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GRAPHICAL ANALYSIS OF MULTI-ENVIRONMENT YIELD TRIALS USING BIPLOT METHOD TO STUDY PERFORMANCE STABILITY FOR SOME EGYPTIAN COTTON GENOTYPES

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ABSTRACT

New hybrids, generally, need to be tested at several locations before being recommended for release. The main objective of this study was the selection for the stability among genotypes of trial B to access genotypes reliable to cultivate in different environment in Middle and Upper Egypt area. Twenty long staple Egyptian cotton genotypes were evaluated at four environments, i.e. Sids, El-Fayoum, Assiut and Sohag in 2016 season as yield trials of a cotton breeding program. Results showed that the variance of components of environments, genotypes, and environments by genotypes interaction were significant (p<0.01) for lint cotton yield. The E component was always the most important source of yield variation. When GGE model was fitted, the first two PCs explained 79.77% (PC1=63.04% and PC2=16.73%) of GGE variation for lint cotton yield. Genotypes ((G 91 × G 90) × {(G83 × G80)× Dandara}), ((G 91 × G 90) × {(G83 × G80)× G89}) and ((G 91 × G 90) × G80) with means over the two control genotypes (Giza 90 and Giza 95) plus the promising hybrid ({(G83 × G80)× G89}×Australian). Genotypes, ((G 91×G 90) × {(G83×G80) × Dandara}) and ((G 91×G 90)×G80) was identified as high yielder and stable genotype. Three genotypes were the winning genotypes for respective environments, ((G 91 × G 90) × G80) was adaptable in both Sids and Sohag region, (CB 58×G90) adaptable for El-Fayoum region, while Assiut region were ((G 91×G 90)×{(G83×G80)×G89}),((G 91 × G 90) × {(G83 × G80) × Dandara}) and ({(G83 ×G80)× G89} ×Karashinky). Positive correlations between Sids and Sohag region reveals that similar information about the genotypes. The fiber quality of genotypes under study they were in the same category for long staple cotton in Middle and Upper Egypt.

Key words: ***Egyptian cotton, GGE-Biplot, Stability.***

INTRODUCTION

Egyptian cotton (*Gossypium barbadense* L.) is an economically important crop in Egypt. In Egypt, the breeding program of cotton research institute aimed to develop more productive genotypes with higher-quality fibers. To achieve this, a large number of genotypes (G) are tested annually in different environments (E), before final recommendation and multiplication. In most cases, these environments vary substantially, and there are interactions between genotypes and environments (GE), that arise from differential genotypic responses to the environment. Understanding GE interactions affords an assessment of the real impact of selection and ensures greater reliability when recommending genotypes to maximize productivity and other agronomic traits of interest in a specific location or group of environments.

Significant GE component reduces correlations between genotype and phenotype values (Kang 1998) and affects breeding for genetic improvement, especially for quantitative traits. In a yield trial of 31 cotton varieties in three Mediterranean countries, the ratio of G×E component to genotypic component was 6.4 (Baxevanos *et al* 2008a). Meredith *et al* (2012) reviewed six studies conducted worldwide between 1964 and 2011 for G×E effects on lint cotton yield and fiber quality. The average attributes of E, G, and G×E to the total variation of lint cotton yield was 86%, 5%, and 9%, respectively. In summary of these previous studies, G×E effects were greater than genotype effects for lint cotton yield, whereas the effects of G×E were usually small relative to genotypic effects for fiber properties.

Over the last three decades, numerous statistical methods have been developed to appraise the stability of cultivars across test locations (Moreno-Gonzalez *et al* 2003). As one of the most important analysis methods, the additive main effects and multiplicative interaction model (AMMI) have been extensively applied to assess the stability of varieties or to group test environments in the case of multi-environment variety trials. Nevertheless, test location evaluation requires integrating the genotype main effect (G) with genotype by environment interaction (GEI) as in the genotype main effect plus genotype by environment interaction (GGE) biplot method (Yan and Kang 2003; Yan and Holland 2010). The concept of biplot was first proposed by Gabriel (1971) to, graphically, display two-way data. AMMI analysis can be used efficiently for identifying superior environmental conditions for the agricultural holding (selection of growing regions) and higher mean performance genotypes (Gauch et al., 2008). In contrast the GGE biplot model is best suited to identifying mega-environments, selecting representative and discriminative environments, and appointing more adapted and stable genotypes to specific environments.

The phenomenon of GEI is characteristic of multi-environment trials (METs) and represents permanent interest for breeders and biometricians along with practical and theoretical aspects (Kempton and Fox 1997). Genotype stability estimation and GEI are specifically interrelated. While it would be nearly impossible to package into one cultivar all high-yield genes and genes conditioning all possible stresses that might be encountered from location to location and year to year, identification of cultivars that are both high yielding and stable in performance across multiple environments (locations or years or locations-years combination), or that have specific adaptation, is an appropriate strategy (Kang *et al* 2005).

