GENETIC DIVERGENCE EVALUATION OF SOME COTTON COLLECTION (*Gossypium barbadense L.*)

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ABSTRACT

This research was to study the genetic divergence evaluation of some cotton collection (*Gossypium barbadens L.*) to select the most suitable genotypes as well as to investigate the importance of evaluate characters, by using multivariate analysis. Based on these data, the first three factors which accounted for 83% of the total variance are important. Factor I included lint%, lint index, lint cotton yield and fiber fineness and its accounted 43% of the total variance. Only fiber length had negative loading indicates the direction of the relationship between the factor and variable. Factor II included seed index, fiber strength and fiber length accounted 25%. Factor III included boll weight and fiber strength and its accounted 14% of the total variance. The most divergent genotypes were Australian 12 and Giza 45 × Sea Island at genetic distance (23.88%). In contrast, the level of similarity was high (95% and more) between 84% from extra long genotypes and between 88% from long stable genotypes.

INTRODUCTION

The prehistoric distribution of *Gossypium barbadense* was wide spread south America, southern and Caribbean basin (Fryxell, 1979). The development of *G. barbadense* cotton during colonial times, Sea Island cotton was developed in the Caribbean basin in the late 18th century and in Egypt in the first 19th century largely through the introduction of Sea Island type *Gossypium barbadense* stocks (El-Zik and Thaxton, 1989). Germplasm from Egyptian cotton varieties especially Giza 16 (meet afifi) was utilized in the development of pima cotton (Calhoun *et al.*, 1994). Although Egyptian cotton breeding programme can to introduce ninety two different varieties that carry Giza numbers as a result of serious research since 1919, the Egyptian cultivated cotton varieties are closely related and are descended from crosses between Jumel cotton and some introduce germplasm. Rigid selection and inbreeding through during the previous period has eliminated a great deal of the original variability.

The main objectives of the present study was to estimate genetic diversity and phonetic relationship among sixty genotypes of some cotton collection (*Gossypium barabadense L.*) and for determining of genetically unique germplasm as potentially important source of alleles for cotton improvement.

MATERIALS AND METHODS

Sixty genotypes from *Gossypium barbadense* included in this study (Table 1).

Table (1): Description of sampled genotypes

No.	Genotypes	Origin	Category
1	G.90	Egypt	Long
2	G.80 x pima S_6	-	-
3	Brown colur	U.S.	-
4	Pima high Percentage	-	-
5	Sea Island	-	Extra long
6	G.75	Egypt	long
7	G.81	-	-
8	G.77	-	Extra long
9	G.86	-	long
10	G.85	-	-
11	G.75 x sea Island	-	-
12	G.75 x5844	-	-
13	G.81 x Termes16 XG.81	-	-
14	Sea Island XG.76	U.S.	Extra long
15	BBB	-	Long
16	Australian12	Australia	-
17	G.67	Egypt	-
18	G.87 x (G.84 xG.70xG.51 B)	-	Extra long
19	G.84	-	-
20	Zero type	India	long
21	G.69	Egypt	-
22	G.81 xG.77	-	-
23	G.75 xG.70	-	-
24	G.84 xF108	-	Extra long
25	G.75 x Sea	-	long
26	G.84 x(G.70x G.51B)x Pima S_6	-	Extra long
27	G.71	-	-
28	G.76 xG.77	-	-
29	G.77 x Pima S_6	-	-
30	G.77 x G.70	-	-
31	C.B 58	U.S.	-
32	G.77 Radiation	Egypt	-
33	G.45 x Sea Island	-	-
34	G.45 xG.77	-	-
35	((G.70x G.51B) x G.45)	-	-
36	(G.70 x G.51) x(G.77x G.45)	-	-
37	G.76	-	-
38	G.84 xG.77	-	-
39	G.45 Radiation	-	-
40	G.74	-	-
41	G.87 x G92	-	-
42	(5844 x Termes 16) x pima S_7	U.S.	long
43	G.87 x Pima 62	Egypt	Extra long
44	(G.84 xG.85)x (G.45x Sea Island	-	long
45	Sea	U.S.	-
46	G.87 x (G.77 xG.70)	Egypt	Extra long
47	(G.83xG.80)xG72	-	long
48	(G.83xG.80)x Dandera	-	-
49	G.76 x(G.45 x S.I)	-	Extra long
50	G.83 x Pima S_6	-	Long
51	G.72 x Pima S_6	-	-
52	(G.84 xG.45)x Pima S6	-	Extra long
53	(G.83xG.80)xG75	-	long
54	G.85 xG.86	-	-
55	G.87 xG.77 x G.70	-	Extra long
56	(G.89 x Karchenky) xG.86	-	Long
57	(G.89 xG.86)xG.81 mutant	-	-
58	Karchenky xG.86	-	-
59	(G.86 x Karchenky) x C.B 58	-	-
60	G.83 x(G.85 x Pima S6)	-	-

