MULTIVARIATE ANALYSIS OF SOME ECONOMIC CHARACTERS IN COTTON (*Gossypium barbadense* L.)

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ABSTRACT: *Multivariate techniques were used to assess variability among genotypes and to evaluate morphological parameters contributing to the variation in each genotype of sixty three-way crosses and six parents. The study of agronomic variability among genotypes was reflective of genetic variability and gave graphical, non numerical assessments of genetic variability. Analysis of variance revealed significant differences among genotypes, parents or crosses, for most studied characters reflected differenced in genetic background. Principal component analysis revealed that PC1 had a higher coefficient for lint index, lint percentage, days to first flower, micronaire reading and reflectance percentage, respectively. While, the largest coefficient in PC2, were 2.5% span length, uniformity ratio and elongation %, PC3 seemed to be effected principally by yellowness degree, reflectance percentage, boll age, seed index and boll weight, respectively. The first five principal components explained no less than 81.7% of the total variability among sixty three-way crosses and six parents. The maximal amount of variation is shown in the first principal component were 36.6%. Principal component analysis separated the genotype, while the six parents were grouped into 5 groups. Based on the extent of relative dissimilarity the 66 cotton genotypes were grouped into 7 clusters, while the six parents were grouped into 4 major clusters. The parental genotype Giza 86 was separated into a wide group while Giza 88 and Pima S_6 were separated into the same group. The hybridization between parents from distant clusters may give progeny which surpassed their parents in most yield characters.*

Key words: *Multivariate analysis, Genetic divergence, Cotton.*

INTRODUCTION

Exploiting heterosis is one of the methods used to increase cotton yields that have stagnated in recent years. The success of hybridization is largely dependent on the correct selection of parents. It is now established that exploitation of heterozygotes and success in getting useful heterosis in breeding programmes depends on the degree of the genetic divergence between parents.

According to quantitative genetic theory, the genetic variance, and hence the probability of producing transgrassive segregates, increases in proportion to the number of loci for which parents carry different alleles. The use of multivariate methods, more common in other disciplines, is seen

increasingly in plant breeding. Though plant breeders often measure several traits in cultivar development, few examples of applications of multivariate methods exist.

Multivariate technique could resolve phenotypic measurements into fewer and easily visualized dimensions (Hamman, 1972). This analysis which used principal components seemed to elucidate patterns of variation in agronomic attributes and to obtain the initial factor solution using eigen values. These values could measure the explained variance associated with each factor (Hair *et al.,* 1987). Godshalk and Timothy (1988) compared principal component and factor analysis as alternatives to index selection and found that selection based on PCA to have a high correlation with that based on Smith-Hazel index selection. Seyam *et al.* (1984) used factor analysis in determining traits that could be selected for high yield. Brown (1991) and Abd El-Sayyed *et al.* (2000) used principal component and cluster analysis to create genetic variability in Upland and Egyptian cottons, respectively. Vega and Chapman (2006) found that the two and three mode PCAs revealed GCA x E and SCA x E interactions were able to identify the best tester for either broad or specific adaptation and this analysis accounted for all sources of variation.

In the analysis presented here, principal component and cluster analysis were used on agronomic trial data to give graphical presentation of relative genotypes performance and to show interrelationship of cotton genotypes based on agronomic performance and fiber quality measurements. The analysis also gives a general over view of genetic variability among cotton genotypes. Such information may identify the breeding strategies that are most likely to produce improved progeny.

MATERIALS AND METHODS

Sixty three-way crosses and six parents were used in this study. The parents were chosen primarily for their diversity of yield and fiber characters. The six parents were crossed in 6 x 6 half diallel to generate a total of 15 hybrids. These 15 hybrids along with 6 parents were grown and crossed using triallel mating system to obtain 60 three-way crosses [n (n-1)(n-2)/2]. The parental cotton genotypes used in this study were Karshenky$_2$ as Russian early variety, Pima S$_6$ American long stable variety, Suvin as Indian variety and three Egyptian varieties Giza 70, Giza 86 and Giza 88. The six parents and 60 three-way crosses were grown at Sakha Agric. Res. Station in 2007 season. The experimental design was randomized complete block with three replications. Each entry was planted in single row with intra and inter row distances of 25 and 65 cm, respectively. Conventional were applied in a field. Data were recorded on 20 guarded plants basis for each entry for the following 14 characters: days to first flower (DFF), boll age (BA), boll weight (BW), seed index (SI), lint percentage (L%), lint index (LI), seed cotton

yield/plant (SCY/P), 2.5% span length (2.5% SL), uniformity ratio (UR), fibre strength (g/t) (FS), micronaire reading (MR), reflectance percentage (Rd%) and yellowness degree (+b).

Statistical analysis:

The data were subjected to the analysis of variance of triallel set of crosses for every character separately. This analysis provides a test of significance between genotypes (parents and crosses). Useful heterosis was determined as the deviation of three-way cross mean from its better parent (Steel and Torrie 1960). Correlation coefficients were calculated as outlined by Steel and Torrie (1960).

Multivariate techniques were used to assess the dissimilarities among genotypes and to evaluate morphological parameters contributing to the variation in each genotypes. Principal component analysis were performed on the correlation matrix of traits of each trial. The principal components of the contributed characters were expressed was eigen value and manifested in eigen vector for all the studied characters in each PC axis (Hair *et al.*, 1987). The principal component analysis was also plotted in a diagram displaying the component score of genotypes based on all characters. Hierarchical clustering was then carried out on each data set using Ward's minimum variance method, which minimizes within-cluster sum of squares. The results from clustering analysis are presented as dendrograms. The dendrogram is constructed on Euclidean distance basis. According to Anderberg (1973) and Nei (1973) and developed by Johnson and Wichern (1988). All these computation were performed using Minitap and SPSS (1995) computer procedure.

