

**BIPLOT ANALYSIS OF GENOTYPE BY ENVIRONMENT INTERACTION FOR
 GRAIN YIELD IN MAIZE
 BY**

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ABSTRACT

Twelve maize hybrids developed at Giza Research Station, Agriculture Research Center, which have been denoted hereafter as G1 to G12, were used in this study. All genotypes were field evaluated in replicated METs at nine locations *i.e.* Behaira (E1), Kafr El Seikh (E2), Dakahlia (E3), Menoufia (E4), Sharkia (E5), Beni Suef (E6), Minia (E7), Assiut (E8), and Sohag (E9). Randomized complete block design (RCBD) with six replications was the design used. The environment effects were considered random effects in the statistical analysis. Analysis of variance indicated significant ($P < 0.01$) genotype by environment interaction (GE) and illustrated the different responses of the evaluated genotypes to environmental factors affecting yield performance on different locations. Variability of grain yield attributed to environments (E) explained about 68% of the total (G + E + GE) variation, whereas genotypes (G) and GE, which were significant ($P < 0.001$), accounted for 15% and 17%, respectively. Applying singular value decomposition resulted significant principal components PC1 and PC2, explaining 61.7% and 17.8% of GGE sum of squares, respectively. Therefore, any graph depending on them illustrates 79.5% of data variation, so these two components were regarded disrespecting other significant PCs. Both crossover and non-crossover GE were existed. Genotypes G7, G8, G6 and G1 are the most staple genotypes in the target region as their markers are concentrated beside the abscissa. E7 is apparently the most discriminative environment as having the longest vector. Two location groups, (E1, E2, E3, E5 and E9) and (E4, E6, E7 and E8) are differently interacting with maize genotypes. The winning genotypes in the "which-won-where" pattern were G2, G11, G12, and G9. This study indicates the possibility of improving progress from selection under different environments conditions via GGE (G+GE) biplot analysis.

Key words: Maize, Corn, Biplot analysis, GGE analysis, Genotype by environment interaction, Multi-environment trials.

INTRODUCTION

Promising genotypes must be evaluated on the basis of multi-environment trials (METs) and multiple traits to ensure that the selected genotypes have acceptable performance in variable environments within the target region and to meet the many-facets of the demand from the producers, processors, and the consumers (Yan and Rajcan, 2002). A genotype is considered to be more adaptive or stable if it has a high mean yield and a low degree of fluctuation in yielding ability when

grown in diverse environments (Arshad *et al.* 2003). Therefore, successful performance of a genotype in METs is essential requirement to register and nominate it as new cultivar.

The yield of a cultivar (or any other measure of cultivar performance) in an environment is a mixed effect of genotype main effect (G), environment main effect (E), and genotype \times environment interaction (GE). Both Gauch and Zobel, (1996) and Yan *et al.*

(2000) reported that, E effect accounts for 80% of the total yield variation and each G and GE effects account for about 10% of METs variations. Significant GE interaction results from changes in the magnitude of the differences among genotypes in different environments or from changes in relative ranking of the genotypes (Allard and Bradshaw, 1964). The GE interaction reduces the correlation between phenotype and genotype and selection progress (Comstock and Moll, 1963).

To understand and illuminate the obstacle problem of GE, many statistical methods have been developed for GE including joint regression (Finlay and Wilkinson, 1963; Eberhart and Russel, 1966; Perkins and Jinks, 1968). Another accomplish to study GE has been suggested by Gauch (1992) known as Additive Main Effects and Multiplicative Interaction (AMMI) depending on principal component analysis, which compile additive main effects with the first principal component in one graph representing interaction patterns. However, Gauch and Zobel, (1996) stated that for the purpose of cultivar evaluation either G or GE are relevant. Furthermore, Yan *et al.* (2000) have been considered those effects in cultivar evaluation using a new model named GGE biplot analysis (Yan, 1999; Yan and Kang, 2003; Yan and Tinker, 2006). Nevertheless, Biplot technique was firstly proposed to summarizing patterns of response that exist in the original data by Gabriel (1971 and 1978).

As documented momentarily, the GGE literature claims that (i) GGE graphs are superior to AMMI for visualizing patterns in yield-trial data, especially for showing which genotype won where and thereby delineating

METs, and (ii) GGE is equivalent to AMMI for gaining predictive accuracy (Gauch, 2006).

