FACTOR ANALYSIS AND ITS RELATIONSHIP WITH GENETIC DIVERSITY IN COTTON.

M.E. Abd El-Salam, M.A. Al-Ameer and Y.M. El-Mansy
Cotton Research Institute, Agricultural Research Center, Egypt.

ABSTRACT: *The relationship between the biometrical methods depended on single trait and multivariate analysis of genotypes in breeding programs are very important. Therefore, this study was carried out to access factor analysis and diversity among 13 parents and 36 F_1 hybrids performance to evaluate 12 variables into separate groups at the Agricultural Research Station, Sakha, Kafr El-sheikh governorate, Egypt during 2008 and 2009 seasons. The analysis of variance revealed that highly significant genotypic differences for the most traits among parents and hybrids. Multivariate analysis reported that, the first factors which accounted for 70 % of the total variance are important. Factor 1, which accounted for about 25.3 % and it was associated with micronaire reading (mic), lint index (L.I.), lint percentage (L.P. %) and degree of yellowness (+ b). Factor 2, which accounted 17.3 % and it was associated with lint quality traits i.e., fiber length (F.L.), uniformity ratio (U.R. %) and lint color {yellowness} (+ b).*

The male parents Kar.2, Seuvin, G.75 and G.76 were grouped into 4 separate groups, these parents varied in general combining ability for the most traits. The female parents were also grouped into 4 different groups .Some of these were grouped with male parents in the same cluster showing nearly related and the other grouped in the same cluster.

Specific combining ability (S.C.A.) effect revealed that most of the combinations having high of (S.C.A.) effect were found between genetically diverse parents. The cross combination Kar.2 x (Pima S 6 x G.89) surpassed all crosses for earliness index and the common parents were distantly related .Also, not only the genetic divergence might be used choose parents for crossing, but also their performance of parents and the F_1. However, (G.C.A.) and (S.C.A.) effects are more informative than performance values.

Generally, the breeder can use the parents according to divergence with performance. Also, breeder might be evaluates characters to know the relative importance of such characters in genetic variability and divergence.

Kay Words *: Factor analysis, Combining ability, Genetic diversity, Cotton.*

INTRODUCTION

Genetic relationships among various genotypes can be measured by similarity of any number of quantitative characters, where characters are agronomic parameters of plant. In determining the potential of genetically different lines and cultivars, breeders have to observe among, many different

characters that influence yield. Accurate evaluation of those characters is made more difficult by genotypes x environment interaction. Thus multivariate technique which using factor analysis have analogous efficacy to determine the most suitable combination of characters Suinaga *et al,* (2005). Few research workers were studied factor analysis such as Walton (1972) who suggested factor analysis as a new technique to identify growth and plant characters as related to yield in spring wheat. Seyam *et al,* (1984) used factor analysis in determining traits that could be selected for high yield in cotton program. Tadess and Bekele (2001) indicated the selection of variable in factor 1 could enable breeder to better realize the desired increment in seed yield of grass pea.

Multivariate analysis of quantitative characters has been used previously to measure genetic relationships within cotton genotypes. Categorizing genotypes accession into morphological similar groups is most useful for analysis of cultivar variability (Cox *et al*, 1986), selection parents for hybrids (El-Lawendey *et al*, 2008, Abo El-Yazeid *et al*, 2009 and El-Mansy *et al*, 2010) and for predication of variances for some characters in the F_2 and inbred generations (Cowen and Frey 1987). However, (Hemada *et al*, 2006 and El-Mansy *et al*, 2008) used canonical analysis and principal components analysis respectively to create the genetic variability in some Egyptian cottons and estimate the relative importance of each character on total variability.

This study was undertaken in order to determine the dependence relationship between morphological characters of thirteen cotton parents and 36 hybrids using factors analysis. The study was extension to determine genetic divergence among cotton genotypes as related to general and specific combining ability to select the most suitable combinations and parents.

MATERIALS AND METHODS

Nine female parents comprising a broad range of Egyptian cottons and characters viz (Giza 77, Giza 80, Giza 81, Giza 85, Giza 86, Giza 88, Giza 89, promising cross (Giza 89 x Pima S 6) and (Giza 86 x Giza 89) and four genetically diverse male parents. These male parents have earliness, high seed cotton yield and high lint quality characters i.e., Karshenky 2 (Kar.2) as a Russian genotype, Seuvin as Indian genotype, Giza 75 and Giza 76 as Egyptian genotypes were crossed during 2008 growing season to generate a total of 36 hybrids.

These 36 hybrids along with 13 parents were grown in randomized block design with three replications at Agriculture Research Station, Sakha during 2009 season having 4.0 m plot length with spacing of 70 x 30 cm. Five competitive random plants were chosen from each replicate of each genotypes to record data on earliness index (E.I.), Lint yield per plant (L.Y./p.), boll weight (B.W.), lint percentage (L.P. %), lint index (L.I .), seed

index (S.I.), fiber length (F.L.), uniformity ratio (U.R.), fiber strength (Press.), micronaire reading (Mic.), lint reflectance { brightness} (R.D. %) and yellowness (+ b).

