USING STABILITY PARAMETERS AND VARIANCE COMPONENTS FOR SELECTION GENOTYPES UNDER DIFFERENT ENVIRONMENTAL CONDITIONS IN EGYPTIAN COTTON.

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ABSTRACT

Plant breeder use yield traits to identify promising genotypes. This goal depends the magnitudes of genotype by environments and stability performance of genotypes. Therefore, twenty Egyptian extra long genotypes were grown in three locations under two years for yield, yield components earliness and fiber traits to identify promising stability genotypes. The genotype x environment interaction was significant for yield and fiber traits. It also noticed that variation due genotype x environment were further partitioned into linear and non-linear components. Genotype x environment linear was insignificant for all studied traits except for MC trait, insignificant of genotype x environment linear indicated that genotypes didn't differ genetically in their response to different environments. Pooled deviation mean squares were significant for all studied traits , indicated that the major components for differences in stability were due to deviation from the linear function. Therefore, it could be concluded that the relatively unpredictable components of the interaction maybe more important than the predictable components.

The results illustrated that lines 3, 5 and 15 were stable for seed cotton yield (x = high, b =1 and s^2d =0).While, the line (7) has high mean performance and regression coefficient equal to one but the deviation from regression was larger than zero. However, for lint percentage, some lines has high mean performances over grand mean (2, 3, 7, 8,9,12 and 14) but these lines did not parallelism with the stability parameters. Therefore, the best performing, highest value in this trait or genotypes was not necessary. The best stable genotype for fiber length is 2, 10, 11 and 12 when had mean performances same the check variety (Giza 70) and regression coefficient (bi)was equal unity for all genotypes and deviation from regression was significant differ from zero The best genotypes according to these criteria (three indexes) are also identified in this when selection based on mean yield a lone when have yield ranks of one because all lines were similar for mean performance for yield due to low variability of these material (Extra long staple) while , selection based on index3 the top lines were 1, 3,5,6,9,11,15and16. Using principal components analysis to selection the better stability lines to comparison regression model, the results shown that the percentage contribution of PCA components of seed cotton yield. Each PAC1and PCA2 were more important. In addition results show that the strains 1and 3 which PCA1 equal unity and PCA2 equal zero. The two strains were stable by using regression model (x=high=1 and s^2=0).On the other hand, lines 5 and 15 were stable by using regression model but the values of PCA equal zero and PCA2 close to unity. Therefore, using the two models to identify promising genotypes stability in cotton breeding programs is very useful.
Keywords: Stability, Interaction, Selection and Cotton.

INTRODUCTION

Cotton is one of the oldest fiber crops. Four species of the genus Gossypium have contributed to a great demand for modern cultivated cotton. Upland cotton (*Gossypium hirsutum*, L.) and Egyptian cotton (*Gossypium barbadense*, L.) account for more than 99 percent of the world supply of raw cotton for factory use. The *Gossypium barbadense*, L. produced high fiber characters

Due to its importance, plant breeders have been working for improving its yield and quality. Consequently, they achieved a great success in this respect through the evaluation of varieties having high yield and better qualities. Hybridization program requires selection of bendable parental lines to be used to produce genetically modified and potentially rewarding germplasm with collection of fixable gene effects relatively in a homozygous line. Cotton is one of the most important fiber crops of the world and is likely to enjoy this advantage in the future in Egypt, cotton is important for both export and local textile industry . Now, cotton area is low and decrease from year to year in Egypt , because environmental conditions vary from one environment to another . Cotton as other filed crops is greatly influenced by seasons, location and any changes for growth environments .Therefore genotype x environments interaction (GE) are a continuing challenge to plant breeders because of the complications they cause in selecting genotypes evaluated in divers' environments. Plant breeder's use yield traits to identify promising genotypes and agronomists use a recommendation for farmers. The level of success in meeting these goals depends critically on two factors (1) the accuracy of yield estimates and (2) the magnitudes of genotype by environments (Gauch, 1988).

The GE interaction reduced the correlation between phenotypic and genotypic values and has been shown to reduce progress from selection Comstock and Moll, (1963). When GE interaction is presence estimates of genetic parameters such as heritability and genetic correlation may vary (Larsson *et al* 1997). Therefore, evolution and stability parameters for genotypes under different environment are very important especially in breeding programs. The gene expression for most cotton traits changes under different environments. Screening of genotypes for stability under varying environmental conditions has thus becomes as essential part of modern breeding program Falconer (1960) and Gill and Singh (1982). Stability of a lines and cultivar refers to its consistency of in performance a cross environments, which is a affected by the presence of genotype x environment interaction stability parameters were estimated to determine the superiority of individual genotypes a cross the range of environments. Finaly and Wilkinson (1963) used the slop of the regression line (b) to estimate stability and adaptability for several genotypes. While, Eberhart and Russel (1966) suggested that it should refer to the deviation from regression (S^2d). Lin *et al.*, 1986 reported that a particular genotype may be considered to be stable if it's among environments variance is small. Studies on stability parameters for comparing Egyptian Cotton Cultivars and lines were made by

several workers i.e. EL-Marakby *et al* ., (1986) , Shofshak *et al*., 1993, EL-Shishtawy *et al*. , 1994, Bader 1999 , Abdel-Hafez *et al*., 2000 and Shaker 2009 .

Therefore, the main objectives of this investigation were to estimate the stability parameters for 14 lines in addition to six check varieties in order to select the best lines (high yield, high fiber properties and stable) with check varieties to using in general farm.

MATERIALS AND METHODS

The experiments were carried out under three locations (Kafre el Sheikh, Damieta and El baheria Govern.) over two growing seasons 2007and 2008, to evaluating 14 lines and six check varieties. The Characterization and Pedigree of lines and Check varieties in this investigation are presented in Table 1:

Data were recorded to many traits as follows:

1- Seed cotton yield per fed. (S.C.Y.), lint percentage (L. %), Boll weight (B.W.) in gram. and earliness index. (E. I.) .

