergence among Cotton Genotypes:

The genetic diversity of plants determines their ability to improve efficiency and thus is used for breeding, which ultimately lead to increase yield potential. Many modern cultivars in cotton and in other crops are often genetically similar, with a rather narrow genetic base. Therefore in breeding we need to take advantage of new sources of diversity. Hence new variation can be created by hybridization between different parental cultivars. Thus developing Cotton varieties with desirable traits require adequate knowledge about the current genetic variance, the more of genetic diversity parents, the greater the chances of obtaining higher heterotic expression in F1 and broad spectrum of variability in segregating population. (ELMansy et al., 2014).

The matrix data of the dissimilarity coefficients on the basic of Euclidean distance are presented in Table (4). The dissimilarity coefficients among eleven cotton genotype corresponding to 55 possible comparisons showed that about 95% of the values were significant as Chi squares values. These coefficients were ranged from 6.1 among the parents (Giza 69) and Giza 93 to 47.5 between parents (Giza45) and Giza94. 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.

This is a dissimilarity matrix

The eleven cotton parental genotypes evaluated in this study were grouped into five major clusters by using hierarchical clustering method on the basis of dissimilarity among parents and contribution of evaluated characters as shown in Figure (1). It is clear that the female parents Kar₂, Suvin, Giza89*_{p_{s6}} and Giza94 grouped at three wide clusters and divergent distance from each others. These parents varied in general combining ability for yield and fiber traits and most of them having large dissimilarity coefficients with other parents (Table 5). The extra-long varieties Giza 96, Giza 93 and Giza 92 grouped at the same cluster and closely related with Giza 45 (cluster 5) and divergent distance with the other groups. These differed slightly for general combining ability for some yield traits but it characterized as good combiner for fiber quality traits. The male parents Giza 85, Giza90 and the female Kar₂ grouped at the same cluster (1) and characterized as a good combiner for earliness index, but it inferior in most yield traits.

Table 4: Dissimilarity coefficients among eleven parental cotton genotypes

Parents	Euclidean Distance										
	1:Kar.2.	2:Suvin.	3:P*G.89	4:G.94	5:G.45	6:G.85	7:G.86	8:G.90	9:G.92	10:G.93	11:G.96
1:Kar.2	0.0	41.071	28.074	27.849	30.281	14.046	27.739	9.161	25.653	27.917	31.492
2:Suvin.		0.0	27.013	38.224	32.396	32.729	19.552	35.323	20.309	21.209	15.806
3:P* .89			0.0	12.085	41.493	28.354	9.835	23.139	27.029	31.185	28.849
4:G.94				0.0	47.497	31.426	19.186	23.996	34.327	38.938	37.364
5:G.45					0.0	18.871	33.789	28.053	15.588	12.221	17.714
6:G.85						0.0	23.247	9.418	13.886	17.123	19.973
7:G.86							0.0	21.155	18.554	23.148	19.655
8:G.90								0.0	20.060	24.141	25.777
9:G.92									0.0	6.505	6.111
10:G.93										0.0	7.610