In Egypt, Various researches have been explored to study GEI and to predict the phenotypic response to changes in the environments. Baker (2008) indicated that the five parents were classified as good combiners for cotton yields and some of them were classified as stable in their mean performance for yielding ability based on seed cotton yield (SCY) and/or lint cotton yield (LCY). Abd El-Bary (2013) found that the genotypes no. 10, 11, 13, 16 and the two promising crosses 10229 × Giza 86 and Giza 89

× Giza 86 had average level of stability and surpassed mean performance for seed and lint cotton yield. Abd El-Moghny and Max (2015) used seven stability parameters to determine stability of 22 Egyptian cotton genotypes. They found that the Genotypes; G6, G9, G18 G19, G20, G22 and G23 were the most stable genotypes across these different methods, and some of them could be recommended for further use in the breeding program. Said (2016) found that using Yield-stability statistic (Ysi) values indicated that, the four genotypes, ((G 91 x G 90) x [(G83 x G80)x Dandara]) , ((G91 x G90)x G80) , ([(G83 x G80) x G89] x (G83 x Delta Pine703)) and ([(G83 x G80)x G89]x Australian) were stable and they surpassed the control variety (Giza 90) and the grand mean in seed cotton yield, lint cotton yield and lint percentage. Therefore, these four crosses could be recommended as stable high yielding genotypes and be incorporated as breeding materials in future breeding programs to produce stable and high yielding cultivars.

The objectives of this study were to: 1) apply a GGE biplot to evaluate the magnitude of the effect of GE interaction on lint cotton yield, 2) determine the best performing and stability genotypes across environments, and 3) analysis of the ideal genotype and ideal environment for cotton production region in Middle and Upper Egypt.

MATERIALS AND METHODS

This investigation was conducted during 2016 season through the advanced yield trial B. Trial B was cultivated at four environments represented Middle and Upper Egypt regions, i.e. Sids (E1), El-Fayoum (E2), Assiut (E3)and Sohag (E4). Each Trial consisted of 20 long staple genotypes of Egyptian cotton (*Gossypium barbadense* L.), 16 lines which were numbered from 1 to 16 descending from 11 crosses plus four control genotypes were numbered from 17 to 20. The code of genotypes and their pedigrees are given in Table (1). In all environments, experimental design was randomized complete block design with six replications; each plot consisted of five rows. The row was four meters long, 60 cm width and 20 cm between hills within a row. Standard cultural practices were applied as recommended for growing cotton. The hills were thinned to two plants each. The middle three rows of each plot were hand harvested to determine lint cotton yield (LCY) in kentar/feddan (k/f).

At maturity, a random representative sample of 50 open bolls was picked from the two outer rows per plot to determine fiber properties: Upper half mean length (UHM, mm), fiber uniformity ratio (UR, %), yarn strength (YSt., unit), Micronaire reading (Mic,unit), Yellowness (+b, unit) and Maturity. The lint cotton samples were tested at Cotton Technology Laboratory, Cotton Research Institute, ARC. High Volume Instrumentation (HVI) was used for determinations of fiber traits.

Table 1. Code and pedigree of 20 cotton genotypes, their parents and their origins.

Code	Genotypes	Parent	Origin
1	H5 120/2014	H_4 74 / 2013	(G91 × G90) × G85
2	H5 125/2014	H4 77-+ / 2013	(G 91 × G 90) × {G83 × (G75× 5844)}
3	H5 141/2014	H4 90 / 2013	(G 91 × G90)× (G 85 × G 83)
4	H5 149/2014	H4 95 / 2013	{(G83 × G80)× G89} × Karashinky
5	H5 158/2014	H4 99 / 2013	(G 91 × G 90) × {(G83 × G80)× G89}
6	H6 181/2014	H5 131 / 2013	(G90 × Australian)×{G83 × (G75× 5844)}
7	H6 195/2014	H5 149 / 2013	(G91 × G90)× Karashinky
8	H7 202/2014	H6 157 / 2013	(G 91 × G 90) ×{(G83 × G80)× Dandara}
9	H7 212/2014	H6 160 / 2013	« «
10	H7 222/2014	H6 172 / 2013	{(G83 × G80)×Dandara}×(G90×Australian)
11	H7 237/2014	H6 191 / 2013	(G 91 × G 90) × G80
12	H7 240/2014	H6 193 / 2013	« «
13	H7 242/2014	H6 194 / 2013	« «
14	H7 247/2014	H6 197 / 2013	« «
15	H9 272/2014	H8 248 / 2013	[(G83 x G80) x G89] x (G83 x Delta Pine703)]
16	H9 278/2014	H8 249 / 2013	« «
17	Promising hybrid	Family mixed	CB 58 × G90
18	Promising hybrid	Family mixed	{(G83 × G80)× G89}× Australian
19	Giza 95	Commercial Cultivar	{G83 × (G75× 5844)}× G 80
20	Giza 90	Commercial Cultivar	Giza 83 × Dandara

The lint cotton yield data for 20 genotypes in 4 environments were subjected to combined analysis of variance (ANOVA) to determine the effects of environment (E), genotype (G) and their interactions.

The data were graphically analyzed for interpreting GE interaction using the GGE biplot. GGE biplot methodology is composed of two concepts, the biplot concept (Gabriel 1971) and the GGE concept (Yan *et al* 2000). The data were analyzed by using Genstat 14th ed. (GenStat 2011). Only variables with significant effects of G and GE were appropriate for analysis using GGE biplot (Blanche *et al* 2006).

RESULTS AND DISCUSSION

Trial B in 2016 is the advanced strains test for the promising genotypes that were selected from Trial A 2015. Trial B was carried out at four environments in Middle and Upper Egypt, i.e. El-Fayoum, Sids, Assuit and Sohag in order to study the breeding behavior of the genotypes grown under different environments to evaluate the genotype stability in different environments.