RESULTS AND DISCUSSION

Estimated mean squares of 60 three-way crosses and 6 parents for the studied characters are presented in Table 1. The results showed significant mean squares of genotypes, parents and crosses for most studied characters. The observed significant variation among the parental genotypes might reflect partially their different genetic background and this variability could be exploit through hybridization. Mean squares of parents vs. crosses as indication to average heterosis over all crosses were significant for days to first flower, lint percentage, seed cotton yield/plant, 2.5% span length, uniformity ratio, reflectance percentage and yellowness degree.

The average performances of parents in their crosses are presented in Table 2. It is clear that the crosses which involved Kar. $_2$ exhibited low values (desirable values) for two earliness traits, but gave low values for all yield components. In the reverse trend triple. crosses with Giza 86 gave high means for yield and its contributing characters with low value for yellowness degree. Pima S$_6$, Giza 70 and Giza 88 in their triple crosses showed significant values for 2.5% span length.

Table 1.   Mean square estimates of 60 three-way crosses and 6 parents for the fourteen studied characters.

S.O.V.	d.f.	DFF	BA	BW	SI	L%	LI	SCY/P	2.5%SL	UR%	S(g/tex)	E%	MR	Rd%	+b
Replications	2	3.899*	2.864*	0.020	0.047	1.327	0.137	2133.96**	2.073	3.667	15.185	0.060	0.087	4.898	3.299**
Genotypes	65	49.215**	22.081**	0.275**	2.020**	8.318**	1.595**	149.69**	4.421**	3.518	19.914**	0.235**	0.218**	23.947**	2.497**
Parents(P)	5	86.856**	16.056**	0.200**	4.320**	24.346**	4.645**	48.89	21.801**	8.340*	59.696**	0.460**	0.570**	53.334**	9.786**
Crosses(C)	59	45.858**	22.930**	0.286**	1.857**	7.022**	1.358**	145.96**	2.703**	2.931	16.650**	0.213**	0.192**	21.299**	1.854**
P Vs. C	1	59.073**	2.134	0.007	0.171	4.597**	0.308	873.61**	18.930**	14.001*	13.600	0.393	0.000	33.280**	4.010**
Error	130	1.073	0.864	0.036	0.185	0.564	0.089	29.13	0.890	2.881	7.768	0.117	0.075	4.436	0.376

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

Table 2. Averages of parents in their crosses for the fourteen studied characters.

Estimate	DFF #	BA #	BW	SI	L%	LI	SCY/P	2.5%SL	UR%	S(g/tex)	E%	MR #	Rd%	+b #
10-Crosses(one-line) for Kar.2	67.4**	45.0**	2.8	9.2	35.0	5.0	35.6	33.8	87.4	40.9	6.5	3.4	69.3	10.6
20-Crosses(two-line) for Kar.2	69.0**	45.0**	2.9	9.4	36.5	5.4	30.9	33.8	87.8	40.8	6.7	3.8	71.2	10.3
10-Crosses(one-line)for Pima S₆	71.4*	46.6	3.1	10.0	36.7	5.8	30.6	34.2*	87.6	42.1	6.7	3.7	72.3	10.2
20-Crosses(two-line) for PimaS₆	71.7*	46.7	3.0	9.6	36.9	5.6	34.9	33.7	87.6	40.3	6.6	3.8	71.4	10.4
10-Crosses(one-line) for Suvin	70.0**	47.0	3.2	10.2	36.3	5.8	37.9*	32.6	86.9	38.3	6.5	3.8	72.9	10.0
20-Crosses(two-line) for Suvin	72.0	47.4	3.1	9.8	37.1	5.8	33.8	33.9	87.8	40.9	6.7	3.8	71.5	10.3
10-Crosses(one-line) for G.70	73.2	48.0	3.0	9.2	37.3	5.5	33.7	34.2*	88.0	41.9	6.7	3.8	72.3	10.1
20-Crosses(two-line) for G.70	71.2*	47.6	3.1	9.6	36.6	5.6	32.9	33.5	87.1	40.4	6.6	3.8	71.5	10.3
10-Crosses(one-line) for G.86	74.8	47.8	3.2	10.0	38.7**	6.3**	37.8*	33.5	87.8	40.7	6.8	4.1	73.4	9.6*
20-Crosses(two-line) for G.86	72.5	47.5	3.2	10.0	37.7*	6.0	36.7*	33.7	87.5	40.9	6.6	3.7	73.0	10.0
10-Crosses(one-line) for G.88	72.1	47.6	3.1	9.8	37.1	5.8	31.4	34.2*	87.6	41.4	6.6	3.8	70.1	11.2
20-Crosses(two-line) for G.88	72.7	48.2	3.1	9.8	36.8	5.7	37.9*	34.0	87.5	41.8	6.7	3.8	71.7	10.4
60-Crosses	71.5*	47.0	3.1	9.7	36.9	5.7	34.5	33.8	87.5	40.9	6.6	3.8	71.7	10.3
6-Parents	73.4	47.4	3.1	9.6	36.3	5.6	27.2	32.7	86.6	41.8	6.5	3.8	70.3	10.8
LSD5%	1.7	1.5	0.3	0.7	1.2	0.5	8.8	1.5	2.8	4.6	0.6	0.6	3.4	1.0
LSD1%	2.3	2.0	0.4	0.9	1.6	0.7	11.7	2.1	3.7	6.1	0.7	0.6	4.6	1.3

\# Low values are desirable.