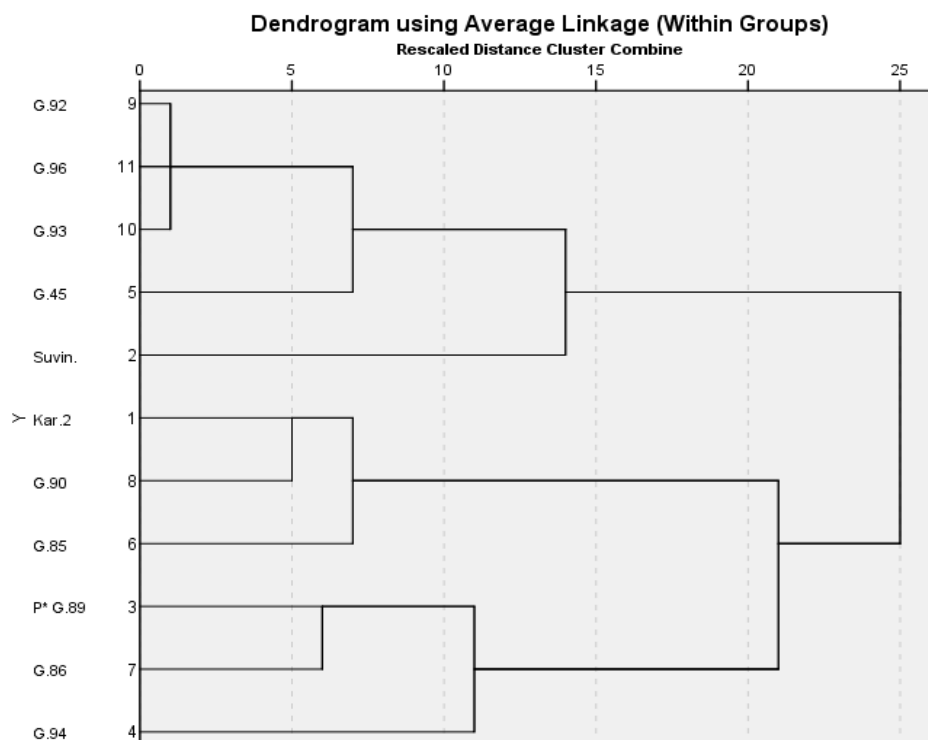


Figure 1: Dendrogram presentation of eleven cotton parental genotypes based on dissimilarity coefficients.

The Egyptian variety Giza94 and the Indian genotype Suvin formed unique two groups (clusters 2 and 4) and pose most genes which controlling general combining ability for yield traits. The commercial variety Giza 86 and the promising cross Giza 89* P_{s6} grouped at the same cluster (3) and closely related with Giza 94 but it widely divergent distance from the other clusters. In this respect Nizamani *et al.* (2017), arranged the 15 cotton genotypes into four different groups based on eight yield and fiber traits, while Farooq *et al.*, (2017). grouped 20 cotton genotypes / varieties into 3 major clusters based on different traits Cluster 3 was the superior in yield clusters with lowest Micromere value. Cluster I was educate with superior in fiber length and moderate yield.

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 (5) revealed that the inter cluster distance was higher than the intra cluster indicating wide genetic divergent among the genotypes (Figure 2). The highest inter cluster distance was observed between clusters 4 and cluster 5 (40.02) followed by clusters 2 and 4 (36.96) indicating wider genetic divergence between the genotypes in these clusters. On the other side clusters number 3 and 4 as well as clusters 2 and 5 were nearly related.

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 generation enabling further selection and improving Verma *et al.*, (2013). Machado *et al.*, (2002) noticed that in order to obtain the best combination choose parents which have greatest genetic divergence, However not only the

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genetic divergence might be used to choose parents for crossing but also the performance of parents and their F₁s. In addition GCA and SCA effects are more

informative than performance values Abdel-Sallam *et al.*, (2010) and EL-Mansy *et al.*, (2014).

Table (5): Inter and intra cluster distance between the five clusters.

Cluster	1	2	3	4	5
1	7.200	30.110	24.129	27.176	21.510
2		0.00	22.271	36.961	16.615
3			4.91	15.261	28.901
4				0.00	40.023
5					6.925