Results of the combined analysis of variance for lint yield of 20 genotypes across the four environments are shown in Table (2). Mean squares of the genotypes (G) were significant, which indicated the presence of large genetic variation among genotypes. Environment (E) mean squares were significant, indicating the presence of wide range of variation across environments sampled (Table 2). Significant GE interactions suggested that genotype performances were not the same across environments. Additionally, many quantitative traits display interactions between genetic and environmental effects known as genotype by environment interaction (G×E). This phenomenon can pose difficulties in selecting superior genotypes that are adapted to wide geographic areas, a goal of most cultivar/hybrid development programs. These results are in agreement with those reported by Abo El-Zahab et al (2003), El-Feki et al (2002) and Khalifa et al (2010).

Table 2. Mean squares for the combined analysis of variance across four environments for 20 genotypes for lint cotton yield (k/fed.).

SOV	df	SS	MS	%(E+G+GE)
Rep/L.	**20**	**454**	**22.69****	
Env. (E)	**3**	**848**	**283.73****	**49.94**
Geno. (G)	**19**	**207**	**10.92****	**12.19**
G × E	**57**	**643**	**11.28****	**37.87**
Error	**380**	**1,810**	**4.76**	
Total	**479**	**3,509**		

**** Significant at 0.01 levels of probability.**

The results of combined ANOVA for lint cotton yield data showed the environment (E), Genotype (G) and G × E interaction effects accounted for 49.94, 12.19 and 37.87% of the total sum of squares, respectively (Table 2). Significant differences for all sources of variation indicated the effect of environments in the GE interaction, genetic variability among the genotypes and possibility of selection for stable genotypes. Similar significant differences in the effects of G, E, and GE interaction were obtained by El-

Akhedar *et al* (2011), when evaluating cotton genotypes in multi-environment trials (new reclamation region) in Egypt. They found that the new promising line 10229xG86 was the best under these conditions for seed and lint cotton yield.

The mean performance of genotypes across 4 environments (Table 3) ranged from 11.99 k/f for G_{20} (Giza90) to 14.91 k/f for G_8 ((G 91 × G 90) × {(G83 × G80) × Dandara}). The results accentuated in superiority of the genotypes; G_8, G_5, G_{13}, G_4, G12, G_9, G_{10} and, G_{18} their means were more than the grand mean. Nevertheless, their ranks changed from an environment to another, which was one aspect of significant GEI. Mean of environments varied from 11.83 k/f for E_4 (Sohag region) to 15.95 k/f for E_3 (Assiut region).

Table 3. Mean lint cotton yield (k/f) of 20 genotypes across 4 environments in Middle and Upper Egypt in 2016 season.

Code	Genotypes	E_1	E_2	E_3	E_4	Mean
1	(G91 × G90) × G85	14.71	13.47	15.38	10.87	13.6
2	(G 91 × G 90) × {G83 × (G75× 5844)}	14.16	13.36	15.70	10.74	13.6
3	(G 91 × G90) × (G 85 × G 83)	12.98	13.63	16.60	11.13	13.6
4	{(G83 × G80)× G89} ×Karashinky	13.68	13.14	18.81	11.44	14.3
5	(G 91 × G 90) × {(G83 × G80)× G89}	12.79	13.60	19.76	12.97	14.8
6	(G90 × Australian) × {G83 × (G75× 5844)}	13.80	12.81	16.80	11.21	13.7
7	(G91 × G90) × Karashinky	13.77	13.18	15.87	11.57	13.6
8	(G 91 × G 90) × {(G83 × G80)× Dandara}	14.04	14.08	18.30	13.22	14.9
9	« «	13.23	12.98	15.99	13.17	13.8
10	{(G83 × 80) × Dandara} × (G90×Australian)	13.87	15.19	14.83	13.00	14.2
11	(G 91 × G 90) × G80	12.23	13.59	15.69	12.91	13.6
12	« «	14.66	13.87	16.50	12.04	14.3
13	« «	15.54	13.00	16.12	12.90	14.4
14	« «	13.26	14.50	15.27	11.16	13.6
15	[(G83 × G80) × G89] × (G83 × Delta Pine703)]	14.46	13.13	14.28	12.54	13.6
16	« «	13.61	14.52	11.41	11.76	12.8
17	CB 58 × G90	14.07	14.95	10.89	12.46	13.1
18	{(G83 × G80)× G89} × Australian	13.33	16.09	15.59	12.07	14.3
19	Giza 95	15.28	14.07	14.09	9.91	13.3
20	Giza90	11.04	13.35	13.96	9.60	12.0
Mean		13.73	13.83	15.59	11.83	13.7
LSD $_{0.05}$		1.94	ns	3.22	2.07	1.23

The partitioning of GGE through GGE biplot analysis showed that PC1 and PC2 accounted for 63.04% and 16.73% of GGE sum of squares, respectively explaining a total of 79.77% variation (Figure 1). This revealed that there was a differential yield performance among genotypes across environments due to the presence of GEI.

Performance and stability were evaluated by an average environment coordinate (AEC) or ATC (average tester coordinate) view of the GGE biplot. It is also referred to as the "Mean vs. Stability" view because it facilitates genotype comparisons based on mean performance and stability across environments. In this method, an average environment is defined by the average values of PC1 and PC2 for all the environments, represented by a small circle (Figure 1).