*,**Significant at the 0.05 and 0.01 levels of probability were of the desirable difference among the crosses mean and parents mean.

Percent useful heterosis are given for each trait in Table 3. The manifestation of heterosis for most characters clearly indicated that hybrids did not follow regular trend. Heterosis for boll weight was significant in two combinations (13.3% and 20.8%), while for lint percentage and lint index were observed in 2 and 1 combinations, respectively. Heterosis for seed cotton yield/plant was significant in 18 triplet combination, ranging from 30.4% to 52.3%.

It is interesting to note that the cross-combinations exhibiting high per-se performance for other yield-contributing characters also involved one of the parents as good general combiner. Also, the results indicated that the higher seed cotton yield/plant does not necessarily depend on the high heterotic behavior of the combination of all the yield components which are ultimately associated with yield be sufficient to enhance the yield. Duhoon (1990) and Pavasia et al. (1999) also reported almost identical results. Useful heterosis for fiber properties was observed in 3 crosses of 2.5% span length, 2 crosses of elongation % and (Kar.$_2$ x G. 88) x Pima S$_6$ of both reflectance percentage and yellowness degree.

From the present study it can be concluded that the selection of parents for a crossing programme on the basis of phenotypic performance may not prove useful, a modified selection type, which involves intermating, can be successfully used for carrying over and crossing the breeding material for the desirable traits of both yield and fiber properties. Thus lines developed with the accumulation of desirable genes may also act as breeding lines for heterosis breeding programme. Similar conclusion was found by Tuteja et al. (2003).

Simple correlations between the various traits are presented in Table 4. The correlations between two earliness characters and yield components, micronaire reading and reflectance percentage were positive and high. The crosses of higher maturity are expected to possess higher cellulose percentage. Thus, increasing late maturity can be expected to result in desirable changes of yield components and fiber properties. Yield components were high positively correlated between them, but were low positively correlated with seed cotton yield. Interpret of yield increases may become more complex. Because yield components were not involved bolls/plant in this study. However, the relationships among fiber properties were sizable and logical. These results coincided with those reported by Singh et al. (1985) and Smith and Coyle (1997).

Multivariate technique which used principal component analysis was performed on 14 agronomic and fiber characters to extract important component of variation in agronomic attributes which are economic important and to obtain the initial factor solution using eigen value Table 5. The relative magnitude of the coefficient of each characters relating to the first six principal components from the component analysis can often provide an interpretation for each component axis. The sign of the coefficient

Table 3. Useful heterosis for the fourteen studied characters.