2- Fiber properties i.e., micronair reading (M.C.), Fiber length (2.5% span length) elongation.

Hair – weight in terms of millitex (10^{-8}g/cm) (FIN) and Yarn strength (STR.) is product lea strength x Yarn count" by The Good Brand Tester.

Table (1): Pedigree of genotypes used in this study.

Number	Genotypes	Origin
1	F.5 1141/2005	{ G.87 x (G.77x G.70)} x)G.45 x Sea Iland)
2	F.5 1145/2005	{ G.87 x (G.77x G.70)} x)G.45 x Sea Iland)
3	F.5 1200/2005	G.87 x G. 92
4	F.5 1215/2005	G.87 x G. 92
5	F.5 1224/2005	G.87 x G.92
6	F.5 1243/2005	G.88 x G. 92
7	F.5 1250/2005	G.88 x G.92
8	F.5 1264/2005	G.88 x G. 92
9	F.6 1272/2005	G.87 x (G.74 x Sea Iland)
10	F.6 1286/2005	G.87 x (G.45 x Sea Iland)
11	F.6 1304/2005	(G.84 x G. 45) x Pima62
12	F.7 1387/2005	{ G.84 x (G.70 x G.51 B) } x Pima 62
13	F.7 1396/2005	{ G.84 x (G.70 x G.51 B) } x Pima 62
14	F.8 1415/2005	G.45 x { G.84 x (G.70 x G.51 B)}
15	G. 92	(G. 84 x G. 74) x G. 62
16	G.77 x Pima S6	G.77 x Pima S6
17	G.87	G.77 x G.45 (A)
18	G.88	G.77 x G.45 (B)
19	G.45	G.28 x G.7
20	G.70	G.59 A x G.51 B

Analysis of variance for randomized complete blocks design was made according to Snedecor and Cochran (1961) for each environment. The combined analysis of variances was calculated for 20 genotypes under three locations over two years according to Le Clerg *et al*., (1962). The analysis of

variance and estimates of it is components were partitioned to genotypes (σ^2 g) and it is interactions with environmental conditions. Variance components were used to estimate the broad sense heritability ($h_b^2\%$) phenotypic (PCV) and genotypic (GCV) coefficients of variability.

Stability parameters:

The statistical analysis for stability was done according to Eberhart and Russell (1966), parameters of regression coefficient (bi) and mean squares of deviation from regression (s^2d) for each variety. A coefficient of determination (r^2) was suggested by Pinthus (1973).

To combine the estimate of yield and stability, rank index was used. Ranks were assigned for mean yield with the genotype giving the significant highest yield receiving the rank of 1, ranks were assigned for (s^2d) with the insignificant estimated value receiving the rank of 1. And also, ranks were assigned for b the lower value than unity receiving the rank of 1.

Three indices were calculated.

1- Index (1) was derived from the sum of yield rank and b rank.

2- Index (2) from the sum of yield rank and s^2d- rank.

3- index (3) from the sum of yield rank, b - rank and s^2d-rank according to Kang (1988).

Multivariate technique were conducted by using principal components analysis and cluster according Haire *et al.*, (1987) and Anderberg (1973) all these computations were performed using SPSS (1995) .

RESULTS AND DISCUSSION

The results in Table 2 revealed that differences among genotypes and environments which were significant for all traits for 14 lines and 6 check varieties under different environments except for strength of genotypes B.W., F.L., FIN, This finding revealed that the presence of a variability among genotypes included in this study for yield, yield components and micronair reading.

Mean performance for 14 lines and six check verities in Table 3 reveled that all lines were close to the best chick variety (G.88) but , there are some lines were high in mean performance for seed cotton yield i.e. 2, 5, 7 and 12 compared to all check varieties. The any increase for a seed cotton yield especially from extra long staple lines in Egyptian cotton verities are very important and necessary because there are negative linkage between fiber traits and cotton yield ,.although some new verities are high fiber quality and medium seed cotton yield i.e. G. 88 and G.92 . Breeding for improvement quantitative characters are very difficult, therefore, selection and evaluation of new lines under different environment are very important to help us for choosing available environment to cultivation the new varieties as well as helping the cotton breeder to correct selection for any new varieties.One line (1415/2005) were higher lint percentage than best check variety and some lines were higher than grand mean (i-e, 2, 3, 7, 8, 9 and 12)while for fiber length all lines were similar with best check varieties.

Table 2: Mean square for yield and lint quality characters for all genotype grown at different environmental conditions

S.O.V.	df	B.W.	S.C.Y./P.	L%	EI	FL	MC	FIN	STF	STR
ENV	5	0.181**	261.3**	49.6**	99.19	24.26**	5.743**	8664**	133.8**	7E+05**
Error (a)	18	0.052	5.760	4.25	1886	0.012	0.008	3.769	0.113	2218
G	19	0.079	5.745*	30.29**	296.1**	3.148	0.783**	5.69	17.41	87346
G*E	95	0.064**	3.355**	6.257**	114**	3.606**	0.267**	207.5**	15.52**	60671**
Env. Linear	1	0.026	1306.368**	991.424**	49596.64	119.696	29.428	43318.12	668.828	3582896
G*Env.(Linear)	19	0.0732	4.328	17.504	61.896	0.7392	1.7**	241.276	11.8444	47224.8
Pooled Dev.	80	0.058	2.956	25.552**	121.32	4.1336	0.2768**	189.08**	15.6224**	60831.2**
Error(b)	342	0.037	1.547	0.323	54.19	0.025	0.009	2.851	0.093	1886
Poold error	360	0.038	1.757	0.519	145.8	0.024	0.009	2.897	0.094	1902

B.W.: boll weight, S.C.Y. : Seed cotton yield , L. %: lint percent , E...I.: Earliness index, F.L.: fiber length at 2.5%, M.C. Micronair reading, FIN: fiber fineness, STF. : Fiber strength and STR; yarn strength.