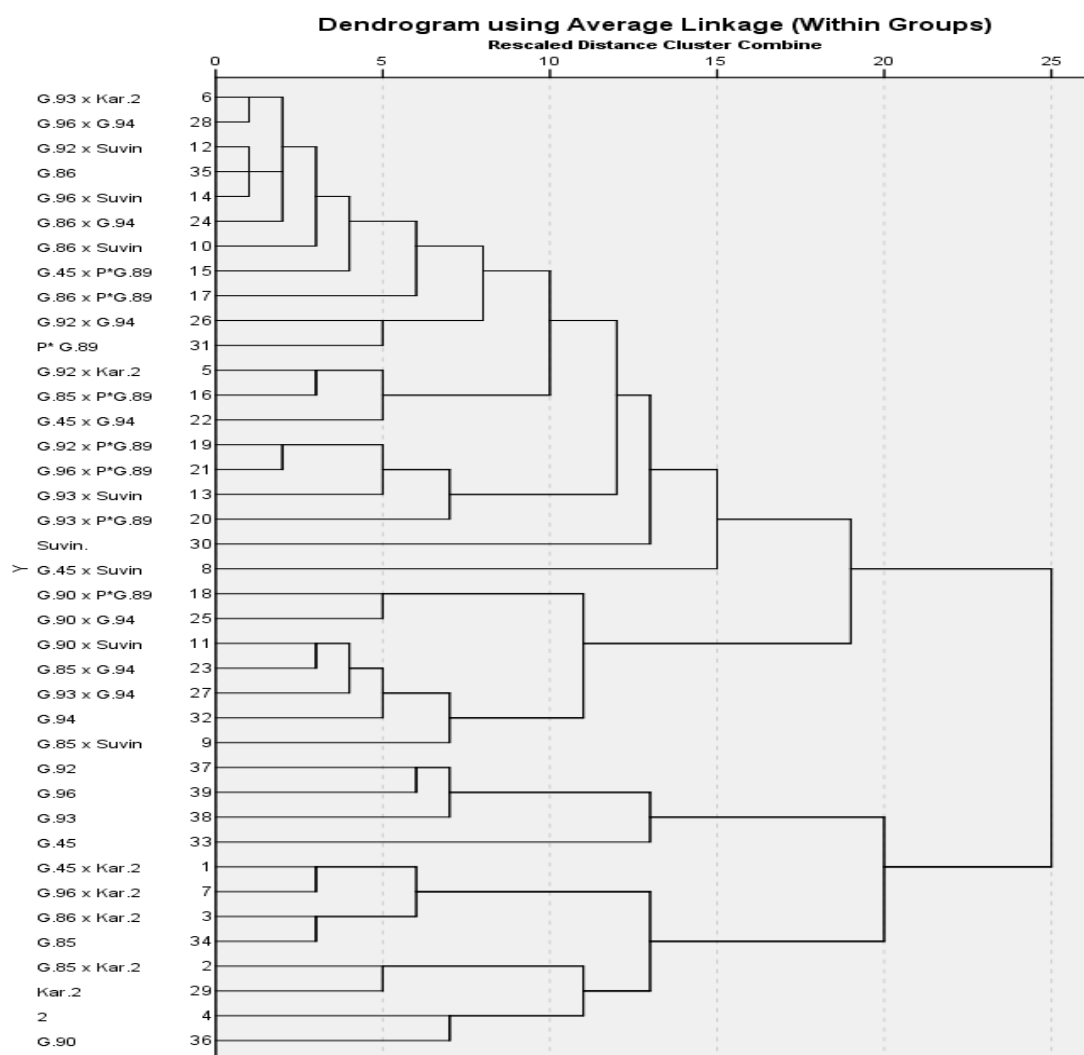


Figure 2: Genetic distance among 39 cotton genotypes in dendrogram

The genotypes formed cluster 3 showed the lowest intra cluster distance which might nearly related, the parental lines belonging to these clusters were relatively closer to each other, in comparison to lines which grouped on other cluster, however the maximum intra cluster distance was observed in cluster 1. 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 Singh *et al.*, (2010) and Farooq *et al.*, (2017).

The relative distribution of 39 cotton genotypes, eleven parents and their 28 F₁ heterozygous are illustrated in Figure (2). The data showed that the 36 genotypes were grouped into 12 major clusters based on relative dissimilarity among genotypes. The distribution of parental genotypes and their F₁ heterozygous in dendrogram reflects a broad parallelism between divergence distance, general and specific combining ability. The distribution pattern of F₁ heterozygous was more or less influenced by their parents as expected on the basis of close affinity between the parents and their F₁ progenies. Similar results were obtained by Shaker *et al.*, (2016). Data illustrated from Figure (2) revealed that the parental genotypes were grouped into three major clusters, while F₁ combinations grouped into nine major clusters and wide divergent from parents.

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. Parents for hybridization could be selected based on large inter cluster distance to isolate useful recombinants through segregates which agree with Suinaga *et al.*, (2005),

AL-Akheder *et al.*, (2006) and EL-Mansy *et al.*, (2014).

Cotton breeder desire to increase genetic diversity among new cultivar 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.

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القدرة علي التآلف والتباعد الوراثي في اقطان الباربادنس

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الملخص العربي

تم اجراء التجارب البحثية بهدف تقدير كل من القدرة العامة والخاصة علي التآلف ودرجة التباعد الوراثي لصفات المحصول والتيلة باستخدام تحليل السلالة *الكشاف حيث تم تقييم سبعة اباة وأربعة أمهات و ٢٨ هجين من اقطان الباربادنس في قطاعات كاملة العشوائية لصفات المحصول وجودة التيلة بمزرعة محطة البحوث الزراعية بسخا.