Crosses	DFF #	BA #	BW	SI	L%	LI	SCY	2.5%S L	UR%	S(g/t)	E%	MR#	Rd%	+b #
(Kar.2 x Pima S₆)x Suv.	2.6	0.8	-20.6	-11.8	-7.1	-22.1	26.6	-1.4	-0.2	-8.5	-0.5	19.8	-0.4	5.8
(Kar.2 x Pima S₆)x G.70	6.8	-0.7	-17.7	-21.5	-4.1	-26.7	-12.6	-4.6	-0.7	-12.3	-3.5	16.7	-6.7	6.0
(Kar.2 x Pima S₆)x G.86	17.7	-3.7*	-12.1	-17.0	-7.3	-27.1	33.0*	-1.0	0.4	-10.1	-10.2	24.0	1.3	8.7
(Kar.2 x Pima S₆)xG.88	9.9	1.6	-22.9	-15.6	-5.5	-23.1	-15.8	-4.8	-1.7	-14.6	-7.0	10.4	2.3	1.7
(Kar.2 x Suv.) x Pima S₆	3.7	3.1	-22.5	-9.3	-3.4	-13.8	-1.0	7.3**	2.3	-1.0	3.5	25.0	-2.4	9.8
(Kar.2 x Suv.) xG.70	6.8	-0.7	-10.8	-7.0	0.5	3.1	-1.2	-2.3	0.7	-7.6	8.5	18.8	-7.5	17.8
(Kar.2 x Suv.) xG.86	7.8	2.3	-15.7	-7.4	-6.6	-17.8	-2.2	-1.4	-0.4	-5.8	-8.3	26.0	-10.8	19.3
(Kar.2 x Suv.) xG.88	4.7	3.1	-9.8	-9.5	-0.9	-0.6	-4.9	-3.1	1.5	-8.4	9.0*	16.7	-6.6	28.6
(Kar.2 X G.70) xPimaS₆	5.8	2.3	-17.7	-15.3	-5.6	-22.6	-27.4	-2.5	-0.2	-7.5	-2.0	14.6	-4.5	2.5
(Kar.2 x G.70) x Suv.	4.2	1.6	-5.9	-5.1	-0.8	3.1	4.1	-11.9	-2.5	-19.3	-0.5	14.6	-3.7	1.1
(Kar.2 x G.70) xG.86	10.4	6.8	-10.1	-12.7	-7.1	-23.1	-5.3	-6.4	0.6	-9.5	-2.3	34.4	-3.8	2.3
(Kar.2 x G.70) x G.88	7.8	3.1	13.3**	1.5	1.4	3.8	-27.3	-2.8	-0.2	-6.0	11.6**	20.8	-8.1	19.6
(Kar.2 x G.86) x PimaS₆	3.7	0.8	-1.0	-3.4	-8.4	-16.4	-19.2	-1.5	-2.0	-7.7	-9.7	18.8	-1.8	18.2
(Kar.2 x G.86) x Suv.	5.8	0.8	-1.0	-0.3	-12.6	-20.4	19.0	-3.0	0.0	-11.1	-9.7	20.8	2.0	4.5
(Kar.2 x G.86) x G.70	7.8	2.3	-12.1	-18.5	-10.1	-32.0	-9.0	-3.8	0.3	-7.7	-6.5	13.5	-4.6	6.4
(Kar.2 x G.86) x G.88	11.5	0.8	-16.2	-6.5	-9.9	-20.9	4.4	1.0	1.0	-9.1	-8.8	15.6	-5.2	24.6
(Kar.2XG.88)x Pima S6	5.2	3.1	-22.9	-17.1	-3.7	-21.5	-2.5	-3.0	-1.1	-15.6	-5.5	18.8	6.3*	-13.9**
(Kar.2 x G.88) x Suv.	3.2	3.8	-25.5	-8.6	-4.5	-4.9	-3.9	-0.3	1.0	-17.8	1.6	21.9	-2.7	19.6
(Kar.2 x G.88) xG.70	7.8	0.1	0.0	-2.9	-0.5	-3.2	7.2	-1.5	2.6	-6.8	9.0*	21.9	-6.9	7.0
(Kar.2 x G.88) x G.86	12.0	-2.2	-4.0	-16.0	-7.3	-25.8	37.5**	-4.9	-0.6	-3.0	0.0	25.0	0.8	6.8
(Pima S₆XSuv.) x Kar.2	2.1	3.1	-24.5	-7.5	-10.8	-22.1	-9.6	2.3	0.2	-3.0	-3.5	7.3	-6.2	14.5
(Pima S₆ x Suv.) x G.70	2.3	2.8	-17.6	-17.4	-0.2	-17.9	26.5	-4.0	0.5	-12.8	0.5	11.4	-4.0	9.1
(Pima S₆ x Suv.) x G.86	6.1	5.0	5.9	4.6	-5.7	-5.3	44.0**	6.0*	0.0	-10.0	-7.9	20.0	1.8	9.5
(Pima S₆ xSuv.) x G.88	3.7	1.4	-1.0	-4.7	-2.1	-7.7	33.4*	-1.5	-2.0	-13.1	-7.5	1.0	-2.6	16.3
(Pima S₆x G.70) x Kar.2	2.1	4.6	-13.5	-19.3	-11.6	-33.3	-19.7	-6.8	-2.5	-16.9	-10.4	-4.2	-12.6	22.1
(Pima S₆ x G.70) x Suv.	-1.5	1.4	-7.8	-9.3	-5.2	-16.4	-5.9	-11.4	-1.8	-24.7	-8.5	11.4	-8.0	10.9
(Pima S₆ x G.70) x G.86	7.5	5.0	2.0	0.0	-4.2	-7.6	-26.0	-4.7	0.8	-6.1	-0.5	22.9	-1.5	7.2
(Pima S₆XG.70) x G.88	6.1	5.7	-6.3	-14.3	-1.9	-16.9	12.4	-3.0	-0.8	-15.3	-4.5	12.4	-8.9	20.0
(Pima S₆x G.86) x Kar.2	9.4	2.3	-18.2	-18.5	-5.3	-25.8	11.7	-3.3	-0.5	-9.2	-9.3	24.0	3.4	7.2
(Pima S₆ x G.86) x Suv.	2.8	1.4	3.9	-2.5	-8.0	-15.1	45.2**	-2.5	-2.2	-8.2	-6.0	14.3	0.0	12.9

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.
#Low value desirable and therefore low parent value used.

Table 3. Continued.