Data analysis followed three steps (i) fisher's analysis of variance, combining ability effects were computed following Singh and Chaudhry (1977). Heterozygous superiority was determined as the mean average of heterosis of F_1 over the mean average of their homozygous parents for each characters (ii) factor analysis as a multivariate analysis methods which aims to explain the correlation between a large set of variable in terms of a small number of underlying independent factors. It is assumed that each of the variables measures depends upon the underlying factors. The principal factor analysis method explained by Harman (1976) was followed in the extraction of the factor loading. The array of communality, the amount of the variance of a variable accounted by the common factor together, was estimated by the highest correlation coefficient in each array as suggested by Seiller and Stafford (1985). The factor loadings of the rotated matrix, the percentage variability explained by each factor and the communalities for each variable were determined. The third step (iii) clustering genotypes 13 parents and 36 hybrids into similarity groups using principal components coefficient according to principal component axis. All these computation were performed by using SPSS evaluation version 10.0 production mode facility and Minitab computer programs.

RESULTS AND DISCUSSION

The analysis of variance for 12 characters studied was presented in Table 1. It's revealed highly significant genotypic differences for all characters. Factorial analysis of population indicated significant differences among parents for all characters except for boll weight, seed index and Presley index. The female parents showed differences for majority of the characters.. The interaction between female and male parents was found to be significant for the characters *viz* lint yield per plant (L.P./P.), (F. L.), (U.R.), (mic.), (press.) and (+ b). Hybrids showed significant differences for most characters.

The previous results indicating that the experimental material possessed considerable amount of variability, while general and specific combining ability were involved in the genetic expression of these characters.

The magnitude of (S.C.A.) variances were greater than (G.C.A.) for the traits i.e., (L.Y./P.), (B.W.), (E.I.), (F.L.), (U.R.%) and (PRES.) , indicating that non additive type of interactions were higher among hybrids which could be exploited by heterosis breeding (Tuteja and Kumer, 2003 and Abo El-Yazied *et al*, 2009).

Multivariate analysis which used factor analysis was performed on 12 agronomic and fiber characters to determine which factor more effect on total variability than other, also to extract important component of variation in agronomic attributes and to obtain the initial factor solution using eigen value.

Table (1):

The results of factor analysis of 13 cotton parental and 36 hybrids for 12 variables are presented in Table 2. The total variance explained by factors showed that, only the first 4 factors which accounted for 70 % of the total variance are important. While the first two factors accounted for 42.6 % of the total variability. A principal factor matrix after orthogonal rotation for these four factors is given in Table 2 and Figure 1 and 2. The values in this table or loadings, indicate the contribution of each variable to the factor .For the purpose of interpretation only those factor loadings greater than 0.5 were considerable important.

Table (2): Proportion of variance explained by the under loading factor

| Variable	Factor1	Factor2	Factor3	Factor4	Communality
L.Y./p.	-0.490	-0.061	0.093	0.320	0.354
L.P.	-0.676	-0.410	0.368	-0.399	0.920
B.W.	-0.510	-0.206	-0.273	0.110	0.389
S.I.	-0.218	-0.083	-0.222	0.885	0.886
L.I.	-0.773	-0.431	0.203	0.213	0.870
E.I.	0.314	0.404	0.150	0.340	0.400
F.L.	0.418	-0.687	-0.473	-0.046	0.873
U.R.	0.250	-0.664	-0.553	0.095	0.818
MIC.	-0.783	-0.099	0.089	-0.091	0.640
Press.	-0.142	-0.044	-0.666	-0.302	0.556
R.D.%	-0.416	0.536	-0.623	-0.074	0.854
+ b	0.545	-0.547	0.494	0.081	0.847
Variance	3.042	2.081	1.945	1.339	8.408
Variance %	0.253	0.173	0.162	0.112	0.701
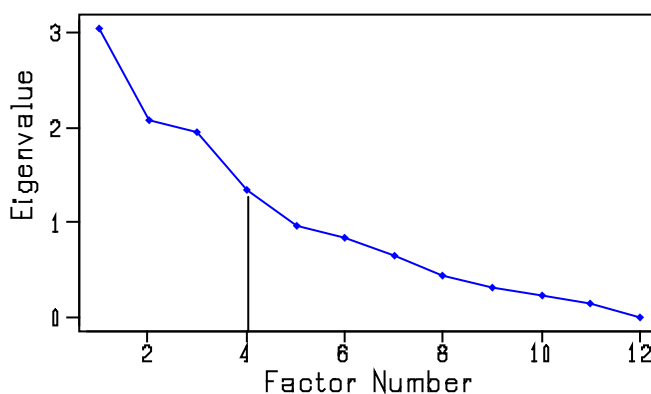
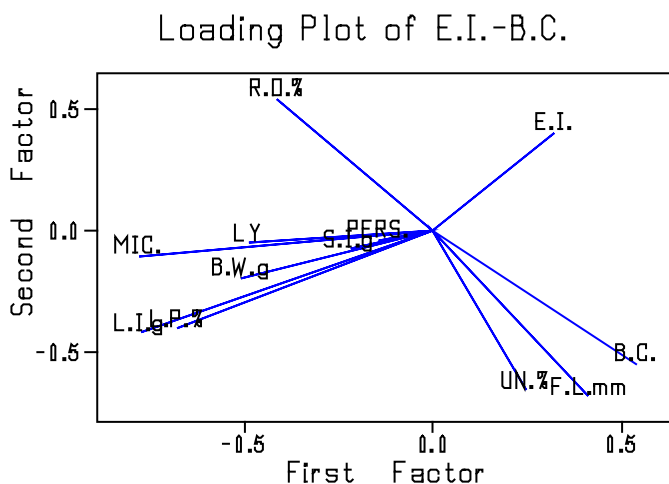Fig. 1. Scree plot of 12 characters on total variance.