وأظهرت النتائج ما يلي:-

- اظهر تحليل التباين وجود اختلافات معنوية لكل من التراكيب الوراثية والاباء والهجين لكل الصفات تحت الدراسة مما يدل على وجود كمية كبيرة من الاختلافات الوراثية.
- كانت الاختلافات الراجعة لتفاعل الإباء والهجن معنوية لمعظم الصفات مما يدل على وجود التأثيرات الهجينية.
- ايضاً اظهر التفاعل بين الإباء والامهات معنوية لمعظم الصفات مع زيادة التباين الراجع للاباء "الاباء والامهات" مما يدل علي احتواء التراكيب الوراثية تحت الدراسة علي قدر كبير من الاختلافات الوراثية وتضمنها لكلاً من القدرة العامة والخاصة علي التآلف.
- اظهر التفاعل بين كل من الاباء المذكرة والمؤنثة معنوية عالية لمعظم الصفات مما يدل علي أهمية كلاً من الفعل الجيني المصنف والغير مصنف.
- من بين التراكيب الاموية اظهر التركيب الروسي كارشنكي ٢ احسن قدرة عامة علي التآلف لكل من صفات معامل التباين وقراءة الميكرونير في حين اظهر الصنف المصري جيزة ٩٤ قدرة عالية علي التآلف لصفات معامل التباين ومعظم صفات المحصول.
- اظهر الصنف جيزة ٤٥ وجيزة ٨٦ قدرة عامة علي التآلف لصفات جودة التيلة بينما اظهر الصنف جيزة ٩٣ معنوية موجبة للقدرة العامة علي التآلف لصفات المحصول وصفة متانة التيلة.
- أظهرت التراكيب الهجينية جيزة ٨٦ X جيزة ٩٤ وجيزة ٩٣ X جيزة ٩٤ قدرة خاصة علي التآلف لصفات وزن اللوزة - معامل البذرة ومعامل الشعر.
- اظهر تحليل التباعد الوراثي معنوية معامل عدم التشابه بين الإباء المستخدمة في الدراسة لأكثر من ٩٥٪ من القيم.
- توزعت التراكيب الابوية ال ١١ المستخدمة في الدراسة على خمس مجاميع رئيسية كبيرة باستخدام تحليل المجاميع المتباعدة على أساس عدم التشابه النسبي بينهما ومساهمة الصفات تحت الدراسة.
- توزعت التراكيب الاموية كارشنكي ٢, سيوفين, جيزة ٨٩ X بيما س ٦ وجيزة ٩٤ علي ثلاث مجاميع كبيرة مع وجود درجة من التباعد بينهما في حين وقعت الاصناف فائقة الطول (جيزه ٩٢, جيزه ٩٣, جيزه ٩٦ وجيزة ٤٥ في مجموعة واحدة "المجموعة الخامسة" وكانت اكثر تباعداً عن المجاميع الأخرى.
- توزعت التراكيب الابوية جيزة ٨٥ وجيزة ٩٠ والتركيب الاموي كارشنكي في نفس المجموعة ويمكن وصفها بتمييزها بالقدرة العامة علي التآلف لصفات معامل التباين.

- الصنف المصري جيزة ٩٤ والتركيب الهندي سوفين كونوا مجموعتين منفردتين وتحتوي علي معظم الجينات الخاصة التي تتحكم في القدرة العامة علي التألف لصفات المحصول .
 - توزعت الـ ٣٦ تركيب وراثي "الإباء والهجن" على ١٢ مجموعة كبيرة على أساس عدم التشابه النسبي بين التراكيب الوراثية، كما اظهر النسل الناتج من الهجين بين الإباء في المجاميع المختلفة درجة كبيرة من عدم التشابه النسبي والتباعد الوراثي.
- اوضحت النتائج وجود علاقة بين التباعد الوراثي و كلا من القدرة العامة و الخاصة علي التألف و علي ذلك يمكن للمربي من استخدام هذه النتائج في فصل التراكيب الوراثية المتباعدة و استخدامها في برامج التربية لتحسين المحصول و الجودة في القطن .

أسماء السادة المحكمين

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