Crosses	DDF#	BA#	BW	SI	L%	LI	SCY/P	2.5%SL	UR%	S(g/tex)	E%	MR#	Rd%	+b#
(Pima S₆ x G.86) x G.70	4.7	7.8	1.0	-13.0	-6.3	-21.8	16.1	-0.3	1.2	-12.4	-0.9	16.2	-2.3	9.8
(Pima S₆ xG.86) x G.88	0.9	0.7	5.1	-4.6	-5.5	-13.3	11.2	0.4	-0.1	-1.8	-3.7	4.8	-2.0	26.5
(Pima S₆ X G.88) x Kar.2	4.2	3.1	-11.5	-9.7	-10.5	-24.1	10.7	-2.1	-0.7	-8.7	-1.5	7.3	-3.5	-1.4
(Pima S₆ x G.88) x Suv.	0.0	2.1	-4.9	-4.4	-3.5	-9.2	44.2**	-3.8	-0.6	-6.7	3.5	8.6	-2.7	15.2
(Pima S₆ x G.88) x G.70	9.9	1.4	-10.4	-15.6	-1.8	-17.9	38.0*	-1.3	-0.3	-8.2	0.5	8.6	-5.4	11.2
(Pima S₆ x G.88) x G.86	8.0	3.5	2.0	-13.3	-4.3	-19.6	36.8**	-1.6	0.7	-14.7	-8.3	19.0	-0.4	14.4
(Suv. X G.70) x Kar.2	3.7	3.1	-9.8	-13.7	-7.7	-16.0	14.1	-5.6	0.5	-19.2	1.6	4.2	-10.4	24.3
(Suv. X G.70) x Pima S₆	-1.0	-0.8	-5.9	-15.3	-3.4	-20.0	0.4	-6.8	-1.7	-14.1	-3.5	1.9	-6.3	14.9
(Suv. X G.70) x G.86	2.8	9.4	-15.7	-12.7	-3.9	-18.7	52.3**	-5.0	0.1	-16.0	-6.9	15.3	-1.4	3.4
(Suv. X G.70) x G.88	-2.2	6.5	-7.8	-6.3	3.2*	9.9*	-22.3	-4.1	1.3	-11.1	8.5	5.4	-6.8	19.6
(Suv. X G.86) x Kar.2	6.3	-1.4	-14.7	-14.2	-12.3	-30.7	-3.5	1.2	-2.3	0.9	-10.2	5.2	-2.3	16.3
(Suv. X G.86) x Pima S₆	8.0	2.1	3.9	1.9	-6.5	-8.9	-14.2	4.5*	0.9	-3.1	-6.5	5.7	0.9	5.3
(Suv. XG.86) x G.70	6.9	10.1	-9.8	-11.7	-3.7	-17.3	1.6	-5.9	-1.2	-9.2	-5.6	2.7	-1.6	10.2
(Suv. X G.86) x G.88	6.4	13.1	-2.0	2.2	-6.0	-8.0	9.2	-3.1	0.2	-12.3	-9.3	2.7	-1.8	20.8
(Suv. X G.88) x Kar.2	4.7	0.1	-22.5	-16.8	-1.6	-9.3	37.2*	-1.9	0.8	-7.5	6.9	6.2	-2.0	5.1
(Suv. X G.88) x Pima S₆	4.2	2.8	-3.9	0.9	-0.9	-0.5	2.9	-0.4	0.7	-10.5	2.0	11.4	-1.7	12.3
(Suv. X G.88) x G.70	4.1	20.4	-5.9	-17.8	4.5**	-1.9	12.6	-6.7	-0.6	-7.0	7.9	-1.8	-4.6	15.9
(Suv. X G.88) x G.86	7.3	13.1	2.0	2.2	-4.8	-6.2	6.6	-6.0	-1.0	-13.0	-6.9	5.4	2.1	10.2
(G.70 x G.86) x Kar.2	5.2	-1.4	-6.1	-13.3	-16.5	-35.6	32.3*	-5.9	-0.7	-11.0	-11.6	2.1	-3.6	1.5
(G.70 x G.86) x Pima S₆	6.1	-4.3**	-5.1	-16.7	-8.5	-28.0	-1.0	-3.4	0.0	-1.0	-0.9	3.8	-0.8	10.2
(G.70 x G.86) x Suv.	-3.6**	5.8	-7.8	0.0	-8.2	-13.3	24.4	-8.9	-2.0	-20.0	-13.0	4.5	-1.4	5.7
(G.70 x G.86) x G.88	-3.6**	7.6	-8.1	-13.6	-9.2	-26.7	34.0*	-4.9	-0.9	-18.1	-11.6	-1.7	-6.2	22.7
(G.70 x G.88) x Kar.2	5.8	3.1	1.1	2.9	-2.6	-1.3	52.0**	-1.7	0.0	-9.0	5.8	9.4	-13.3	22.8
(G.70 x G.88) x Pima S6	4.2	6.4	20.8**	4.0	-4.6	-3.6	47.8**	-1.5	-1.9	-3.9	-1.5	2.9	-6.4	14.7
(G.70 x G.88) x Suv.	-0.9	10.1	-6.9	-8.9	0.3	1.9	19.3	-6.8	-1.1	-14.8	3.2	-0.9	-1.8	12.3
(G.70 x G.88) x G.86	3.5	8.3	-3.0	-1.5	-2.0	-5.3	13.1	-4.5	-2.1	-10.5	-4.2	5.1	-0.5	11.7
(G.86 x G.88) x Kar.2	4.7	0.1	-13.1	-13.0	-12.3	-30.2	30.4*	-0.5	1.3	-8.0	-4.2	13.5	-7.5	24.2
(G.86 x G.88) x Pima S6	8.0	8.5	-3.0	2.2	-13.0	-18.7	31.3*	-2.0	-1.1	-5.8	-6.9	4.8	0.0	20.1
(G.86 x G.88) x Suv.	4.1	13.1	2.9	4.6	-9.0	-10.7	48.3**	-6.0	-0.8	-19.0	-9.3	6.3	1.5	12.5
(G.86 x G.88) x G.70	2.6	8.3	0.0	-4.9	-9.0	-19.1	34.7*	-3.5	-0.6	-11.8	-12.0	-9.4	-1.6	17.0
LSD 5%	1.7	1.5	0.3	0.7	1.2	0.5	8.8	1.5	2.8	4.6	0.6	0.5	3.4	1.0
LSD 1%	2.3	2.0	0.4	0.9	1.6	0.7	11.7	2.1	3.7	6.1	0.7	0.6	4.6	1.3

*,** Significant at the 0.05 and 0.01 levels of probability, respectively. Low value desirable and therefore low parent value used.

Table 4. A matrix of simple correlation coefficients for the fourteen studied characters.