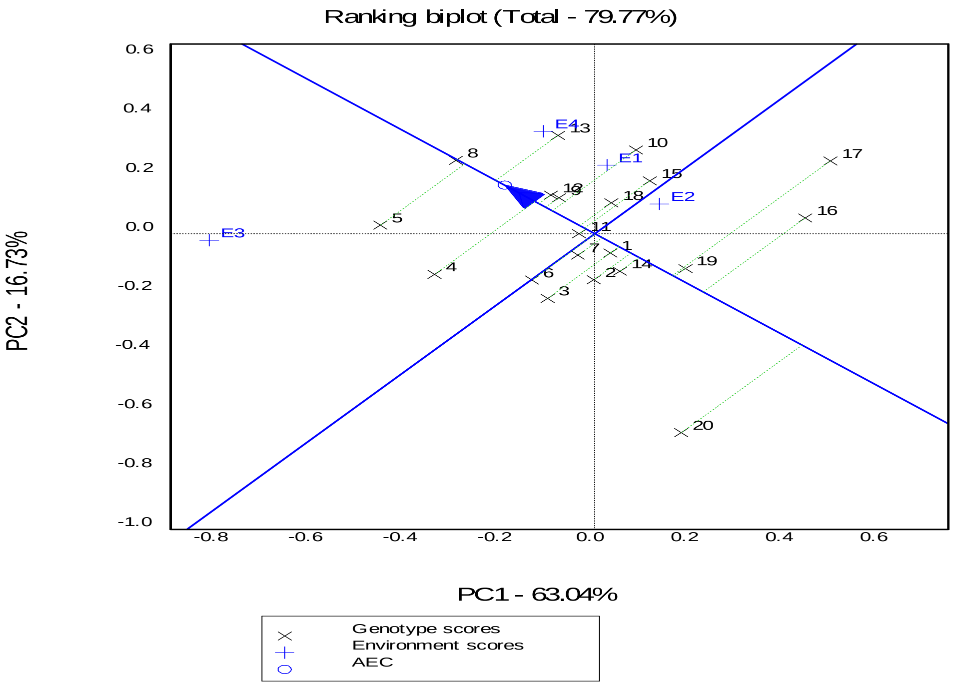

Fig. 1. The "Mean vs. Stability" view of the GGE biplot ranking for lint cotton yield of 20 genotypes across 4 environments in Middle and Upper Egypt in 2016 season.

A line is then drawn to pass through this average environment and the biplot origin; this line is called the average environment axis (AEA) and serves as the abscissa of the AEC. AOE or the ordinate of the AEC is the line that passes through the origin and is perpendicular to the AEC abscissa (Figure 1). Unlike the AEC abscissa, which has one direction, with the arrow pointing to greater genotype main effect, the AEC ordinate is indicated by a thick line or double arrows, and either direction away from the biplot origin indicates greater GEI effect and reduced stability. This line

(AOE) divides or separates genotypes with below-average means from those with above-average means. Furthermore, the average yield of genotypes is approximated by the projections of their markers to the AEC abscissa. Thus, on the AEC abscissa (Figure 1), the ranking of the genotypes was as follows: G8 > G5 > G13 > G4 > G12 > G9 > G10 > G18> G15> G11 ≥ grand mean > other genotypes. Stability of the genotypes depends on their distance from the AE abscissa. Genotypes G8 ((G 91 × G 90) × {(G83 × G80) × Dandara}), G5 ((G 91 × G 90) × {(G83 × G80)× G89}) and G13((G 91 × G 90) × G80) with means over the two control G19 (Giza 95) and G20 (Giza 90) genotypes plus the promising hybrid G18 ({(G83 × G80)× G89}×Australian) could be selected.

On the other hand, genotype stability is very important, in addition to yield mean. A longer projection to the AEC ordinate, regardless of the direction, represents a greater tendency of the GEI of a genotype, which means it is more variable and less stable across environments or vice versa. Thus, among tested genotypes G8, G9 ((G 91×G 90)×{(G83×G80) × Dandara}) and G12 ((G 91×G 90)×G80) was identified as high yielder and stable genotype Therefore, these two crosses could be recommended as high yielding and stable genotypes and be incorporated as breeding materials in future breeding programs to produce stable and high yielding cultivars. While G16, G17 and G20 were identified as low yielding with poor stability (long vector length). Conversely, G4, G5 and G10 were high yielding, but more variable. This results agreement with Said (2016) that found ((G 91×G 90)×[(G83×G80)xDandara) and ((G91×G90)×G80) were stable and they surpassed the control variety (Giza 90) and the grand mean in lint cotton yield.

The GGE biplot model indicated that ideal genotype should have a large PC1 (high mean performance) and near-zero PC2 (more stable). The genotypes ranking is shown on the graph of genotype so-called “ideal genotype” (Figure 2). An ideal genotype is defined as genotype that is the highest mean performance and it’s absolutely stable in performance that ranks the highest in all test environments (i.e. perform the best in all environments) (Yan and Kang 2003) it should also possess both high mean performance and high stability within a mega-environment (Yan *et al* 2007). Ideal genotype to be on average environmental coordinate (AEC) on positive direction and has vector (the line connect the biplot origin and marker of the genotype) length equal to the longest vector of the genotype and indicated by an arrow pointed to it. The ideal genotype is located in the first concentric circle in the biplot. Desirable genotypes are those located near to the ideal genotype (Thus, using the ideal genotype as the center).