Table 3: Meanperformance of 20 genotypes over environments for studied traits.

Genotypes	B.W	S.C.Y./P.	L%	EI	FL	MC	FIN	STF	STR
1	2.99	9.18	34.35	63.49	35.79	3.70	132.50	50.27	3306.3
2	3.00	9.30	36.03	64.07	36.13	3.86	134.67	47.79	3277.5
3	3.05	9.14	35.65	60.07	35.50	3.70	131.75	48.47	3190.8
4	3.01	9.02	35.03	59.38	34.98	3.55	128.67	50.31	3225.4
5	3.00	9.28	33.15	69.38	35.83	3.37	123.50	49.06	3253.3
6	3.04	8.56	33.71	71.50	35.91	3.40	123.33	48.86	3266.3
7	2.97	9.24	35.67	65.83	35.96	3.76	131.21	49.35	3317.5
8	2.94	8.77	35.84	64.78	36.10	3.70	132.46	50.14	3339.2
9	3.06	8.85	35.91	60.38	35.70	3.59	132.00	49.07	3208.8
10	3.03	8.97	34.11	60.88	36.10	3.57	133.33	48.87	3224.2
11	3.21	8.21	34.36	64.78	36.39	3.47	127.67	49.58	3348.8
12	3.00	9.12	36.34	63.13	36.35	3.56	130.42	49.01	3277.5
13	3.06	8.87	35.76	62.55	35.18	3.66	128.88	47.98	3133.3
14	3.06	9.20	37.80	60.25	36.08	3.63	131.17	49.91	3266.7
15	3.08	9.12	35.50	67.06	35.79	3.27	124.88	48.00	3213.3
16	3.07	8.80	35.35	67.80	35.58	3.33	120.17	49.06	3179.6
17	3.07	8.43	33.68	60.71	35.93	3.22	117.63	48.63	3283.6
18	3.06	8.88	36.66	63.24	35.65	3.85	135.00	49.86	3287.5
19	3.01	7.34	35.25	61.63	35.46	3.58	133.67	47.43	3140.0
20	2.99	8.09	35.46	58.27	36.10	3.63	130.08	48.17	3223.3
LSD.05	-	0.706	0.32	4.17	-	.05	-	-	-

B.W. , FL, FIN, STF and STR : These traits showed non significant differences among genotypes .

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There are some lines were higher fiber strength than the check variety (G.77 x Pima S6) i-e, 4, 7, 8 ,11 and 13 while ,the lines i-e 7, 8, 11, were the highest in Yarn strength. The pervious results reported that there are some lines are mean performed for strength similar to check variety (G.88) with high seed cotton yield i-e, 1, 2, 7, 14 and 15. Therefore, these lines considered the promising lines and able to cultivate in general cultivation.

Estimation of variance components, heritability in broad sense, phenotypic and genotypic coefficient of variability for yield and fiber properties are presented in Table 4, The results indicated that the genotypes behavior affected by different environmental conditions. This affect of environments appeared on heritability values estimates for these traits which were low 16.2, 35.9, 7.2 and 22.9 for B.W., S.C.Y., S.T.F., and S.T.R., respectively. Heritability and genetic variation would give the best indication of the amount of genetic variance to be expected from selection (Burton 1952). Therefore, estimation of these parameters under different environments is very important for breeding programs. Also, mean squares were partitioned to environments and their interaction with genotypes. High heritability of lint percentage, earliness index and micronair reading indicating that the phenotypic expression of these traits was indicated of their genetic behavior. While, low heritability for the rest traits indicated that these material are similar of performance, the similarity due to the Egyptian cotton breeder for breeding programs maintenance of limit level of fiber traits for the selection. Therefore, the low variability between the produced lines was observed programs. F or most fiber traits, the genotype by environments interaction was high indicated that these genotypes differed in their performance under different environments. Falconer (1960). suggested that a character measured in two different environments could be regarded not as one character but as two. Therefore, the evolution of new strains in breeding programs in early generation is very important to correct selection for any promising strains.

Table 4: The variance components, heritability, Phenotypic and genotypic of variation for all studied traits.

Prameters	B.W	SCY	L%	EI%	FL	MC	FIN	STF	STR
SP	0.00385	0.23	1.386	13.59	0.21	0.038	27.97	1.05	4864
SG	0.00063	0.10	1.001	7.567	-0.02	0.022	15.06	0.08	1111
$H^2 b$	16.2162	35.9	72.26	55.66	-	56.58	53.85	7.52	22.85
PCV	-	0.15	3.34	5.81	1.28	5.46	4.10	2.09	2.15
GCV		0.10	2.83	3.60	-	4.15	3.01	0.58	1.03

B.W.: boll weight, S.C.Y. : Seed cotton yield   , L. %: lint percent , E...I.: Earliness index, F.L.: fiber length at 2.5%,   M.C. Micronair reading, FIN: fiber fineness, STF. : Fiber strength and STR; yarn strength.

Table 2 cleared that the genotype x environment interaction was significant for yield and fiber traits. If the G X E interaction components were larger relative to the genotypic components and if they were related to predictable environment factor (such as geographic areas, major pest problems), the breeder searches for a cultivar to meet the specific requirements of that environment, while the interaction is small and

unpredictable (microclimatic or yearly variation in weather and management practices) the breeder searches for a cultivar that has general adaptability and universal performance over the range of environments

It also noticed that variation due genotype x environment were further partitioned into linear and non-linear components. Genotype x environment linear was insignificant for all studied traits except for MC traits, insignificant of genotype x environment linear indicated that genotypes didn't differ genetically in their response to different environments, while significant indicating that the regression coefficient of some verities more or low than unity (b=1) and some lines were more stable than others over the environments.