Characters	DDF	BA	BW	SI	L%	LI	SCY/P	2.5%SL	UR%	S(g/t)	E%	MR	Rd%
BA	0.72**												
BW	0.50**	0.43**											
SI	0.36**	0.36**	0.67**										
L%	0.71**	0.49**	0.39**	0.33**									
LI	0.63**	0.52**	0.66**	0.84**	0.78**								
SCY/P	0.22	0.18	0.28*	0.23	0.18	0.24*							
2.5%SL	0.00	0.02	-0.20	-0.20	0.04	-0.16	-0.03						
UR%	0.03	-0.06	-0.16	-0.06	0.28*	0.11	0.02	0.63**					
S(g/t)	0.18	0.04	0.02	-0.15	0.16	-0.01	-0.18	0.62**	0.36**				
E%	0.23	0.11	0.24*	0.15	0.52**	0.39**	0.10	0.23	0.55**	0.53**			
MR	0.49**	0.31**	0.23	0.27*	0.74**	0.59**	0.13	-0.04	0.33**	-0.05	0.47**		
Rd%	0.53**	0.32**	0.36**	0.25*	0.53**	0.46**	0.34**	-0.16	0.01	-0.07	0.24*	0.50**	
+b	-0.26*	-0.05	-0.18	-0.15	0.37**	-0.31**	-0.30*	0.29*	-0.06	0.20	-0.25*	-0.49**	-0.82**

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

Table 5. Principal component coefficients of 60 three-way crosses and 6 parents according to the first six components for the fourteen studied characters.

Variable	PC1	PC2	PC3	PC4	PC5	PC6
DFF	-0.348	-0.016	-0.172	-0.448	-0.056	0.009
BA	-0.274	0.036	-0.331	-0.464	-0.101	-0.204
BW	-0.293	0.153	-0.311	0.235	-0.136	0.338
SI	-0.277	0.180	-0.318	0.477	0.040	-0.064
L%	-0.377	-0.137	0.040	-0.140	0.206	-0.120
LI	-0.394	0.044	-0.191	0.235	0.155	-0.105
SCY/P	-0.162	0.111	0.126	0.178	-0.798	-0.237
2.5%SL	0.040	-0.508	-0.124	-0.057	-0.309	-0.189
UR%	-0.075	-0.489	0.170	0.238	-0.024	-0.370
S(g/t)	-0.024	-0.486	-0.193	-0.107	-0.100	0.538
E%	-0.223	-0.377	0.110	0.289	0.087	0.305
MR	-0.323	-0.096	0.257	-0.021	-0.339	-0.300
Rd%	-0.314	0.099	0.367	-0.198	-0.173	0.248
(+b)	0.239	-0.124	-0.561	0.000	0.067	-0.229

is irrelevant, and in fact arbitrary, though negatively correlated traits will generally have opposite signs on a given axis. Though no clear guidelines existed to determine the significance of a treat coefficient, one rule of thumb is to treat coefficient > 0.3 as having a large enough effect to be considered important (Hair *et al.*, 1987). Each characters was an important source of variation in one principal component axis. Some characters may have greater importance in determining plant phenotypic than other (Brown, 1991).

Lint index was a primary source of variation with a higher coefficient in the first PC axis. Lint percentage appeared to have the second highest coefficient followed by days to first flower and micronaire reading as well as reflectance percentage. Hence, the higher PC1 score for a genotype, the higher values for the above traits would be. As all these traits deal with yield component, earliness and fiber properties. Thus the PC1 axis dealing with all group of traits.

This trend was changed in PC2 since fiber properties showed large coefficient in this axis. 2.5% span length had the smallest coefficient in the first PC axis, but it exhibited the largest coefficient in the second PC axis followed by uniformity ratio, fiber strength and elongation %. An intercorrelation is implied among traits with high coefficients on the same axis.

Similarly, for PC3, the large coefficients are on yellowness degree, reflectance percentage, boll age, seed index and boll weight, respectively. It is clear that, no axis contained all yield and its contributing characters, but these characters were separately according degree of association with each other. This trend was reverse, since most of fiber characters were involved in the same factor.

Generally, the previous results reflected the importance of fiber characters in the total variation among the studied genotypes. The association of yield component characters such as lint index with lint percentage and seed index with boll weight were more important also in the variation among genotypes. In this connection Brown (1991), Cai *et al.* (1996) and You *et al.* (1998).

The first five principal components accounted for no less than 81.7% of the total variance of all characters (Table 6). Since, each component score is a linear combination of the traits, similar to an index, such that the maximal amount of variance is shown in the first principal component 36.6%. The second amount in the second component about 18.7%. While, the first five PC axes accounted for 81.7% of variation. In this respect Stanton *et al.* (1994), Cai *et al.* (1996) and Abd El-Sayyed *et al.* (2000).

Table 6. Eigen values and variation percent among 60 three-way crosses with 6 parents accounted by first six PCs.

Parameter	PC1	PC2	PC3	PC4	PC5	PC6
Eigen value	5.13	2.62	1.65	1.05	0.99	0.80
Proportion	36.6	18.7	11.8	7.5	7.0	5.7
Cumulative	36.6	55.3	67.1	74.6	81.7	87.4

Furthermore, each genotype could be plotted at the component score on each PC axis. The two dimensional distance between genotypes might reflect at a summary of differences based on all characters measured to the extant that the first two PC axes are effective in capturing the combined variance of all characters (Hair *et al.*, 1987). Therefore, the first two PC axes were used for representation the sixty three-way crosses along with six parents as shown in Figure 1. It is clear that the second PC axis separated most genotypes, since the fiber characters were associated with the second PC axis and were important in total variation. Thus the second PC axis, separated the genotypes with high fiber characters. Cheng and Liu (1988) separated 11 parents into 5 group by using principal component analysis. From the previous results we could obtain visual idea of amount of genetic variability existing among the studied genotypes.