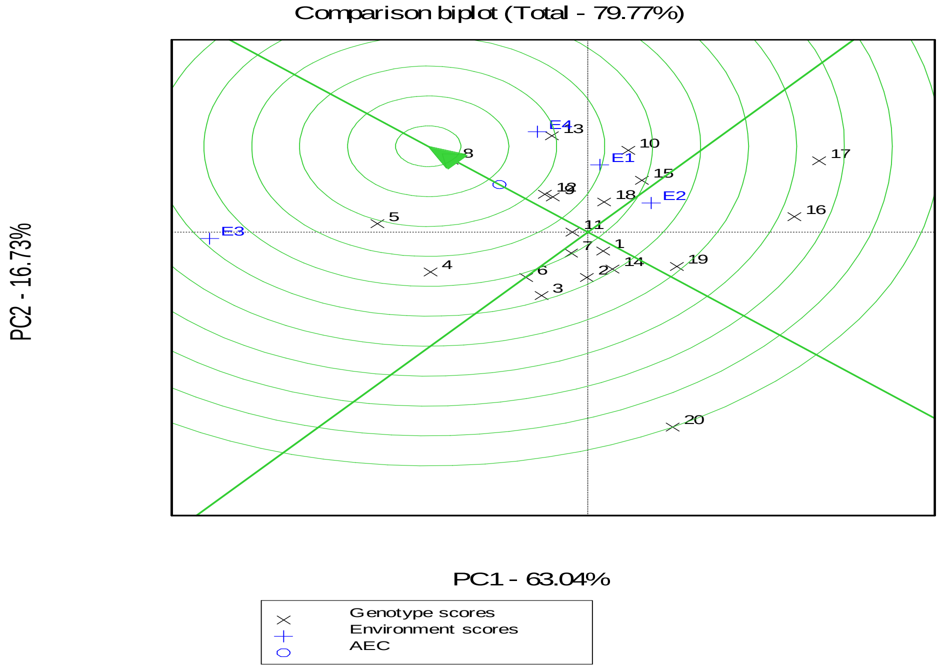

Fig. 2. GGE biplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype.

Thus, starting from the middle concentric circle pointed with arrow concentric circles was drawn to help visualize the distance between genotypes and the ideal genotype (Yan and Tinker 2006).

The ideal genotype can be used as a benchmark for selection. Genotypes that are far away from the ideal genotype can be rejected in early breeding cycles while genotypes that are close to it can be considered in further tests (Yan *et al* 2009). Although, such an “ideal” genotype may not exist in reality. It can be used a reference for genotype evaluation (Mitrovic *et al* 2012). A genotype is more desirable if it is located closer to the ideal genotype. Thus, using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype. Figure 2 revealed that G8 ((G 91 × G 90) × {(G83 × G80) × Dandara}) which fell into the center of concentric circles, were ideal genotype in terms of higher yielding ability and stability, compared with the genotypes. G13, G12 ((G 91 × G90) × G80) and G5 ((G 91 × G 90) × {(G83 × G80) × G89}) were located near the ideal genotype, thus being desirable genotypes. Four genotypes, the three control genotypes, G20 (Giza 90), G19 (Giza 95) and G17 (CB 58 × G90) plus G16 ([(G83×G80) × G89] × (G83× Delta Pine703)]) were undesirable genotypes.

Farias *et al* (2016) using biplot analysis of phenotypic stability in upland cotton and they found that the genotypes BRS ARAÇÁ and LD 05

CV had high cotton productivity and phenotypic stability, and could be grown in all environments across Mato Grosso State.

The "which-won-where" pattern is represented by a polygon formed by connecting the markers of genotypes that are further from a biplot origin (so that all other genotypes are contained within the convex hull) , and a set of lines drawn from the biplot origin perpendicular to each side of the polygon (convex hull) . A perpendicular line does not necessarily intersect the convex-hull side; it may only intersect the extension of the convex-hull side. These perpendicular lines divide the biplot into several sectors, each having its winning genotype which is the vertex genotype for that sector (Yan *et al* 2000). If environment markers fall into a single sector, this indicates that a single genotype won in all environments. If environment markers fall into a different sector, this indicates that different genotypes won in different environments. The twenty genotypes located in the vertex formed a seven-sided polygon having seven possible sectors (Figure 3). The vertex genotype for each sector is the one that yielded the highest for the environments filling within that sector. The vertex genotypes were the best or the poorest genotypes in some or all of the environments because they were farthest from the origin of the biplot (Yan and Kang 2003). G17, G13, G8, G5, G4 and G20 were vertex genotypes.