Pooled deviation mean squares were significant for all studied traits , indicated that the major components for differences in stability were due to deviation from the linear function therefore, it could be concluded that the relatively unpredictable components of the interaction maybe more important than the predictable componemnts, similar results were reported by Awaad(1989), Ismail .*et al* .1992,   EL.Harony.*et al.,(2000)*   and Shaker (2009)

Eberhart and Russell (1966) proposed that an ideal genotype is one which has the highest yield over abroad rang of environments regression coefficient (b) value of 1.0 and deviation mean Square (s^2d) of zero. Characterization of mean performances of individual genotypes coupled with different stability parameters for yield, yield components and earliness genotype   grown index, (E.I.) are presented in Table 5. The results illustrated that lines 3,5 and 15 were stable for seed cotton yield ($\bar{x}$=high, b =1 and s^2d =0). While, the line (7) has high mean performance and regression coefficient equal one but the deviation form regression was larger than zero and determinations coefficient were small. However, for lint percentage some lines has high mean performances over grand mean (2, 3, 7, 8, 9, 12 and 14) but these lines did not parallelism with the stability parameters. Therefore, the best performing, highest value in this trait or genotypes was not necessarily to be best stable genotype. Similar results reported by EL-Harony. *et al* (2000) found that correlation between $\bar{X}$ and r^2, b and S^2d) was insignificant for seed cotton yield.

Earliness index (E.I.) trait is very important parameter for breeding method to selection early verities in Egyptian cotton breeding programme. Therefore, selection lines have high yield, more earliness and high stable are important. Most lines and check verities have regression coefficient and deviation form regression did not differe from one and zero but, line (6) which has high mean (over best check variety (G.92), and more stable than the rest genotypes. Therefore can be using this line for stock in breeding program to produce verities more earliness with selection to high yielding. In this respect, Allard and Work man (1963) reported that heterozygote's were more buffered than homozygotes. However, Kohel (1969) and Kohel (2003) stated that the buffering ability had no relation with heterozygosity, but, Bahatade and Bhale (1983). Reported that the stability of genotypes could be resulted from balanced and optimal combinations of development traits in such genotypes.

Table 5: The mean performances and stability parameters for all traits .

Genotype	B.W				S.C.Y./P.				L%			
	Mean (X)	Regression coefficient (b_i)	s^2d	Coefficient of determinations R^2	Mean (X)	Regression coefficient (b_i)	s^2d	Coefficient of determinations R^2	Mean (X)	Regression coefficient (b_i)	s^2d	Coefficient of determinations R^2
1	2.990	4.2155 **	0.0061 *	0.7629	9.184	0.8235	-0.2628	0.9401	34.35	1.4766	3.5287 **	0.3158
2	3.003	0.5813	-0.0038	0.1432	9.296	1.0535	0.6753 **	0.8026	36.03	0.3247	0.5823 **	0.1029
3	3.050	1.7431	-0.0060	0.7080	9.135	0.8141	0.2787	0.7903	35.65	0.2599	1.4767 **	0.0315
4	3.012	0.9423	-0.0077	0.5887	9.021	0.9828	0.3188 *	0.8387	35.03	1.1311	-0.0741	0.9469
5	3.000	2.3594	-0.0039	0.7365	9.285	1.2205	-0.0760	0.9436	33.15	0.6368	0.0267	0.6675
6	3.038	0.3010	0.0174 **	0.0095	8.563	1.1593	-0.2360	0.9643	33.71	1.7365	1.0539 **	0.6637
7	2.972	0.9670	-0.0075	0.5669	9.244	1.0835	0.9495 **	0.7753	35.67	1.5444	0.7780 **	0.6705
8	2.945	0.9947	-0.0016	0.2609	8.771	1.1194	0.7153 **	0.8159	35.84	0.2771	1.0291 **	0.0488
9	3.062	1.7300	-0.0051	0.6558	8.849	1.0411	-0.2114	0.9510	35.91	0.6891	0.4261 **	0.3982
10	3.030	0.1713	-0.0009	0.0095	8.968	1.0543	-0.0547	0.9219	34.11	0.8187	0.0847 *	0.7076
11	3.217	1.6121	0.0185 **	0.2079	8.205	0.5298	0.6899 **	0.5037	34.36	1.1859	1.2453	0.4420
12	2.998	2.0952	0.1042 **	0.0985	9.119	1.4792 *	0.2826 *	0.9252	36.34	2.0484	6.6606 **	0.3237
13	3.065	1.3718	-0.0014	0.3965	8.869	0.7611	0.7773 **	0.6603	35.76	1.6580	4.6511 **	0.3081
14	3.057	2.0580 *	-0.0076	0.8637	9.195	0.7888	0.5241 **	0.7250	37.80	0.3890	0.4863 **	0.1598
15	3.087	-0.1195	-0.0022	0.0055	9.119	0.9289	0.1951	0.8474	35.50	1.4912	0.3904 **	0.7680
16	3.073	1.5909	-0.0089	0.9266	8.801	0.8316	0.2340	0.8075	35.35	0.6867	1.1951	0.2161
17	3.078	0.1932	-0.0026	0.0151	8.429	1.4328 *	0.0616	0.9436	33.68	1.2189	0.0781	0.8470
18	3.057	0.9913	-0.0043	0.3485	8.880	1.3671 *	0.0698	0.9375	36.66	0.8824	0.0761	0.7455
19	3.013	0.4365	0.0064 *	0.0327	7.345	0.5756 **	-0.1149	0.8066	35.25	-0.0623	3.3353 **	0.0009
20	2.990	-1.0534	0.0115 **	0.1304	8.092	0.9530	1.1784 **	0.6962	35.46	1.6070	2.3134 **	0.4502