Figure 2 presents results of the hierarchical cluster analysis in the form of dendrogram. This analysis provides visual idea about variabilities presented in the studied cotton genotypes, in addition to, assuring the continued
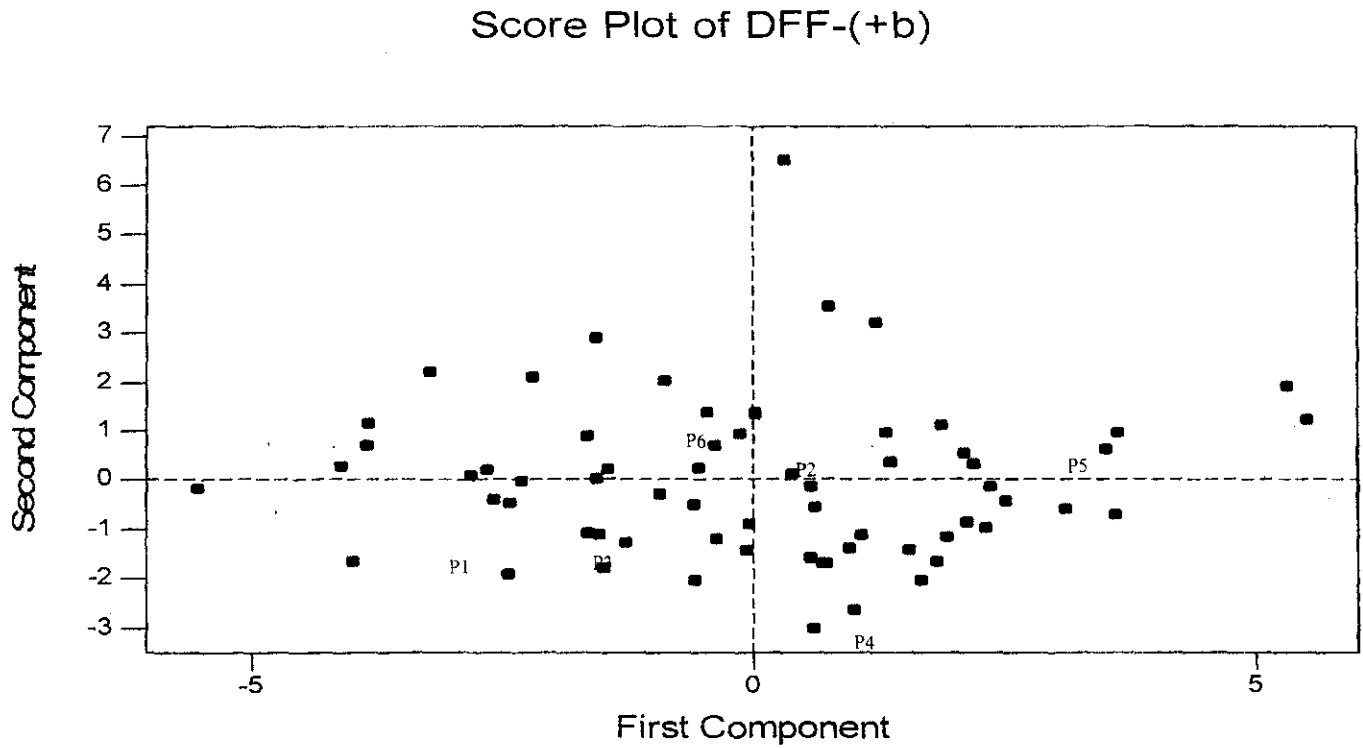
Score Plot of DFF-(+b)

Fig.1: Principal component analysis of 66 cotton genotypes ;plot of individual accessions on the first two PC axes
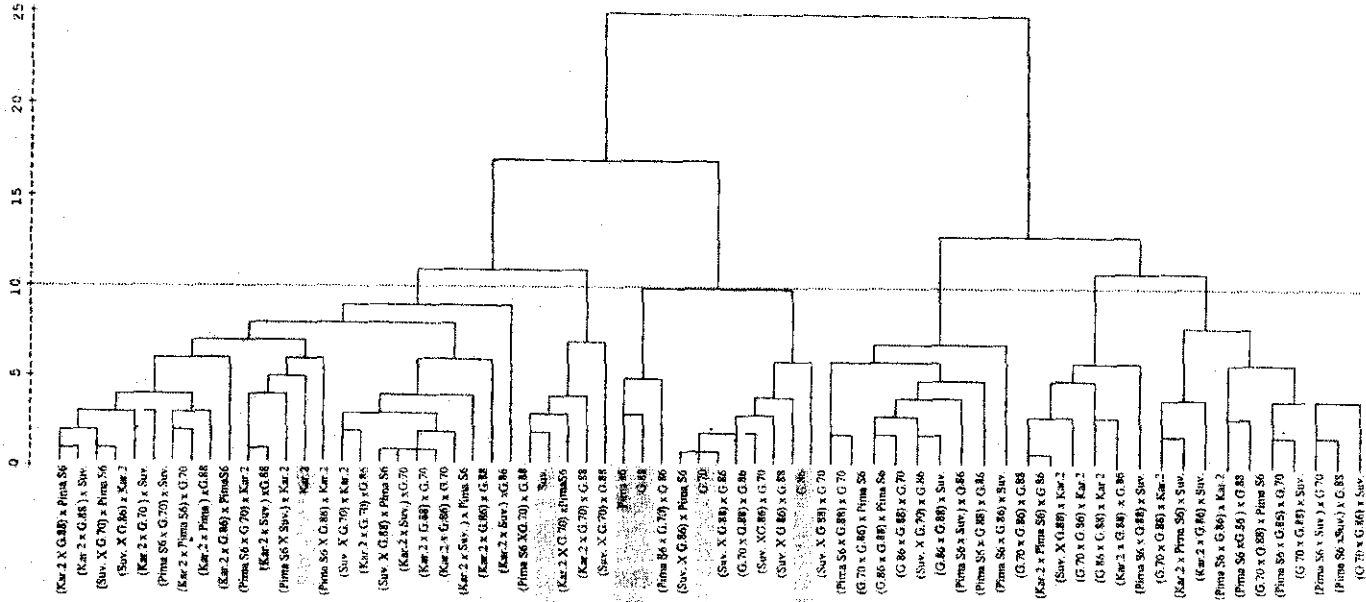
Fig. 2: Results of the hierarchical cluster analysis shown as a dendrogram based on dissimilarity coefficients between the 66 cotton genotypes.