Fig. 2. Loading plot of 12 characters in factor analysis.

Factor 1, which accounted for about 25.3% of total variation was strongly associated with micronaire reading (fiber fineness), lint index (L.I.), lint percentage (L.P. %), boll weight (B.W.) and degree of yellowness (+ b). This factor was affected by quality and yield components. All variable had negative loadings except degree of yellowness had positive loading. The significant of the loading indicates the direction of the relationship between the factor and the variable. Factor 2 which accounted for 17.3 % of the total variability was named lint quality factor since it consisted of most fiber quality characters i.e fiber length, uniformity ratio, degree of yellowness and reflectance {brightness}(RD%). Most of these variables had negative loading. The third factor was affected primary by lint quality characters and accounted about 16.2 % of variation. Factor 4 include 1 variable (weight factor) since it include seed index, and accounted for 11.2% of total variability.

It is great important to note that some characters may have great importance in determining plant phenotypic than other since each character was an important source of variation in one factors. Generally, the previous results reflected the importance of fiber quality characters in the total variability among the genotypes. However, yield components such as lint percentage, lint index, boll weight and seed index were more important also, in the variation among genotypes. Therefore, these traits can be using to screen different the genotypes in breeding programs. In this connection Cai *et al*, (1996), You *et al,* (1998) and El-Lawendey *et al,* (2008) found that lint index, lint percentage, micronaire reading and reflectance {brightness}(RD%)

was the primary source of variation on the first P.C. axis, while fiber properties were the largest affected in the second axis.

One based on the first and second factors variable and on the basis of dissimilarity coefficient between genotypes the 13 cotton parents were grouped into six major grouped (Fig. 3 and Fig. 4).

The two dimensional distance between genotypes might reflected at a summary of differences based on all characters. It is clear that the parental cotton genotypes were grouped on the factor according to which variable were more effecting. The second axis separated most genotypes which posses' variability's in fiber characters such as lint color and length lint. On the other hand, the first factor separated the other genotypes (yield components and fiber).

It is clear that the male parents viz Karshensky 2, Seuvin, G. 75 and G.76 were grouped into 4 separate groups. These parents varied in (G.C.A.) for most characters for example Kar.2 and G.76 were the best genotypes for micronaire reading, uniformity ratio and the latest was the best (G.C.A.) for pressly index only. On the other side, G75 and Seuvin were superior in yield characters. The female parents were also grouped into 4 different groups. Some of these were grouped with male parents in the same cluster showing nearly related and the other grouped in the same cluster. In this regard El-Lawendey *et al,* (2008) and Abdelsalam *et al,* (2010) classified some parental genotypes into varied groups based on principal components axis.
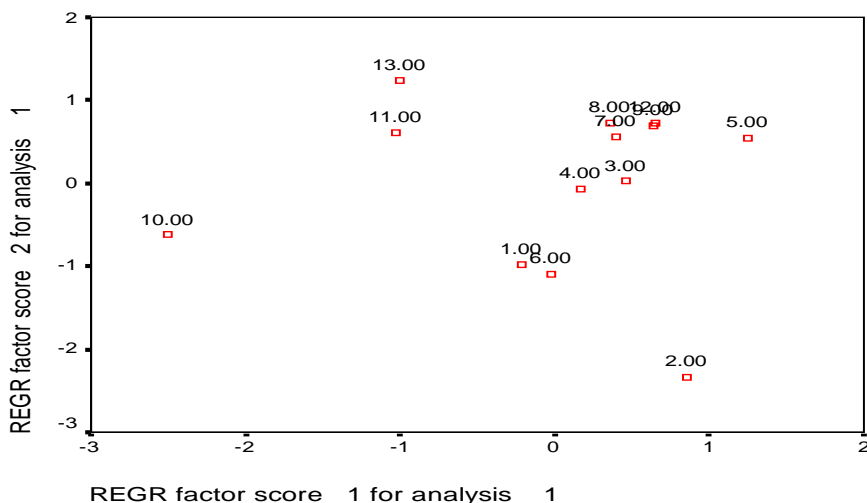
Females: (1-G.77   2- G.80 3- G.81 4- G.85 5- G.86 6- G.88 7- G.89   8- PimaxG.89   9- G.89xG.86)
Males   : (10- Karshensky 2   11- Seuvin 12- G.75 13- G.76)

Fig. 3. Principal axis factoring of 13 parental genotypes according to 12 variables on the first two factors.