Cont. Table 5

Genotype	EI				FL				MC			
	Mean (X)	Regression coefficient (b_1)	S^2d	Coefficient of determinations R^2	Mean (X)	Regression coefficient (b_1)	S^2d	Coefficient of determinations R^2	Mean (X)	Regression coefficient (b_1)	S^2d	Coefficient of determinations R^2
1	63.49	0.9837	-27.8412	0.9457	35.77	1.1628	0.6415 **	0.4385	3.70	1.0915	0.0482 **	0.6847
2	64.07	0.8615	11.0962	0.7075	36.13	1.3329	0.2379 **	0.7315	3.87	1.2247	0.0332 **	0.7958
3	60.08	1.0529	-15.4293	0.8910	35.50	1.0961	0.7646 **	0.3684	3.70	1.0724	0.0770 **	0.5717
4	59.38	0.9824	-21.1037	0.9069	34.98	1.2219	1.2126 **	0.3143	3.55	1.2750	0.0070 **	0.9417
5	69.38	1.0213	0.3842	0.8144	35.83	1.3044	0.4409 **	0.5875	3.37	09080	0.0103 **	0.8583
6	71.50	0.9481	-23.3706	0.9142	35.92	0.6061	0.5037 **	0.2123	3.40	0.5967	0.1050 **	0.2339
7	65.84	0.8392	-26.8944	0.9195	35.97	1.2985	0.0866 **	0.8719	3.75	1.5292	0.0265 **	0.8822
8 .	64.78	0.8281	-23.3043	0.8899	36.10	0.5918	0.5980 **	0.1783	3.70	0.7843	0.0062 **	0.8703
9	60.38	0.9400	-20.1186	0.8934	35.70	1.1242	0.7663 **	0.3797	3.60	0.5519	0.0497 **	0.3501
10	60.88	1.1664	-19.8874	0.9272	36.10	0.8094	0.6190 **	0.2817	3.57	1.2396	0.0198 **	0.8652
11	64.78	1.0401	42.2209 **	0.6806	36.38	0.9672	1.1461 **	0.2330	3.47	1.3117	0.0479 **	0.7595
12	63.13	1.0222	-4.7409	0.8363	36.37	1.1806	1.4510 **	0.2635	3.65	0.9923	0.1010 **	0.4673
13	62.56	1.1869	46.4143 **	0.7249	35.18	0.5111	1.9634 **	0.4727	3.67	1.2519	0.1270 **	0.5273
14	60.25	0.8986	-30.0061	0.9510	36.08	1.3218	0.7826 **	0.4532	3.63	0.7014	0.0408 **	0.5121
15	67.06	1.1562	-13.6806	0.9010	35.78	0.8088	3.3464 **	0.0680	3.27	0.5627	0.1070 **	0.2105
16	67.81	0.9937	10.4979	0.7653	35.58	1.6674	3.8062 **	0.2143	3.33	0.7000	0.0760 **	0.3654
17	60.71	1.1225	5.8552	0.8219	35.93	1.3008	0.3945 **	0.6125	3.22	0.5872	0.0231 **	0.5555
18	63.24	0.9775	-4.9301	0.8245	35.65	0.4745	0.3335 **	0.1988	3.85	1.5006 *	0.0144 **	0.9255
19	61.64	1.3597	0.3139	0.8863	35.47	0.7916	0.7880 **	0.2279	3.58	1.4721	0.1556 **	0.5581
20	58.28	0.6190	-7.8830	0.6752	36.10	0.4281	0.6655 **	0.0926	3.63	0.6470	0.2626 **	0.1269

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Cont. Table 5

Genotype	EI				FL				MC			
	Mean (X)	Regression coefficient (b_i)	s^2d	Coefficient of determinations R^2	Mean (X)	Regression coefficient (b_i)	s^2d	Coefficient of determinations R^2	Mean (X)	Regression coefficient (b_i)	s^2d	Coefficient of determinations R^2
1	132.50	0.9465	14.3733 **	0.8893	50.27	1.3505	1.6128 **	0.6997	3306.3	0.8252	11980.88 **	0.3797
2	134.67	0.9130	10.2626 **	0.9113	47.79	1.1369	12.5182 **	0.1772	3277.5	1.8170 *	4731.83 **	0.8765
3	131.75	0.7737	20.4584 **	0.7928	48.47	1.2872	4.2580 **	0.4472	3190.8	1.3889	13957.25 **	0.5994
4	128.67	1.3137 **	2.9990 **	0.9843	50.31	1.3438	1.3376 **	0.7350	3225.4	1.2702	12565.40 **	0.5807
5	123.50	1.0332	16.1554 **	0.8954	49.06	1.6751	4.4413 **	0.5678	3253.3	1.5045	8102.16 **	0.7471
6	123.33	0.8657	83.6594 **	0.5459	48.86	1.1741	3.5984 **	0.4430	3266.3	0.8694	20786.36 **	0.2847
7	131.21	1.4830 **	7.3906 **	0.9735	49.35	1.0995	1.5949 **	0.6096	3317.5	0.8101	4336.43 **	0.6043
8	132.46	0.7826	6.8131 **	0.9167	50.14	1.4802	1.8229 **	0.7126	3339.2	1.2762	4405.79 **	0.7889
9	132.00	0.5286 **	7.4543 **	0.8222	49.07	-0.3639	6.8080 **	0.3894	3208.8	0.2604	23358.19 **	0.3087
10	133.3	0.5068 **	11.3409 **	0.7424	48.87	0.7241	4.5638 **	0.1928	3224.2	1.1551	2002.92 **	0.8577
11	127.67	1.1831	39.1442 **	0.8262	49.58	1.2227	0.9638 **	0.7599	3348.8	0.5729	21305.08 **	0.1444
12	130.42	1.3183	28.0501 **	0.8910	49.01	0.5027	5.4213 **	0.0884	3277.5	0.8933	23811.32 **	0.2690
13	128.98	1.3691	40.6349 **	0.8599	47.98	0.8408	3.9059 **	0.2733	3133.3	0.6224	5070.41 **	0.4389
14	131.17	0.8207	29.8116 **	0.7491	49.91	-0.2705 **	1.7823 **	0.0781	3266.7	0.6123	17510.76 **	0.1892
15	124.88	1.1034	93.0776 **	0.6373	48.00	1.5106	6.0322 **	0.4406	3213.3	0.2186	28785.43 **	0.0180
16	120.17	0.2739	166.3262 **	0.5732	49.06	0.1939	3.6656 **	0.0209	3179.6	0.1780	48445.95 **	0.0072
17	117.63	0.8255	75.0804 **	0.5489	48.63	1.8434	2.0327 **	0.7755	3283.6	2.0582	12753.88 **	0.7819
18	135.00	1.4044 **	8.2903 **	0.9673	49.86	1.1026	0.7584 **	0.7647	3287.5	1.0762	6366.90 **	0.6546
19	133.67	1.3118	66.6554 **	0.7757	47.43	1.3423	5.2994 **	0.4144	3140.0	1.4659	14478.10 **	0.6167
20	130.08	1.2429	202.9440 **	0.5066	48.17	0.8040	5.2237 **	0.2048	3223.3	1.1254	9890.15 **	0.5777