The evaluated genotypes were represented by 27 extra long and 33 long stable. All genotypes were grown and evaluated in a randomized complete blocks design with three replications in cotton breeding department, Sakha Agricultural Research Station during 2009 and 2010. Entries were sown on ridged plots of 70 cm, 4 m long, and one row per each genotype. Hills of the row were spaced at 30 cm and plants were thinned at one plant per hill. Five randomly selected plants were harvested in every season, on which the following characters were determined, lint cotton yield (g), boll weight (g), lint %, seed index, lint index, 2.5% span length (mm), fiber fineness (Micronaire reading) and fiber strength (Pressly index).

Data analysis:

Analysis of variance as applied by Steel and Torrie (1980). The factor analysis method (Harman, 1976) indicates both grouping and contribution percentage to total variation. It is assumed that each of a small number of underlying independent factors. After loading of the first factor was calculated the process was repeated on the residual matrix to find further factors when the contribution of a factor less than 10% from the total percentage of the trace, the process stopped. After extraction, the matrix of factor loading was submitted as applied by Kaiser (1958). The factor loading of the rotated matrix, the percentage variability explained by each factor and the communalities for each variable were determined. The cluster analysis was performed using the group average linkage Eucliden distance and lined by Anderberg (1973). All the previous estimates were performed by using SPSS computer programs (1995).

RESULTS AND DISCUSSION

In (Table 2) the combined analysis over two seasons shows highly significant differences between 60 genotypes for all measured traits. Present findings were similar to the finding of Abdalla *et al.*, (2001) and El-Akhedar (2007).

Table 2. Mean squares of combined analysis over two seasons for all studied traits among sixty cotton genotypes .

S.o.v	dF	Boll weight	Lint Cotton yield	lint%	Seed index	Lint index	Fiber strength	Fiber length	Fiber Finennes
Year	1	0.07	0.4	0.698	0.003	0.021	0.01	0.05	0.015
Error a	4	0.03	32.3	2.438	0.496	0.53	0.13	0.63	0.064
Genotype	59	0.417**	1118.6**	46.47**	3.2933**	3.798**	1.018**	15.14**	1.24**
Year x gen	59	0.1	40.6**	1.105	0.286	0.126	0.12	0.65	0.046
Error b	236	0.1	26.2	1.623	0.339	0.185	0.24	0.8	0.064

*, ** significantly different at the 0.05 and 0.01 levels of probability, respectively

Factor analysis approach aim to collect knowledge of germplasm distance and relationships among elite breeding materials Multivariate procedures based on morphological of genetic divergence in cotton. Principal component analysis seemed to elucidate pattern of variation in agronomic attributes which are of economic importance and give entail factor solution using Eigen value. These values could measure the explained variance associated with each variable . The results of factor analysis are shown in

Tables (3 and 4) and Fig. (1). The values indicate the contribution of each variable to the factor. The factor was become considerable important when it's greater than 0.5. Factor analysis grouped the eight variables into three main factors which represented for 83% of the total variance in the dependence structure.

Table 3: Principal Component Factor Analysis of the Correlation Matrix Unrotated Factor Loadings and Communalities.

Variable	Factor I	Factor II	Factor III	Communality
Boll weight	0.396	-0.402	0.701	0.810
Lint cotton yield	0.609	0.040	0.248	0.434
Lint%	0.848	0.240	-0.166	0.804
Seed index	0.353	-0.743	-0.062	0.680
Lint index	0.916	-0.185	-0.197	0.913
Fiber strength	-0.051	-0.689	-0.517	0.744
Fiber length	-0.456	-0.601	0.209	0.613
Fiber fineness	0.816	0.067	-0.020	0.670
Variance	3.0870	1.6463	0.9343	5.6676
Var %	43.6	25.6	14.7	83.8

Table 4: Summary of factor loading for eight traits of cotton genotypes.