Machado *et al,* **(2002), reported that in order to obtain the best combination, choose parents which have greatest genetic divergence, however not only the genetic divergence might be used to choose parent for crossing, but also their performance of parents and their F_1. However, (G.C.A.) and (S.C.A.) effects are more informative than performance values (Verma** *et al***, 2004 and Kumar and Patil, 2009).**

```
                         Fig. 4.
     Dendrogram using average linkage (within group)
                    showing the genetic
       relationship among the studied genotypes.


             Rescaled Distance Cluster Combine

     C A S E    0          5          10          15
                    20            25
  Label  Num    +---------+---------+---------+------
                  ---+---------+

            4    ò û ò ò ò ò ò ò ò ò ò ò ø
          7    ò ÷              ù ò ò ò ò ò ø
        3    ò û ò ò ò ò ò ø     ó           ó
          9    ò ÷       ù ò ò ò ÷
  ù ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ø
          5    ò ò ò ò ò ò ò ÷                   ó
                             ó
         12    ò ò ò ò ò ò ò ò ò ò ò ò ò ò ò ÷
                             ó
```

The 36 hybrids were grouped into 10 major groups according to principal factoring axis and the dissimilarities among these genotypes Fig.5. The hybrids were significantly differences among them. The diversity among the parental genotypes were reflected on the correspond F_1'S. In this regard Sandhu and Boparai (1997) reported that the progenies derived from diverse parents have exhibited abroad spectrum of divergence.

From Tables 3 and 4, it is clear that most hybrids which contained the Russian variety (Kar. 2) as a common parents formed a wide group distance while the cross combination G. 88 x Kar. 2 tend to be a unique group and more distantly related to the other hybrids, but it more related with the

Russian variety Kar.2. This combination surpassed the other hybrids for fiber length uniformity ratio and it was brown color. On the other side, the cross combination G. 81 x G. 75 also tended to be unique distantly group showing more divergence. This combination between two related parents and gave best values for pressley index ,but it was course fiber.
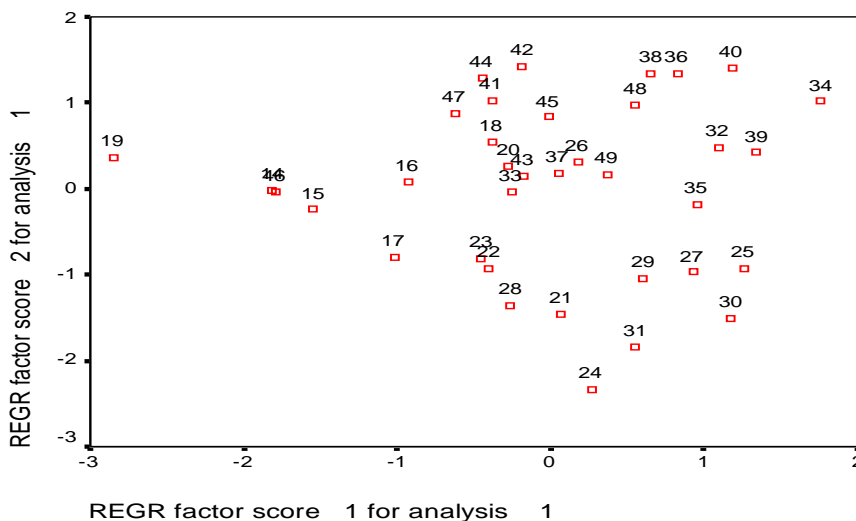

Fig. 5. Principal axis factoring of 36 hybrids according to 12 variables on the first two factors.

Table (3): Estimates of general combining ability (G.C.A.) effects of parental for all characters studied.

	Genotypes	L.Y./P.	L.P.%	B.W.	E.I.	S.I.	L.I.	F.L.	U.R.	MICRO	Pressly	R.D.%	+ b
Males	Kar. 2	-0.401	-0.960*	-0.186*	-0.631	-0.028	-0.269*	0.395*	0.471	-0.240*	-0.092	-2.450*	0.462*
	Seuvin	0.840*	-0.234	0.040	5.881*	0.543*	0.236*	-0.912*	-0.640*	0.101*	-0.188*	0.135*	0.107
	G.75	0.173	1.429*	0.088*	-3.594*	-0.239*	0.247*	-0.279*	-0.203	0.227*	0.134*	2.020*	-0.408*
	G.76	-0.612*	-0.234	0.058	-1.657	-0.276*	-0.214*	0.795*	0.371	-0.088*	0.145*	0.294	-0.160*
	L.S.D. 0.05	0.58	0.24	0.06	2.66	0.20	0.18	0.23	0.49	0.06	0.13	0.88	0.11
Females	G.77	-0.255	-0.20	0.19*	-2.721	0.017	-0.038	0.74*	0.19	-0.134*	-0.02	-0.73	0.498*
	G.80	0.120	0.87*	-0.15*	-3.955	-0.108	0.169	-0.05	0.14	0.024	-0.12	-2.94*	1.815*
	G.81	0.187	0.48*	0.16*	3.620	-0.058	0.094	-0.34	-0.04	0.041	0.10	-0.14	-0.719*
	G.85	-0.130	-0.16	-0.03	3.329	-0.483*	-0.320*	-0.70*	-0.63	-0.268*	-0.03	1.31	-0.419*
	G.86	-0.280	0.50*	0.04	-2.796	-0.158	0.058	0.13	-0.27	0.024	-0.10	1.76*	-0.702*
	G.88	0.054	-0.88*	0.01	-1.471	0.125	-0.161	1.34*	1.15*	-0.293*	-0.17	-2.32*	1.740*
	G.89	-0.305	-0.59*	-0.09*	-7.205*	-0.200	-0.272*	-0.61*	-0.76*	0.132*	0.05	1.00	-0.769*
	Pima S 6xG.89	0.345	-0.02	-0.06	7.254*	0.658*	0.362*	-0.19	-0.06	0.257*	0.44*	0.94	-0.677*
	G.89xG.86	0.262	0.00	-0.06	3.945	0.208	0.107	-0.31	0.28	0.216*	-0.15	1.11	-0.769*
	L.S.D. 0.05	0.87	0.36	0.09	3.99	0.30	0.19	0.35	0.73	0.09	0.19	1.32	0.17

* **Significant at 0.05 probability level.**

Table (4): Estimates of specific combining ability (S.C.A.) effects for all characters studied.