The results in Table (5) revealed that, the lines for fiber length have mean performances were the same as check variety (Giza 70) and regression coefficient (bi)was equal unity for all genotypes and deviation from regression was significant differ from zero. Therefor, the determination (r^2) was low of most genotypes. Therefore, all genotypes were unstable for this trait. Similar trend was in the rest fiber traits EL-Shaarawy 1998 and Seyam *et al* 1994 reported that micronaire reading, fiber strength and fiber length differed significantly in estimated a. The cultivars varied greatly in the estimated λ statistic , the deviation from three liner response. Also, similar results of reported by EL-Marakby *et al.*, 1986 and Shaker 2009. . Although, fiber properties controlled the genetic compare with the yield and yield components but these traits affect by of environment factors. This effect appeared in the expression of these lines. Therefore, all lines nearly were unstable for micronair, fiber length, fiber fineness and fiber strength and this is very important to breeders, because the genetic parameters or the gene expression may vary of the presence of genotype x environment interaction (Larsson *et al.*, 1997).

In over environments are given in Table 6. The superiority of the seed cotton yield ranged between 1.0 for line 2 and line 3-5- 6-15, for check Varity G.45 .Selection is based primarily on Pi values and function of bath genotypic as well as GE interaction values. The small of Pi value indicates general superiority of the cultivar. The results indicated that, there is relationship between the mean performance and regression coefficient with superiority measure (Pi). 1, 3, and 15 were more superior, high stable and above performance. Parameter multiple, to identify and selection the top yielding lines are important in early selection generate for breeding programs because these help the breeder to correct suggesting especially most economic characters are given genes multiple and effect by environments.

Rasmusson and Lambert (1961), Lin and Binns (1988) and Abdel-Hafez *et al.*, (2000)   using the superiority and stability parameters to evaluate some Egyptian cotton varieties and reported that most stable varieties were more superiority over all environments.

The mea n of genotypes, stability parameters and the three indices of 20 genotypes are shown in Table 6 for seed cotton yield. The best genotypes according to these criteria are also identified in this table when selection based on mean yield a lone have yield ranks of one because all lines were similar for mean performance for yield due to low variability of these material (Extra long staple) while , selection was made on the basis of index on the top times included the lines 1, 2, 3 ,4, 5 ,6 ,7 ,8 and 9 when selection of index two the lines 1, 3, 5, 6, 9, 10 ,15 and 16 . While, selection based on index3 the top lines were 1, 3, 5, 6, 9, 11, 15 and 16.

The previous results of lines selection were similar of ranks due to the Low variability of ranks of lines (1, 2, 3) and rank for each b and S^2d depended on and significant for them while, the ranks depended on absolute value are low important for identify of genotypes. Therefore selection in these lines showed is dependent on the three indices. The best lines of exprnel were 1, 2, 5 and 9 (high yield and high stable).

Table 6: The superiority and the mean of genotypes and the three indices of 20 genotypes of the seed cotton yield.

Genotypes	Yield	Rank Yield	Rank b	Rank S ^2 d	Index 1	Index 2	Index 3	Superiority
1	9.148	1	2	1	3	2	4	1.119
2	9.296	1	2	2	3	3	5	1.025
3	9.135	1	2	1	3	2	4	1.460
4	9.021	1	2	1	3	2	4	1.510
5	9.285	1	2	1	3	2	4	1.060
6	99.563	2	2	2	4	4	6	2.077
7	9.244	1	2	2	3	3	5	1.631
8	8.771	1	2	1	3	2	4	2.100
9	8.849	1	2	1	3	2	4	1.660
10	8.968	1	2	2	3	3	5	1.485
11	8.205	2	2	2	4	4	6	3.730
12	9.119	1	3	2	4	3	6	1.518
13	8.869	1	2	2	3	3	5	1.954
14	9.195	1	2	2	3	3	5	1.140
15	9.119	1	2	1	3	2	4	1.320
16	8.801	1	2	1	3	2	4	2.660
17	8.429	2	3	1	5	3	6	2.630
18	8.880	2	3	1	5	3	6	1.850
19	7.345	3	1	1	4	4	5	5.560
20	8.092	2	2	2	4	4	6	3.420

The rank of these materials were little due to, rank of yield, b and S^2d depended on significant for them and low variability of these material. Absolute value ranks (without significant) give us more ranks, but it is not efficiency for screening and selection for genotypes. .Quantitative traits affected by major factors e.g. multiple genes, environmental factors and interaction. Therefore, selections to families' copies are very important in breeding programs for improvement of these traits.