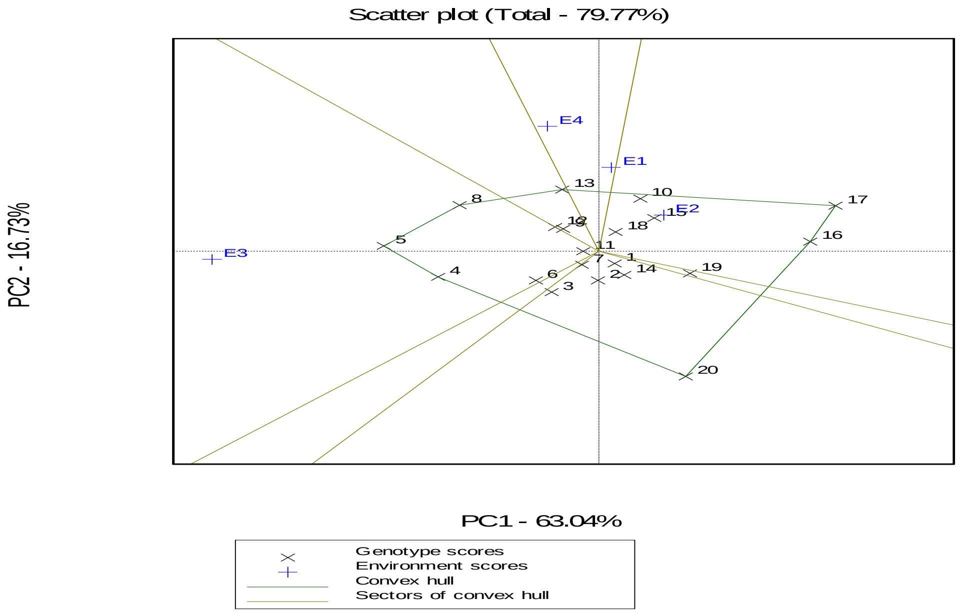

Fig. 3. The which-won-where view of the GGE biplot of lint cotton yield 2016.

From the polygon view of biplot analysis of MET data, four of the sectors had no environments and the four environments fell into three sectors delineated by different winning genotypes. The first section contains two environments, E1 (Sids region) and E4 (Sohag region) with G13 ((G 91 × G 90) × G80) as the best yielder genotype; so (G 91 × G 90) × G80) is adaptable in both environments. The second section contains environment E3 (Assiut region) with G5 ((G 91 × G 90) × {(G83 × G80) × G89}), G8 ((G 91 × G 90) × {(G83 × G80) × Dandara}) and G4 ({(G83 ×G80) × G89} ×Karashinky) as the best yielder genotypes. And the third section contains environment E2 (El-Fayoum region) with the promising hybrid, G17 (CB 58 × G90) as the best yielder genotype. G20 (Giza 90, control genotype) was the poorest-yielding genotype in any environment. The genotypes within the polygon and located nearer to plot origin (for example G11 for E3) are less responsive than vertex genotypes (Yan *et al* 2001).

The ideal environment is representative and has the highest discriminating power (Yan and Tinker, 2006). The biplot (ranking environments based on discriminating ability and representativeness) helps to visualize the ideal environment. The environments that have small angle with AEC, are more representative of the mega-environment than those have larger angles with it. While the environments with longer vectors are more effective in discrimination of the genotypes. Based on figure 4, the environments might be classified into three types: 1) environment had a short vector and provides little or no information about the genotype differences, 2) environment had a long vector and small angle with the AEC abscissa and was ideal environment to selecting superior genotypes, and 3) environment had a long vector and large angle with the AEC abscissa and it used in culling unstable genotypes.

In GGE biplot analysis, test environments are evaluated by defining three parameters: the ability to discriminate between genotypes (discrimination ability), the ability to represent the target region (representativeness) and the biplot distance from an ideal environment (desirability index). The discrimination ability depends on various factors which are either static (or indigenous such as soil type) or dynamic (such as pest pressure). A representative environment implies that varieties selected in that environment would have high probability to perform well in other environments of the same region. Test environments are finally assessed by their “distance” from an ideal one, which is designed to be located on the average test- environment axis and with the longest vector of all test-environments on the GGE biplot (Yan and Hunt 2001). Hence, the discrimination ability of a test environment is measured by the length of its vector on the biplot; the representativeness is measured by the cosine of the angle between the test environment and the “average” environment; and the “distance” from an ideal environment is the product of the discrimination ability and representativeness (Yan and Holland 2010).