Hybrids	L.Y./P.	L.P.%	B.W.	E.I.	S.I.	L.I.	F.L.	U.R.	MIC.	Press.	R.D.%	+ b
G.77xKar.2	-0.55	-0.67	-0.20*	-6.62	0.19	-0.06	-0.10	-0.26	-0.14	0.22	0.44	-0.65*
G.77xSeuvin	-1.72	0.77*	-0.09	9.04*	-0.58	-0.12	0.55	0.01	0.02	-0.15	-3.11*	1.30*
G.77x G.75	1.24	0.17	0.26*	2.11	0.47	0.32	0.15	0.04	0.12	0.12	0.04	0.02
G.77x G.76	1.03	-0.27	0.03	-4.53	-0.09	-0.14	-0.60	0.20	0.00	-0.19	2.63	-0.66*
G.80xKar.2	1.04	0.53	0.04	-6.02	-0.18	0.02	1.13*	-0.25	0.13	-0.05	-0.75	0.76*
G.80xSeuvin	-1.00	-0.30	-0.05	7.27	0.02	-0.05	-2.23*	-0.98	-0.11	-0.19	-0.40	-0.35*
G.80x G.75	0.64	-0.66	-0.10	0.71	-0.27	-0.34	-0.13	0.65	-0.04	-0.38	-2.69*	-0.23
G.80x G.76	-0.68	0.43	0.10	-1.96	0.43	0.37	1.23*	0.58	0.01	0.61*	3.84*	-0.18
G.81xKar.2	0.14	-0.25	0.07	-0.19	-0.06	-0.11	0.52	1.03	-0.15	0.13	-2.42	-0.47*
G.81xSeuvin	0.64	0.49	-0.12	-0.91	-0.67*	-0.24	-0.80*	-1.69*	0.14	-0.08	1.86	0.19
G.81x G.75	-0.96	-0.14	0.03	4.80	0.35	0.17	-0.37	0.54	0.31*	0.73*	0.11	0.37*
G.81x G.76	0.19	-0.11	0.03	-3.70	0.38	0.19	0.65	0.13	-0.30*	-0.78*	0.44	-0.08
G.85x77xKar.2	-1.21	0.43	0.03	0.26	0.26	0.27	-0.79	-1.08	-0.24*	-0.41*	-0.93	0.16
G.85xSeuvin	-1.81*	0.37	-0.10	2.12	-0.31	-0.07	1.45*	1.66*	0.18*	0.25	1.41	-0.15
G.85x G.75	4.65*	-0.36	-0.01	-6.37	0.07	-0.07	-0.65	-1.77*	-0.18*	0.13	-0.60	0.07
G.85x G.76	-1.63	-0.43	0.08	3.99	-0.02	-0.12	-0.02	1.19	0.24*	0.02	0.12	-0.08
G.86xKar.2	-0.12	0.03	-0.01	4.49	-0.56	-0.31	-0.45	-1.84*	0.10	0.33	0.36	-0.12
G.86xSeuvin	0.34	0.17	0.27*	7.38	-0.33	-0.14	0.09	-0.86	0.02	-0.27	-0.79	0.10
G.86x G.75	-2.03*	0.44	-0.21*	-2.78	0.41	0.37	0.35	1.84*	-0.14	0.01	-0.15	0.32
G.86x4	1.82*	-0.63	-0.05	-9.09*	0.48	0.08	0.01	0.86	0.01	-0.07	0.58	-0.30
G.88xKar.2	-0.22	-0.36	-0.18*	-5.20	-0.18	-0.18	0.80*	2.54*	0.11	0.07	0.70	0.50*
G.88xSeuvin	0.07	-0.15	0.03	-8.45*	0.52	0.24	-0.55	0.35	0.24*	0.16	0.41	-0.71*
G.88x G.75	-1.16	0.62	0.21*	8.99*	0.00	0.15	0.25	-1.76*	-0.19*	-0.33	1.13	-0.43*
G.88x G.76	1.32	-0.12	-0.06	4.66	-0.33	-0.21	-0.50	-1.13	-0.17	0.10	-2.24	0.63*
G.89xKar.2	0.80	0.32	0.12	-1.57	0.04	0.11	-0.48	-0.09	0.19*	0.15	1.65	-0.29
G.89xSeuvin	0.33	0.03	0.16	3.55	0.41	0.23	0.70*	-0.44	-0.42*	0.18	0.80	0.14
G.89x G.75	-0.31	0.03	-0.12	-2.11	-0.21	-0.13	0.33	0.99	0.16	-0.18	-0.72	-0.35*
G.89x G.76	-0.82	-0.37	-0.16	0.12	-0.24	-0.21	-0.55	-0.45	0.07	-0.15	-1.73	0.50*
(P x G.89) xKar.2	0.82	0.02	0.13	12.34*	-0.08	-0.05	-0.73*	-0.19	0.03	-0.44*	1.08	0.25
(P x G.89)xSeuvin	0.04	-0.54	-0.16	-13.67*	0.52	0.13	-0.19	0.12	-0.04	0.19	0.29	-0.39*
(P x G.89)xG.75	-1.22	-0.34	-0.15	-3.46	0.00	-0.07	0.41	-0.41	0.06	-0.17	0.54	0.26
(P x G.89)x4	0.36	0.86*	0.18*	4.80	-0.43	-0.02	0.50	0.48	-0.05	0.42*	-1.90	-0.12
(G.86x G.89)xKar.2	-0.70	-0.04	-0.01	2.51	0.57	0.31	0.09	0.15	-0.03	0.01	-0.13	-0.15
(G.86x G.89) xSeuvin	3.13*	-0.83*	0.07	-6.33	0.43	0.03	1.00*	1.82*	-0.03	-0.10	-0.48	-0.13
(G.86x G.89) xG.75	-0.84	0.24	0.09	-1.89	-0.82*	-0.41*	-0.34	-0.11	-0.13	0.05	2.34	-0.02
(G.86x G.89) xG.76	-1.59	0.63	-0.15	5.71	-0.18	0.07	-0.75*	-1.85*	0.19*	0.04	-1.74	0.30
L.S.D. 0.05	1.75	0.72	0.18	8.00	0.60	0.39	0.70	1.46	0.18	0.39	2.65	0.34