Plant breeder's use yield traits to identify promising genotypes and agronomists make recommendations for farmers. The level of success in meeting these goals depends critically on two factors (1)the accuracy of yield estimates and (2) the magnitudes of genotype by environments (Gauch, 1988). These two factors reflect within trail accuracy and between trail predictability.Using principal components analysis to selection the better stability lines to comparison regression model. Therefore, the results in Table 7 shown that the percentage contribution of PCA components of seed cotton yield. Each PAC1and PCA2 were more important. These results agreed with these obtained by EL-Shaarawy (1998 and 2000) and El-Helow. *et al.*,(2002).The results in Figures 1and 2 show that the strains (1and 3)which PCA1 equal unity and PCA2 equal zero. The two strains were stable by using regression model (x=high,b=1 and s^2=0). On the other hand, lines 5 and 15 were stable by using regression model but the values of PCA equal zero and PCA2 nearly equal unity. Therefore, using the two models to identify promising genotypes stability in cotton breeding programs is very useful

Table 7: Percentage contribution of PCA components of seed cotton yield.

Cumulative %	% of Variance	Extraction Sums of Squared Loadings Total	Cumulative %	Eigen values Total	Component
44.376	44.376	2.663	44.376	2.663	1
68.336	23.960	1.438	68.336	1.438	2
84.565	16.228	0.974	84.565	0.974	3
94.026	9.462	0.568	94.026	0.568	4
99.919	5.893	0.354	99.919	0.354	5

(PCA1)
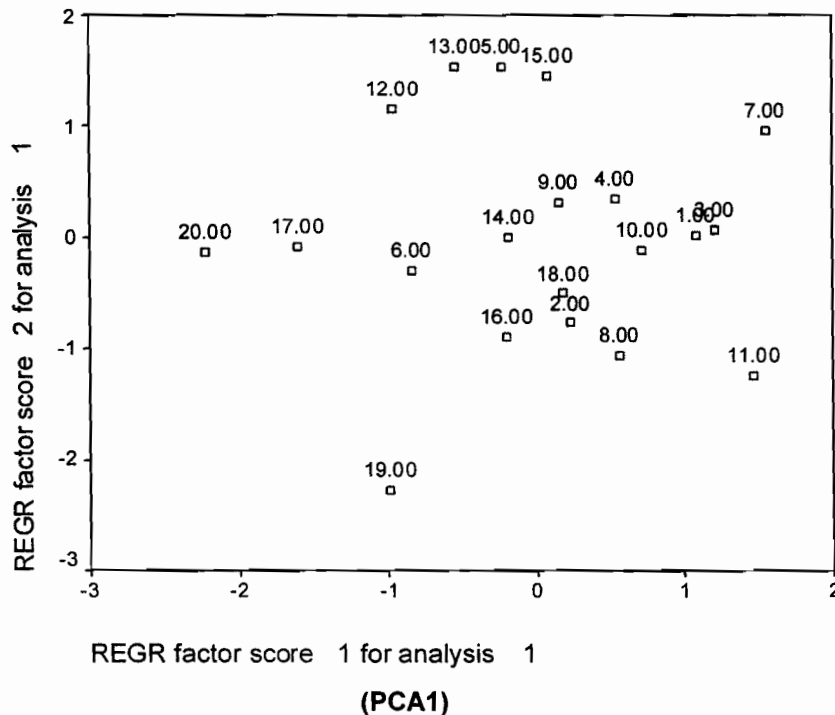
Figure 1: Principal axis factoring of 20 genotype according 6 environments for seed cotton yeiled.

Genetic diversity

In this part of the study all cotton genotypes are accounted for cluster analysis to determine the relative genetic diversity and genetic distances. It is interesting to not that the multivariable analyses were important and very efficient for exploiting the genetic variability existing among the Egyptian cottons varieties. The results in Figure 1 of the hierarchical cluster analysis in the from of dendogrames. It is clear evident that the line 11 was wide divergent from their check of varieties.

Also, check varieties were divided for most clusters (2, 3 and 5 cluster).

The lines are in same cluster indicated that near similar. Therefore selection for lines depends on the relationship between these lines for cluster

analysis. Cluster analysis could efficiently describe the characteristics of group of various genotypes and both gave a sensible and useful integration of the data.

In generally, these results are useful for breeder in classification of the cotton (Gene bank) group according to their genetic similarity.