Traits	Loading	Total Communality
Factor I	**3.087**	**43.6**
Lint cotton yield	0.609	
Lint %	0.848	
Lint index	0.916	
Fiber fineness	0.816	
Factor II	**1.646**	**25.6**
Fiber strength	0.689	
Fiber length	0.601	
Seed index	0.743	
Factor III	**0.934**	**14.7**
Boll weight	0.701	
Fiber strength	-0.517	
Commutative Variance		**83.8**

Factor I included lint index, lint%, lint cotton yield and fiber fineness and its accounted 43% of the total variance. Only fiber length had negative leading indicates the direction of the relationship between the factor and variable.

Factor II included seed index, fiber strength and fiber length accounted 25%. Factor III included boll weight and fiber strength and its accounted 14% of the total variance. These results indicated that lint cotton yield and the most of its components beside fiber properties representing the most variation among plant phenotypic, thus cotton breeder can be used these traits to screen and classification the different stocks in cotton breeding programme. Present findings were similar to the findings of Cai *et al.*, (1996) and Abdel Salam *et al.*, (2010).
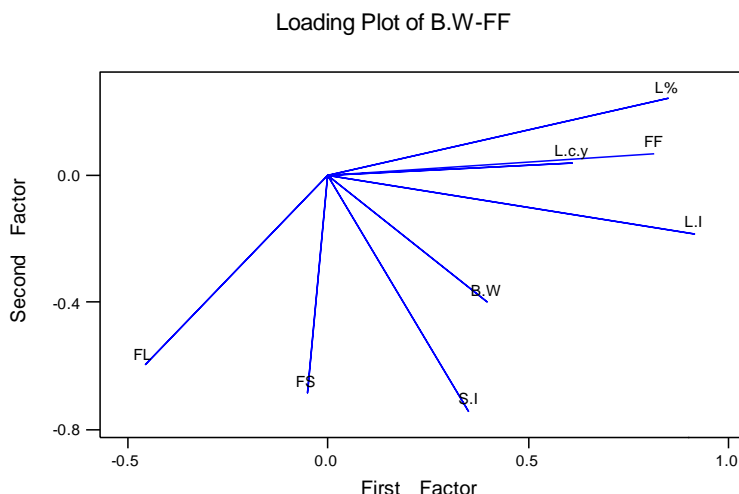
Loading Plot of B.W-FF

Fig. (1): Loading plot of 8 characters in factor analysis.

Genetic distance based on group average linkage Euclidean distance, was shown in Table (5). Genetic distance among all genotypes sampled ranged from (20.64) between cluster I and cluster III to (68.12) between cluster III and cluster IV.

Table (5): Average distance within and between four clusters of sixty cotton genotypes

Cluster(no.of genotypes	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I(1 genotype)	-	23.62	20.64	47.49
Cluster II(4 genotypes)		8.85	44.25	23.88
Cluster III(17genotypes)			11.46	68.12
Cluster IV(38genotypes)				13.7

A dendrogram (Fig. 2) obtained from computer numerical analysis of eight quantitative characters fell into four clusters. One genotype , Australian 12 formed cluster I , 4 into mixed between Egyptian cotton and some divergent origin genotypes , 17 genotypes fell into extra long cluster and 38 into long cluster. We should mentioned that Giza 45 × Sea Island occupied a basal position within Extra long cluster likewise, both Giza 83 × Pima s_6 and Giza 75 × Sea occupied the same basal position within long cluster.

Cluster I containing one genome, Australian 12 at genetic distance (23.88%) with all other clusters. Australian 12 is noted the excellent for lint cotton yield and lint%.

Cluster II was consisted of only four genotypes at genetic distance (23.62) with cluster I. Giza 80 × Pima s_6 was the excellent genotypes for lint cotton yield, lint % and seed index. The most genotypes of this cluster mixed between divergent origin and Egyptian cotton. The distantly related genotypes (5844 × Terms 16) × Pima s_7 and Giza 80 × Pima s_6 (genetic