* Significant at 0.05 probability level.

On the basis of (S.C.A.) effect revealed that most of the combination having high (S.C.A.) effects were between genetically diverse parents (El-Mansy *et al,* 2008). For example the cross combination Kar. 2 x (Pima S 6 x G. 89) surpassed all crosses for earliness index and the common parents were distantly related. However the combination Kar.2 x G. 88, Kar. 2 x G. 80 and G. 76 x G. 80 were given high (S.C.A.) effects for fiber length. Regarding to Lint yield/p the combinations G. 75 x G. 85 and Seuvin x (G. 86 x G. 89) gave the best values. No combinations were surpassed in all yield characters.

The most combinations which had good specific combining ability were having one or two parents of either good x good or good x poor general combiner. Therefore, the performance region of F_1' may be different with the regions of original parents, so this difference is due to complementary between the genes in F_1 generation. The previous results showed that the

most groups in F_1 correlated with the male parental, this was agreement with the relative percentage of contributions for most characters. Male contributions showed great important specially for lint index, lint percentage, seed index and fiber length, so these traits were very important for factor loading communality i.e. 0.87, 0.92, 0.89 and 0.873 respectively for the previous traits (Table 2).

Table 5 gave average parental and hybrid means and number of crosses deviating from mid-parents and better parent for different characters studied. $\overline{F_1}$ was more than $\overline{P}$ for some characters. The magnitude of mid-parent heterosis exhibited by the different characters was variable and being highest for fiber length and micronaire. Such characters were important in factor analysis for grouping various genotypes in different clusters.

The 36 F_1 hybrids were classified into 9 groups on the basis of their performance and similarity between characters. The distribution pattern of the F_1 heterozygous was more or less influenced by their parents as expected on the basis of close affinity between the parents and their F_1 progenies. It is interesting to note that most of F_1 hybrids were segregating around the parents P1, P3, P4, P6, P7, P8, P9, P11, and P12. This result suggested that these parents might involve dominant genes controlling the characters which effecting divergence.

However, the parents P2, P5, P10 and P13 was more widely divergent than all the other genotypes (Fig.3) indicating that these parents might possess different gene complex probably of recessive action governing the same characters.

Table (5): Average parental and hybrid means and number of crosses deviating from mid (M.P.) and better parents (B.P.) for different characters in cotton.

Characters	$\overline{P}$	$\overline{F1}$	< M.P	= M.P	MP <	BP<	>MP
Earliness	48.21	44.538	25	Zero	11	Zero	11
Lint yield	6.287	6.638	11	Zero	6	19	25
Boll weight	2.6	2.756	6	2	6	22	28
Lint percentage	37.323	36.531	16	Zero	17	3	20
Lint index	6.187	6.171	13	Zero	16	7	23
Seed index	10.351	10.717	10	1	5	20	25
Fiber length	33.036	33.927	5	Zero	13	18	31
Uniformity ratio	88.208	89.07	9	Zero	6	21	27
Micronaire	4.277	4.251	6	Zero	26	4	30
Pressely	9.726	9.695	17	Zero	9	12	21
b +	9.877	9.681	15	Zero	6	15	21
R.D.%	70.513	71.269	20	Zero	11	5	16

From the present study, it could be concluded that the performance of parents does not seem to be an index of (G.C.A.) effects in the material. However, good combiner parents for different character can be used for conventional breeding programs. However, both additive and non additive variance is important. Thus, recurrent selection approach would be

appropriate for improvement of such characters. This can be achieved by adopting biparental mating in F_2 among selected crosses (Ramaligeim and Sivasamy 2003).