Rescaled Distance Cluster Combine
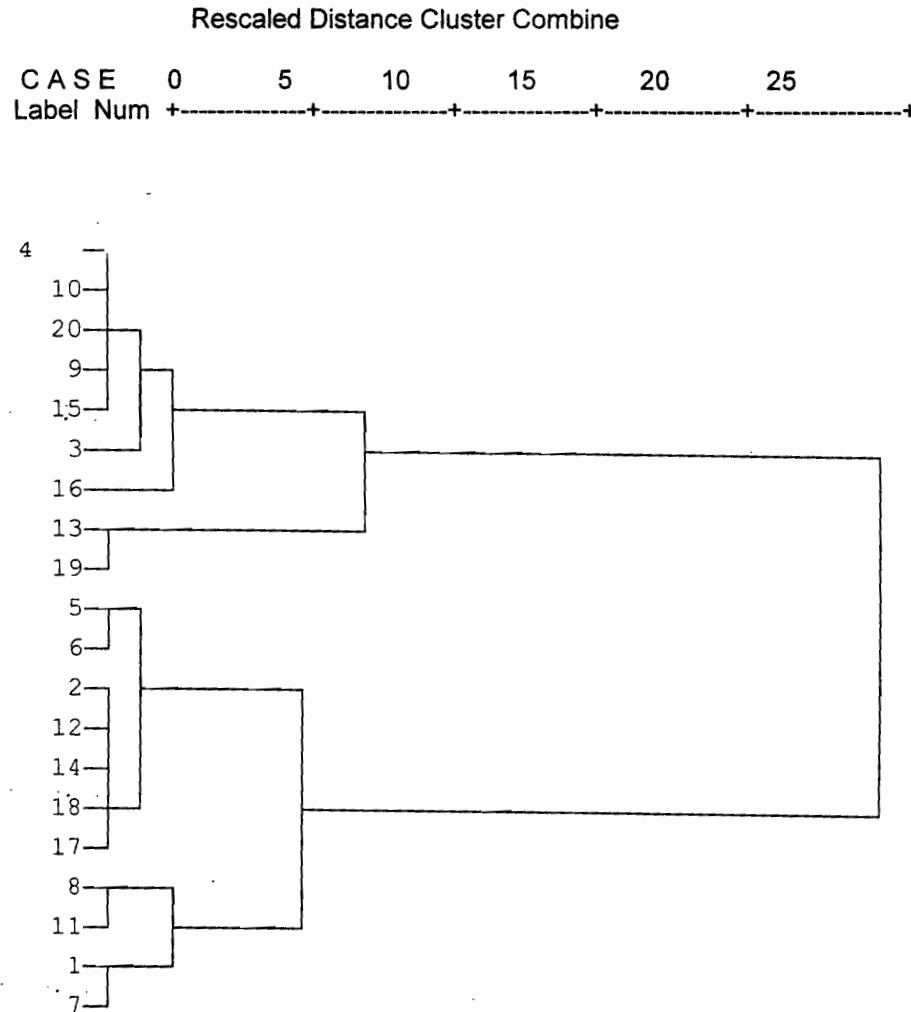
Figure 2: Dendrogram using Average Linkage (Within Group)

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استخدام مقاييس الثبات ومكونات التباين لانتخاب التراكيب الوراثية تحت ظـروف بيئية مختلفة في القطن المصرى
محمد نشأت عبد العزيز نظمي، وليد محمد بسيوني يحيي ، عادل عبد العظيم ابو اليزيـد الاخضر و محمد عزت عبد السلام .
معهد بحوث القطن – مركز البحوث الزراعية – مصر

يستخدم مربي القطن تجارب التقييم المحصولي لتقييم وانتخاب الهجن المبشرة ولاتمام هذا الهدف فانه يعتمد علي اهمية التفاعل ما بين البيئة والوراثة وايضا علي درجة الثبات الوراثي لهذه الهجن . لهذا تم في هذا البحث تقييم ٢٠ تركيب وراثي في ثلاث مواقع زراعية لموسمين زراعيين ومن النتائج المتحصل عليها يتضح الاتي :-

تشير النتائج الي وجود تفاعل عالي بين البيئة والوراثة لكل من صفات المحصول والتيلة وان التفاعل الخطي بين البيئة والوراثة كان غير معنوي لجميع الصفات الموجودة تحت الدراسـة عدا صفة الميكرونير وعدم وجود معنوية يدل علي ان التراكيب الوراثية الموجودة تحت الدراسـة كانت استجابتها للبيئة غير مرتبطة بتركيبها الوراثي وان الجزء الاهم للتفاعل يرجع الي اخـتلاف الانحرافات عن خط الانحدار .

يتضح من النتائج ايضا ان السلالات ٣و٥و ١٥ كانت اكثر ثباتا لـصفة المحـصول (X- $=high$, b=1 and S2d = 0) بينما السلالة ٧ كانت اعلي محصولا ولكن معامل الانحدار اكبر من ١ (الوحدة) و S2d لا يساوي الصفر .

اشارت النتائج ايضا الي انه توجد مجموعة من السلالات كان متوسطها اعلي من المتوسط العام وهي (٢، ٣، ٧، ٨، ٩، ١٢، ١٤) ولكن يعاب عليها انها غير ثابتة ومن ذلك يتضح انـه ليس بالضرورة ان تكون السلالات عالية الاداء ان تكون ثابتة وعلي الجانب الاخر كانـت جميـع السلالات ذات متوسط عادي للصنف جـ٧٠ في صفة طول التيلة ولكن جميع السلالات كانت غير ثابتة في تلك الصفة .

من النتائج يتضح ان انتخاب افضل التراكيب الوراثية علي اساس مؤشرات الانتخاب الثلاثة ان معظم السلالات كانت متساوية في ترتيبها بالنسبة لصفة المحصول ويرجـع ذلـك الـي قلـة الاختلافات والمحصول في طبقة الاقطان فائقة الطول للحفاظ علي مستوي معين فـي الـسلالات المبشرة في صفات التيلة والانتخاب علي اساس الا index 3 فكانت هناك عدد مـن الـسلالات افضل وهي ١، ٣، ٥، ٦,٩,١١ وتعتبر من الهجن المبشرة جدا في برامج التربية.

استخدام تحليل المكونات الاساسية للتراكيب الوراثية والثبات المختلفة لـصفة المحـصول زهر لانتخاب افضل السلالات بالمقارنة بنموذج الانحدار اتضح ان PCA1 , P CA2 كانـت اكثر اهمية واتضح ان السلالتين ١ ، ٣ ذات PCA1 مساوي للواحـد و PCA2 مـساويا للصفر وان تلك السلالتين كانتا اكثر ثباتا باستخدام الانحدار . علي الجانب الاخر الـسلالتين ٥ ، ١٥ كانت اكثر ثباتا باستخدام الانحدار ولكن قيم ال PCA1 يساوي صفر و PCA2 يساوي تقريبا الواحد لذلك تقرر النتائج المتحصل عليها ان استخدام الطريقتين لانتخاب الهجـن المبـشرة الاكثر ثباتا في برامج التربية يكون اكثر فائدة .

قام بتحكيم البحث