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distance 8.85), whereas the level of similarity was high (98.68%) between Giza 80 x Pima s$_6$ and Karshenky × Giza 86.
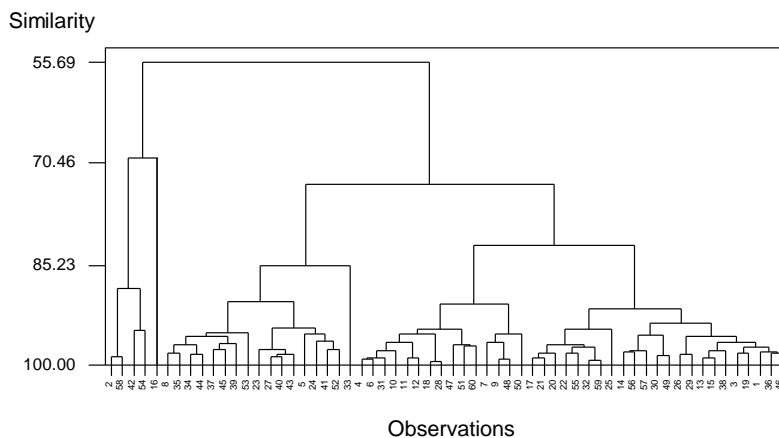

Fig. (2): Comparison of dendrogram based on lint cotton yield and fiber proprieties.

Cluster III was consists of 17 extra long genotypes at genetic distance within cluster (11.46). This cluster divided into two sub clusters, Giza 45 × Sea Island the excellent genotypes for 2.5% span length and fiber fineness make the first at genetic distance (11.42) while, the second sub cluster included 16 genotypes that composed of two sub sub clusters, each of them consisted of eight genotypes.

In this sub cluster, genetic distance was (11.96) between Australy 12 and Giza 45 × Sea Island and (7.03) between Australian 12 and Giza 77. In contrast, on the basis of the level of similarity, both Giza 74 and Giza 71 are closely related genotypes (high similarity, 98.7%). Also, the level of similarity was high, (98.23%) between Giza 77 and (Giza 84 × Giza 70) × (Giza 45 × Sea Island).

Cluster IV was the largest (38 genotypes) at genetic distance of (20.79). Giza 80 × Pima s$_6$ followed by Karshenky × Giza 86 were the excellent genotypes for lint cotton yield. In contrast Giza 75 × Sea occupied a basal position within this cluster. The level of similarity was high (99.30%) between Giza77 Radiation and Giza 86 × (Karshenky × CB 58) and it was (98.83%) between Giza 75 and Giza 89. In the other word, Giza 75 and Giza 89 were closely related genotypes may be resulting from the use of parent Giza 67 a common parent in their pedigree. So, Giza 89 across between Giza 75 and Rissun 6022.

In contrast, the level of similarity was low (82.48%) between Giza 90 and Pima high percentage may be resulting from divergent origin. So, Giza 90 mixed between Giza 83 × Dandera where Pima high percentage descended from Pima cotton.

On the basis of the data for this study, the level of similarity was high (95% and more) between most accessions (84%) for extra long cluster may be resulting from identical by descent (Kempthorne, 1969) from the same origin. Also, quite similar trends were observed for long cluster. So, the level of similarity was high (96% and more) between 88% genotypes for this category. According to pedigree records for most extra long Egyptian cotton varieties that descended from a cross between Sakha 3 and Sakha 4. So, all the respective Egyptian cotton varieties like Giza 12, Giza 36, Giza 68, Giza 77 and the current extra long cotton variety Giza 88 including these two varieties in their pedigree. Also, the succeeded commercial cotton variety Giza 86 descended from Giza 75, the later is a cross between Giza 69 and Giza 67 that were progenitor of Ashmonii stocks.

Indeed genetic uniformity within cotton may be caused by the extensive use of one or more closely related varieties also, the intervarietal hybridization in Egyptian cotton breeding programme that used from 1921 till now followed selfing in subsequent generation would be the most reason for fixation of alleles.

Thus, broadening the genetic resources need to extensive exploitation for a new germplasm to rebuild Egyptian cotton collection of *gossypium barbadense.*

REFERENCES

Abdalla, A.M.;; O.U.K. Reddy and K.M. El zik (2001). Genetic diversity and relationships of diploid and tetraploid cottons revealed using AFIP, Theor Appl. Genetic. (2001), 102: 222-229.

Abdelsalam, M.E.; M.M. El-Lawendy; M.A. El-Ameer (2010). Factor analysis and its relationship with genetic diversity in cotton. J. Agric. Res. Kafr El-Sheikh Univ., Vol. 35, No. 3, 941-955.