In the same time the breeder can used the parents according to their divergence with performance. Also, breeder might be evaluated characters to know relative importance of such characters in genetic variability and divergence.

REFERENCES

Abdelsalam, M. E., Y. M. EL-Mansy and Rokia, M. Hassan (2010). The relative importance of characters affecting genetic divergence in cotton. J. Agric. Res. Kafr EL-Sheikh, Univ., Vol. 36, No. (1) 44 - 63.

Abou EL-Yazied, M. A., H.M. Hamoud and M.A. Abd EL-Gelil (2009). Hybrid performance as related parental diversity in cotton .Egypt J. Appl. Sci.,24(1)240-253.

Agrobase /4 Complete System Analysis Software computer program, Version 1.3b to be used , Serial Number : ICA- 94-003 For Plant Breeders and Agronomists Copyright (©) 1990, 1991, 1992, 1993 by Agronomix Software, Inc. Portage La Prairie, Manitoba, Canada.

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 characters of short season cotton .J. Southwest, Agric. Univ. 18(4) 346-349 .

Cowen. N.M. and K.J. Frey (1987). relationships between three measures of genetic distance and breeding behaviour in oat .Genome (29) 97-106 .

Cox, T.S., Y. T. Kiang, M. B. Gorman and D. M. Rodyers (1985). Genetic relationships among hard red winter Wheat Cultivar as evaluated by pedigree analysis. Crop. Sci. (25) 1058-1063.

EL-Lawendey, M.M., Y. M. EL –Mansy and .Y.A. Soliman (2008). Multivariate analysis of some economic characters in cotton . Minufia, J. Agric. Res. 33(4) 955-972.

EL-Mansy, Y.M.; M.M. EL-Lawendy and M. E. Abdelsalam(2008). Enferior lint quality as a results of off types cotton plants existence in some Egyptian cotton varieties. J. Agric. Res. Kafr EL-Sheikh, Univ., Vol. 34 No. (1)43-53.

EL-Mansy, Y. M., R.M. Hassan and M. E. Abdelsalam (2010) Estimation of genetic components and genetic divergence in diallel hybrids of cotton. J. Agric. Res. EL-Sheikh Univ. Vol. 36, No. (1) 17-32.

Hair, J. F., R.E. Anderson and R. L. Tatham (1987). Multivariate Data Analysis with Reading. MacMillan Pub Co., New York

Harman, H. H. (1976). Modern Factor Analysis ,3nd Ed.Univ.of Chicago Press Chicago.

Kumar, K.J. and R.S. Patil (2009). Genetic analysis of yield components, seed oil and fiber quality traits in cotton. Karnta J. Agric. Sci., 22(2);428-432.

Machado, C.F., G.H. Nunes and D.F. Ferreira (2002). Genetic divergence entra genotypes by using Multivariate technique. Cienciu Rural;32(2)251-258.

Ramalingam, A. and N. Sivasamy (2003). Genetics and order effects of boll number per plant and boll weight in Upland cotton. Madras Agric. J. 90(7):472-477.

Sandhu, B. S. and M.S. Boparai (1997). Genetic divergence in G. arborium3 L. Indian J. Genet. PL. Breed. 57(4) 461 - 465

Seiller, G. J. and R. E. Stafford (1985). Factor analysis of components in Guar. Crop Sci. 25,905-908.

Seyam, S. M., A. A. AboEL-Zahab, F. M. ELRayes and H.N. EL-Rassas (1984). Factor analysis of yield in Egyptian cotton. Agric., Res., Rev., 62(6) 33-40

Singh, R. B. and B. D. Chaudhary (1977). Biometrical Methods in Quantitative Genetic Analysis .Pup New Delhi.

SPSS (1995). SPSS version 10 for Windows a Computer Program Users Guide spss, USA.

Suinaga, F. A., E. C. Freire, C.S. Bastos and L.E.P. Rangel (2005). Multivariate Analysis of Genetic Divergence in Cotton. Revisita Brasileira de Algadeo.

Tadess, W. and E. Bekele (2001). Factor analysis of components of yield in grass pea .Lathyrws Lathyrism.Newaletter.2.91-93.

Tuteja, O. P. Luthra and S. Kumar(2003). Combining ability in Upland cotton (*G. hirsutum*) for yield and its components. Indian J. Agric., Sci., 73(12):671-675.

Verma, S.K., S. L. Ahuja, O.P. Tuteja and D. Monga (2004). Line x tester analysis of yield ,its components and fiber quality traits in cotton . J. India Soc. cotton Improv., 29,151-157.

Walton, P.D. (1972). Factor analysis of yield in spring wheat. Crop Sci. 12, 731-733 .

You, J., J. Liu and J. Z. Sun (1998). Analysis of heterosis and its Components in interspecific crosses between Upland Cotton and breeding lines. Acta. Agron .Sinica 24(6) 834-839.

التحليل العاملى وعلاقته بالتباعد الوراثي في القطن

محمد عزت عبد السلام ، محمد عبد المولى الأمير و ياسر محمد المنسي

معهد بحوث القطن – مركز البحوث الزراعية – مصر

الملخص العربي:

دراسة العلاقة ما بين الطرق الاحصائية التي تعتمد على الصفات الفردية والطرق الاحصائية الأخرى التي تُقيم التراكيب الوراثية على أساس جميع الصفات هدف مهم في برامج التربية.