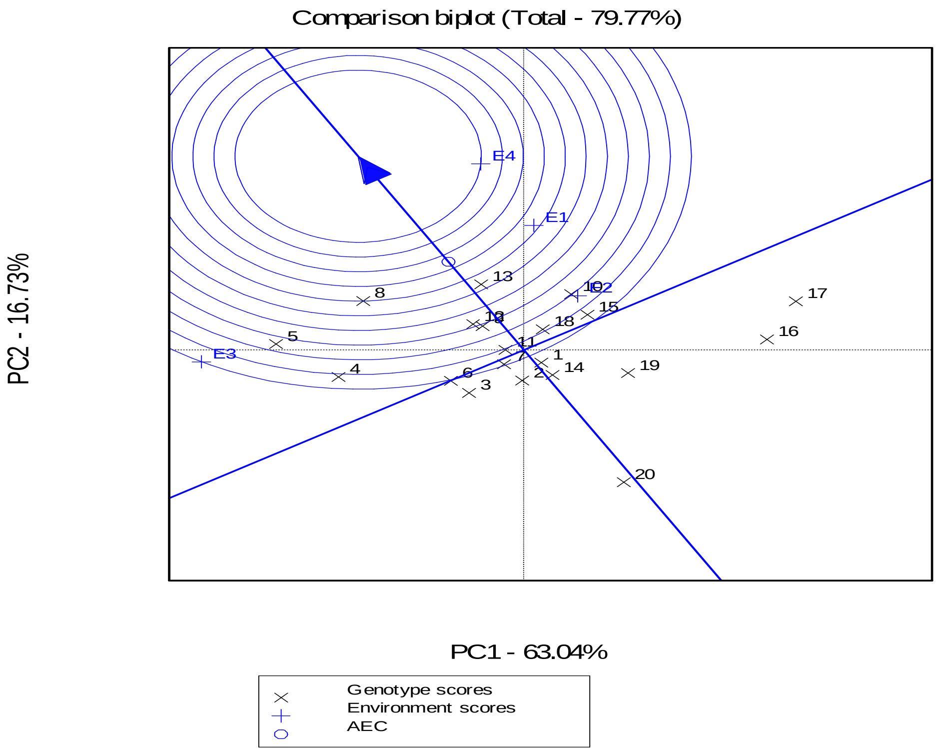

Fig. 4. GGE-biplot showing a comparison of 4 environments with in ideal environment for the lint cotton yield 2016.

Another useful property of the vector is that the length of the vector approximates the standard deviation (CD) within each environment, which is a measure of their discriminating ability of the environment. Thus, E4 (Sohag region) and E3 (Assiut region) were most discriminating (longest vectors). While E1 (sids region) was moderately discriminating (moderate vectors). While E2 (El-Fayoum region) was least discriminating (short vectors).

Similarly to the ideal genotype, the ideal environment is located in the first concentric circle in the environment-focused biplot and desirable environments are close to the ideal environment. Nearest to the first concentric circle, environment E4 (Sohag region) was close to the ideal environment (Fig. 4); therefore, it should be regarded as the most suitable to select widely adapted genotypes.

The length of the average environment vector (the distance from biplot origin and the average environment marker), relative to the biplot size, is a measure of the relative importance of genotype main effect vs. GEI. The longer it is, the more important is the genotype main effect, and the more meaningful the selection based on mean performance. For this study, the length of the average environment vector was sufficient to select genotypes based on yield mean performances.

Thus, in Figure (5) positive correlations were found between E1 (Sids region) and E4 (Sohag region) in a location as the angle between them was less than 90˚. This indicated that environment effect is minimal in the variation of MTY of cotton.

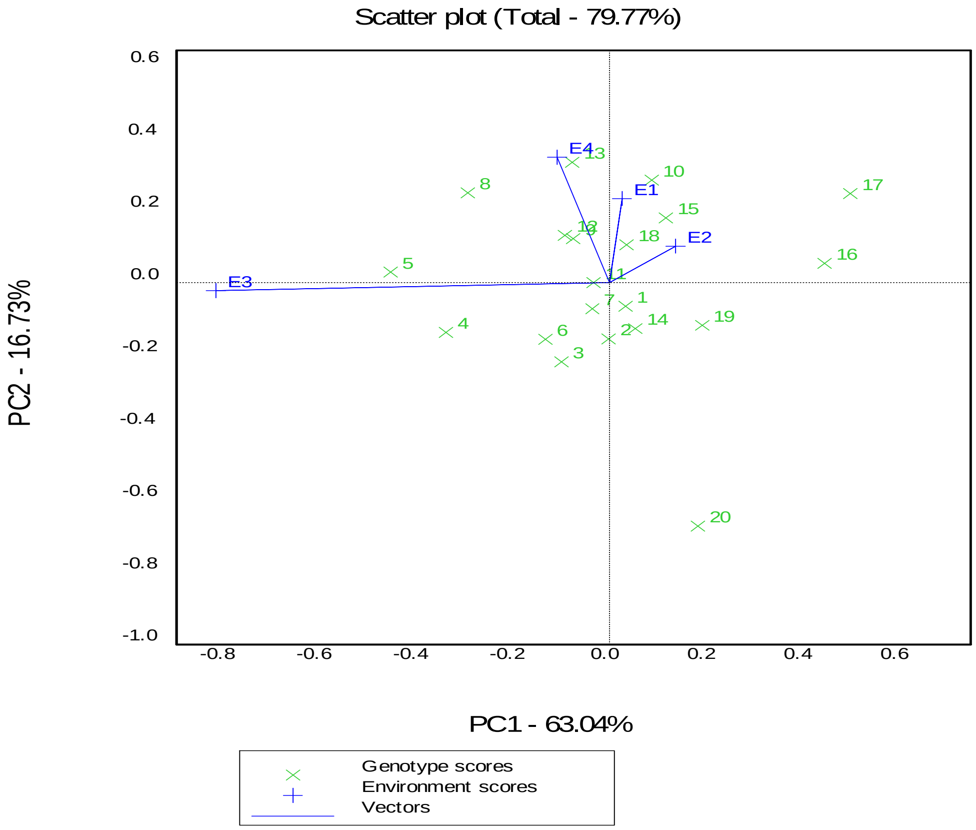

Fig. 5. GGE-biplot view to show relationship among 4 environments, 2016.

The presence of close associations between testing environments reveals that similar information about the genotypes could be obtained from fewer test environments and hence there could be better potential to reduce testing cost under limited resources. Thus, indirect response to selection could be possible between Sohag and Sids region. In addition to, E2 (El-Fayoum region) was different from environment E3 (Assiut region).

Concerning fiber quality had the same Category for long staple cotton in Middle and Upper Egypt (Table 4).

Table 4. Means of fiber properties of 20 genotypes in Trial B at four locations in Middle and Upper Egypt in 2016 season.