genetic improvement. It is clear that the estimates of Euclidean distances corresponding to the 2145 possible comparisons showed that about 42% of the values were significant, more than the corresponding Chi-square value at 0.05 for 14 degree of freedom. These results indicated that the studied genotypes were expected to exhibit similarly a broad spectrum of variability and confirmed the detected significant among these genotypes.

The 60 three-way crosses and six parents were grouped into 7 clusters, based on the extent of relative dissimilarity among these genotypes, while the parental genotypes were grouped into 4 clusters. It is clear that the Russian genotype "Kar.$_2$" and the Indian genotype "Suvin" formed a wide group having divergent distance from the other parents and these two parents appeared to be nearly related. The dendrogram showed that the divergence between P_2, Pima S_6, and P_6, Giza 88, was not clearly pronounced, since these parental genotypes appeared to be closely related. On the other side, the parental genotypes Giza 70, P_4, and Giza 86, P_5, tended to be unique groups and more related to the other parents. The hybridization between parents from distantly clusters may give progeny which surpassed their parents in most yield characters. This was true, since the three clusters, 5, 6 and 7 gave significant differences for useful heterosis for SCY/P and some attributes.

Its worthy to note that, the cluster number 5 contained 9 triplet combination and this cluster surpassed other cluster for yield and fiber characters, since this cluster involved all the six parents in more recombination some of these parents were a good combiner and other was bad combiner. In this regard, Cox et al. (1985) and Sandhu and Boparai (1997) reported that genetically diverse genotypes when used as parents in hybrid breeding programme generate a wide range of variability and provide transgrassive segregates in a hybridization programme.

Finally, the results of principal component analysis and clustering analysis appeared to be in a complete accordance. The application of both analysis seemed to look reasonably straight forward. Thus each of these analysis help the breeder to know interrelationship between the genotypes or how different genetic groups relate to one another when considering may traits simultaneously.

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التحليل المتعدد لبعض الصفات الاقتصادية في القطن
(Gossypium barbadense L.)

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يهدف هذا البحث إلى استخدام التحليل المتعدد لتقدير الاختلافات بــين التراكيـب الوراثيــة وكذلك لتقييم الصفات الكمية المختلفة المساهمة في التباين لكل تركيب وراثي ، ومدى أهميـة ومساهمة كل صفة من الصفات المدروسة في التباين ، ترتيب الصفات تبعا لأهميتها ، ترتيــب التراكيب الوراثية في مجاميع مختلفة تبعا لتحليل التباعد الوراثي.

حيث تم تقييم ٦٠ هجين ثلاثي مع ٦ أباء تتبع النوع G. barbadense وتم دراسة ١٤ صفة تضم صفات التبكير ، المحصول و مكوناته والتيلة.

ويمكن تلخيص أهم النتائج المتحصل عليها كما يلي:

١ – أظهر تحليل التباين اختلافات معنوية لمعظم الصفات المدروسة مما يعكس وجود اختلافات في الخلفية الوراثية.

٢ – أظهر تحليل المكونات الأساســية Principal component analysis أن العامــل الأول PC1 أعطى أعلى معامل لصفات معامل الشعر ، معدل الحليج ، عدد الأيــام حتــى تفتح أول زهرة ، قراءة الميكرونير ونسبة الانعكاس على التوالي. بينما العامــل الثــاني PC2 أعطى أعلى معامل لصفات الطول عند ٢.٥% ، الانتظام (%) والاستطالة (%). في حين أن العامل الثالث PC3 تأثر بصفات درجة الاصفرار ، نسبة الانعكاس ، عمر اللوزة، معامل البذرة ، ووزن اللوزة على التوالي.

٣ – أعطت المكونات الخمسة الأولى ٨١.٧% من التباين الكلى على مستوى جميع الــصفات بين أل ٦٦ تركيب وراثي (٦٠ هجين ثلاثي + ٦ أباء). وتلاحظ أن المكون الأول First PC axis قد أعطى أعلى قيمة للتباين الكلى ٣٦.٦% ثــم المكــون الثــاني ١٨.٧% والثالث ١١.٨% والرابع ٧.٥% والخامس ٧.١%.

٤- على أساس عدم التشابه Dissimilarity تم فصل التراكيب الوراثية إلى ٧ مجموعـات رئيسية وتلاحظ وقوع الآباء الأصلية الست في ٤ مجاميع مختلفة.

٥- تلاحظ أن الصنف جيزة ٨٦ كان أكثر تباعدا عن بقية الآباء حيث وقـع فـي مجموعـة منفصلة. في حين أن الأبوين جيزة ٨٨ ، بيماس، وقعا في مجموعة واحدة.

٦- وجد أن التهجين بين الآباء في المجاميع المتباعدة قد أعطت هجن ثلاثية تفوقـت علـى الآباء الأصلية لها في معظم صفات المحصول.