لذلك أُجري هذا البحث بغرض دراسة العلاقة بين التحليل العاملي والتباعد الوراثي وكذلك المكونات الوراثية لعدد ثلاثة عشر أبا هي جيزة ٧٥ ، جيزة ٧٦ ، جيزة ٧٧ ، جيزة ٨٠ ، جيزة ٨١ ، جيزة ٨٥ ، جيزة ٨٦ ، جيزة ٨٨ ، جيزة ٨٩ ، (الهجين المبشر بيما س ٦ X جيزة ٨٩) ،(الهجين المبشر جيزة ٨٦ X جيزة ٨٩) ، كارشنسكى ٢ و سيوفين و ستة وثلاثين هجيناً لإثنتى عشرة صفة محصولية وتيلة. وقد أُجريت الدراسة في محطة البحوث الزراعية بسخا – كفر الشيخ – مصر خلال الموسمين الزراعيين ٢٠٠٨ و ٢٠٠٩.

وأظهرت نتائج تحليل التباين معنوية ما بين الأباء والهجن فى معظم الصفات المدروسة. كما أظهر التحليل العاملي أن الأربعة عوامل الأولى اشتملت على حوالي ٧٠ % من التباين الكلى وكان العامل الأول ١ يمثل ٢٥.٣ % وكانت أهم الصفات هى قيمة الميكرونير (نعومة التيلة)، معامل الشعر، معدل الحليج و قياسات اللون التي تشمل درجة الإصفرار ودرجة الإنعكاس (R.D.%, + b) في حين احتل العامل الثاني ٢ على ١٧.٣ % وكان مرتبطاً بصفات التيلة.

كما اتضح من الدراسة أيضاً أن الآباء (Males) كارشنسكى ٢ ، سيوفين ، جيزة ٧٥ و جيزة ٧٦ كانت مُقسمة إلى أربع مجموعات مُنفصلة وكانت تلك الآباء مختلفة في القدرة العامة على التآلف لمعظم الصفات المدروسة وأيضاً اختلفت الأمهات (Females) إلى أربع مجموعات منفصلة.

كما اتضح من دراسة القدرة الخاصة على التآلف أن معظم الهجن ذات القدرة الخاصة العالية كانت بين الآباء ذات التباعد الوراثي عن بعضها البعض على سبيل المثال الهجين كارشنسكى ٢ x (بيما س ٦ x جيزة ٨٩) أظهر قدرة خاصة على التآلف عالية في التبكير.

كما اتضح من النتائج أنه يجب استخدام مقاييس التباعد الوراثي مع أداء الآباء و الجيل الأول (F₁) لتقييم الآباء .

كما أظهرت الدراسة أيضاً أهمية استخدام مقاييس القدرة العامة و القدرة الخاصة على التآلف حيث كان أكثر أهمية من أداء الآباء منفرداً.

وعموما فإنه يجب على المربى استخدام التباعد الوراثي مع أداء التراكيب الوراثية و تقييم الصفات لمعرفة العلاقة بينهم في دراسة الاختلافات الوراثية والتباعد الوراثي.

Table (1): Mean squares estimates for all the characters studied.

S.O.V.	d.f.	L.Y./P.	L.P.%	B.W.	S.I.	L.I.	E.I.	F.L.	U.R.	MIC.	PRESS.	R.D.%	+ b
Replications	2	24.62**	2.26	0.26**	2.12*	0.61	667.78**	7.74**	61.52**	0.24**	0.13	28.00	1.74**
Genotypes	48	7.79*	8.94**	0.12**	0.97**	0.67**	260.89**	6.07**	5.69**	0.46**	0.37*	29.54**	4.93**
Parents	12	10.71*	23.23**	0.06	0.54	1.38**	423.96**	9.46**	6.05*	0.99**	0.24	51.14**	7.79**
Hybrids	35	6.92	3.79**	0.12**	1.03**	0.44**	201.40**	4.09**	5.12*	0.29**	0.42*	22.51**	4.08**
Parent vs Hybrids	1	3.53	18.00**	0.70**	3.83**	0.01	386.41*	34.59**	21.46*	0.02	0.06	16.36	0.27
Males	8	0.74	3.64**	0.16**	1.21*	0.58	265.96**	5.22**	3.76	0.46**	0.42	33.68**	14.09**
Females	3	11.44	27.66**	0.43**	3.86**	2.12**	455.72*	15.29**	7.29	1.14**	0.75*	91.70**	3.76**
Males X Females	24	8.41*	0.85**	0.07	0.62	0.18	148.09	2.31**	5.30*	0.12**	0.37*	10.13	0.78**
Error	96	4.57	0.79	0.05	0.55	0.23	95.41	0.74	3.21	0.05	0.23	10.51	0.18
k^2 GCA		-0.114	0.210	-0.004	0.024	0.012	4.372	0.130	-0.014	0.004	-0.004	0.950	0.258
k^2 SCA		1.281	0.022	0.008	0.025	-0.015	17.557	0.522	0.696	0.023	0.049	-0.124	0.202

*,** Significant and highly Significant at 0.05 and 0.01 probability levels respectively