Anderberg, M.R. (1973). Cluster analysis for applications. Academic Press, New York.

Cai, Y.F.; Y.J. Tang and H.H. Hel (1996). Principal component analysis and canonical correlation analysis for earliness, yield contributing characters and fiber quality characers of short season cotton. J. Southwest Agric. Univ., 18(4): 346-349.

Calhoun, D.S.; D.T. Bowman and O.L. May (1994). Pedigree of Upland and Pima cotton cultivars released between 1970 and 1990. Mississippi State University, Agricultural and Forestry Experimental Station, Bulletin, 1017.

El-Akhedar (2007). Genetic distance and its relationship. Heterosis in Cotton. Egyptian J. oF Genetics and Cytology Ain Shams.,1:223-234.

El-zik, K.M. and P.M. Thaxton (1989). Genetic improvement for resistance to pests and stresses in cotton. In: Frishee R.E.; El-Zik, K.T.; Wilson, L.T. (eds). Integrated pest management systems and cotton production. John Wiley and Sons, New York, pp. 191-224.

Fryxell, P.A. (1979). Natural history of the cotton tribe. Texas A & M University Press, College Station, Texas.

Harman, H.H. (1976). Modern factor analysis, 3rd Ed. Univ. of Chicago Press Chicago.

Kaiser, H.F. (1958). The varimax criterion for analytic notation in factor analysis, Psychometricka, 23: 187.

Kempthorne, O, (1969). An introduction to genetic statistics. Iowa State Univ.Press. IA.

SPSS (1995). SPSS version 10 for windows a computer program users guide SPSS, USA.

Steel, R.G.D. and J.H. Torrie (1980). Principles and procedures of statistics. McGraw Hill Co. Inc., New York.

تقييم التباعد الوراثى لبعض الأصول الوراثية لجنس القطن جوسيبيم باربادنس

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قسم بحوث تربية القطن ـ معهد بحوث القطن ـ مركز البحوث الزراعية-مصر

أجرى هذا البحث بمحطة البحوث الزراعية بسخا بموسمى ٢٠٠٩ ، ٢٠١٠م بغرض تقييم التباعد الوراثى بين ستون تركيب وراثى لجنس القطن جوسيبيم باربادنس.

- أظهرت نتائج تحليل التباين وجود فروق معنوية بين معظم المواد الوراثية.

- أظهر التحليل العاملى أن العوامل الثلاثة الأولى اشتملت على ٨٣% من التباين الكلى سجل العامل الأول ٤٣% وكانت أهم صفاته محصول القطن الشعر ـ معامل الشعر ـ تصافى الحليج والنعومة فى حين سجل العامل الثانى ٢٥% وكانت أهم صفاته معامل البذرة-متانة الشعيرات وطول التيلة. بينما سجل العامل الثالث ١٤% من التباين الكلى وكانت أهم صفاته وزن اللوزة والمتانة.

- قسمت التراكيب الوراثية إلى أربعة مجموعات طبقا للتحليل العاملى باستخدام صفات محصول القطن الشعر وصفات التيلة شملت:

المجموعة الأولى: التركيب الوراثى استرالى١٢ والذى امتاز بالمحصول العالى.

المجموعة الثانية : بعض الاتحادات الجديدة بين أصناف مصرية و بعض التراكيب الوراثية الأجنبية و كانت اهم صفاتها النسبة المئوية لتصافى الحليج .

المجموعة الثالثة : ١٧ تركيب وراثى تابعة لطبقة الأقطان الفائقة الطول احتل جيزه ٤٥ × سى ايلند مكانأ منفصلا فيها بنسبة تباعد ١١,٤٧

المجموعة الرابعة : شملت ٣٨ تركيب وراثى تابعة للأقطان الطويلة التيلة. سجل جيزه ٧٥ × س اعلى نسبة تباعد داخلها (٢٠,٧٩).

أتضح من الدراسة أن أكثر من ٨٤% من الأقطان الفائقة الطول ، ٨٨% من الأقطان الطويلة ذات مستوى عالى من التشابه (أكبر من ٩٥%) وأن التباعد الوراثى بينها أقل ما يمكن لذا يلزم إضافة دم جديد للمجموعة النباتية للقطن المصرى بهدف زيادة التحسين الوراثى المتوقع بالانتخاب عند استخدام هذه التراكيب الوراثية ببرامج التربية.

قام بتحكيم البحث

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