Code	Genotypes	Y.St. (unit)	+b (unit)	U.R. (%)	U.H.M (mm)	Mic. (unit)	Maturity
1	(G91 × G90) × G85	2054	11.4	85.0	30.5	3.9	0.94
2	(G 91 × G 90) × {G83 × (G75× 5844)}	2038	11.4	83.8	29.2	3.8	0.94
3	(G 91 × G90) × (G 85 × G 83)	2026	11.7	83.1	29.8	3.7	0.91
4	{(G83 × G80)× G89} ×Karashinky	2020	11.8	85.1	30.1	3.8	0.92
5	(G 91 × G 90) × {(G83 × G80)× G89}	2074	11.4	83.5	30.0	3.8	0.91
6	(G90 × Australian) × {G83 × (G75× 5844)}	2021	11.8	83.4	30.2	4.1	0.93
7	(G91 × G90) × Karashinky	1926	11.8	84.0	30.9	3.9	0.92
8	(G 91 × G 90) × {(G83 × G80)× Dandara}	1966	11.5	84.9	30.6	3.8	0.90
9	« «	2039	12.7	84.5	30.8	3.7	0.92
10	{(G83 × 80) × Dandara} × (G90×Australian)	1935	12.4	84.9	30.4	3.8	0.92
11	(G 91 × G 90) × G80	2113	11.4	83.6	30.1	3.8	0.92
12	« «	2104	11.1	84.0	30.3	4.0	0.92
13	« «	2010	11.2	82.4	30.1	4.0	0.94
14	« «	1985	11.2	84.2	29.1	4.1	0.94
15	[(G83 × G80) × G89] × (G83 × Delta Pine703)]	2088	11.9	84.1	31.2	3.8	0.93
16	« «	2040	12.6	84.5	31.0	3.8	0.93
17	CB 58 × G90	1948	12.0	83.6	30.1	3.9	0.93
18	{(G83 × G80)× G89} × Australian	2003	12.2	83.6	30.2	3.8	0.91
19	Giza 95	1983	11.5	84.7	31.1	3.9	0.93
20	Giza90	2035	11.6	84.0	30.1	3.8	0.93
Mean		2020	11.7	84.0	30.3	3.8	0.90

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التحليل البيانى لتجارب المحصول متعددة البيئات باستخدام طريقة المحاور الثنائية لدراسة ثبات الأداء لبعض التراكيب الوراثية من القطن المصرى

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تحتاج الهجن الجديدة الى الإختبار فى عدد من المواقع قبل ان تكون متاحة للتسجيل.تهدف هذه الدراسة للإنتخاب للثبات بين التراكيب الوراثية لتجربة المحصول المتقدمة (ب) للوصول الى اى التراكيب التى يمكن الإعتماد عليها كأصناف فى زراعتها فى اكثر من منطقة بالوجه القبلى . واشتملت هذه الدراسة على عشرين تركيب وراثى زرعت فى اربع مناطق وهى سدس والفيوم واسيوط وسوهاج فى موسم 2016 كتجارب لقسم تربية القطن. وكانت اهم النتائج كما يلى: كانت جميع مكونات التباين(التراكيب الوراثية-البيئات-التفاعل البيئى الوراثى) معنوية لمحصول القطن الشعر. كانت البيئات هى المصدر الرئيسى فى الإختلافات. فعند استخدام طريقة تحليل المحاور الثنائية GGE اعطى المحور الأول "PC1" ٦٣,٠٤% والمحور الثانى "PC2" ١٦,٧٣% بمجموع ٧٩,٧٧%. كانت التراكيب الوراثية (جـ٩١ × جـ٩٠) × [(جـ٨٣×جـ٨٠)× جـ٨٩] و (جـ٩١×جـ٩٠) × جـ٨٠ الأعلى محصولا مقارنة بثلاثة تراكيب وراثية مقارنة (جيزة ٩٠- جيزة ٩٥ – [(جـ٨٣×جـ٨٠)× جـ٨٩] × أسترالى). كان التركيبين الوراثيين (جـ٩١ × جـ٩٠) × [(جـ٨٣×جـ٨٠)×دندرة] و (جـ٩١×جـ٩٠) × جـ٨٠ الأعلى محصولا والأكثر ثباتا لذا يوصى بهما فى برنامج استنباط اصناف جديدة كتراكيب عالية المحصول وثابتة الاداء. اعطى التركيب الوراثي (جـ٩١×جـ٩٠) × جـ٨٠ أفضل أداء محصول قطن شعر فى منطقتى سدس وسوهاج بينما اعطى الهجين المعزول C.B58× جـ٩٠ أفضل أداء محصول قطن شعر فى منطقت الفيوم بينمااعطت التراكيب الوراثيه الثلاثة (جـ٩١ × جـ٩٠) × [(جـ٨٣×جـ٨٠)× جـ٨٩] و (جـ٩١ × جـ٩٠) × [(جـ٨٣×جـ٨٠)×دندرة] و[(جـ٨٣×جـ٨٠)× جـ٨٩] × كاراشنكى أفضل أداء محصول قطن شعر فى منطقة أسيوط. كانت منطقتى سدس وسوهاج اكثر البيئات ارتباطا حيث اعطت نتائج متشابهة عن التراكيب الوراثية تحت الدراسة. كانت جودة التيلة للتراكيب الوراثية تحت الدراسة ضمن طبقة اقطان طويلة التيلة لمصر الوسطى والعليا.

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