GGE-biplot is constructed by the first 2 principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from subjecting environment centered yield data, *i.e.* the yield variation due to GGE, to singular value decomposition (SVD). This GGE-biplot is shown to effectively identify the GE pattern of the data. It clearly shows which genotype won in which environments, and thus facilitates mega-environments (MEs) identification (Yan *et al.*, 2000). METs not only aim to identify superior genotypes for the target region, but also to determine if the target region can be subdivided into different MEs. Investigation of ME is a prerequisite for meaningful cultivar evaluation and recommendation (Yan *et al.*, 2000). The biplot from the site regression model shows that ideal genotypes should have large primary effects (high mean yield) and near zero secondary effects (more stable) and the ideal sites should have large primary effects (high power to discriminate cultivars) and small secondary effects. Such properties tend to occur if the primary effects of cultivars are highly correlated with the cultivar means (Yan *et al.*, 2000; Crossa and Cornelius, 1997). A full description of the interpretation of the biplots of multiplicative models is given in Gower and Hand (1996).

The objectives of this study therefore were (i) to identify genotypes that combine high yields with stability across environments via GGE (genotype plus genotype x environment) biplot methodology and (ii) to study the relationship between different locations used in the current investigation.

MATERIALS AND METHODS

Twelve maize hybrids developed at Giza Research Station, Agriculture Research Center, which have been denoted hereafter as G1 to G12, were used in this study. All genotypes were field evaluated in replicated METs at nine locations *i.e.* Behaira (E1), Kafr El Seikh (E2), Dakahlia (E3), Monofia (E4),

Sharkia (E5), Beni Suief (E6), Minia (E7), Assuit (E8), and Sohag (E9), during the summer season of 2008. Randomized complete block design (RCBD) with six replications was the design used. Each hybrid was planted in a 4-row plot, 6 m long and 0.8 m apart. Planting was done in hills spaced 0.25

m along the row. Two kernels were planted per hill and then thinned to one plant per hill prior to the first irrigation, giving a plant density of approximately 22000 plants feddan⁻¹ (Feddan = 4200 m²). All cultural practices were applied as recommended at the proper time at each environment. At maturity, ears of

the inner rows of each plot was harvested, and weighed. Grain yield was adjusted to 15.5% moisture content and recorded in ardabs feddan⁻¹, where one ardab = 140 kg. Environment effects were considered as random factor in the statistical analysis.

Table (1): Used location characterization

Symbol	Location	Latitude	Longitude§	Elevation
E1	Behaira	31° 2	30° 28	6.7
E2	Kafr El Seikh	31° 7	30° 57	20
E3	Dakahlia	31° 3	31° 21	7
E4	Monofia	30° 36	31° 1	17.9
E5	Sharkia	30° 35	31° 30	13
E6	Beni Suief	29° 4	31° 6	30.4
E7	Minia	28° 5	30° 44	40
E8	Assiut	27° 11	31° 6	71
E9	Sohag	26° 36	31° 38	68.7

§ both latitude and longitude expressed by degree and minute

‡ average temperature and average moisture calculated for maize growing season via day and night

Using SAS version 9.1 for Windows software, the yield data was analyzed using Proc Mixed procedures (SAS Institute, 1990) considering environment and block as random, and genotype as fixed factor. GGE biplot methodology (which is depended on 2 concepts the GGE concept proposed by (Yan *et al.* 2000) and the biplot concept (Gabriel 1971)), was used to visually analyze the METs data. This methodology considers both G and GE factors that are the main sources of variation in analysis of METs data and important in genotype evaluation (Yan *et al.*, 2000, 2001). The GGE-biplot shows the first 2 principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from subjecting environment-centered yield data (yield variation due to G plus GE factors) to singular value decomposition (Yan *et al.*, 2000). The GGE biplot method of Yan *et al.*, 2000 was employed using a modified SAS program of Vargas and Crossa (2000) relates to the creation of files BILOT and LABELS, as well as the routines for making the graphs using PROC GPLOT to study the genotype by environment interaction of yield. This SAS program could be easily

obtained from the web at www.cimmyt.cgiar.org/biometrics (or in the general CIMMYT web page under BSU in the compressed file BILOT.ZIP). The GGE biplot stepped firstly subjecting the GGE matrix, i.e., the environment-centered data, to singular-value (SV) decomposition. The GGE matrix is decomposed into three component matrices-the SV matrix (array), the genotype eigenvector matrix and the environment eigenvector matrix, so that each element in the GGE matrix is recovered through

$$y_{ij} - \mu - \beta_j = \sum_{i=1}^k \lambda_i \xi_{il} \eta_{lj} + \epsilon_{ij}$$

Where y_{ij} = the measured mean yield of genotype l ($l=1, 2, \dots, n$) in environment j ($j=1, 2, \dots, m$); μ = the grand mean; β_j = the main effect of environment j , ($\mu + \beta_j$) begin the mean yield in environment j ; λ_i = the SV of i th principal component (PC), the square of which is the sum of squares explained by PC i ($i=1, 2, \dots, k$, with $k \leq \min(m, n)$ and $k=2$ for a two dimensional biplot); ξ_{il} = the eigenvector of genotype l for PC i ; η_{lj} = the eigenvector of environment j for PC i ; and ϵ_{ij} = the residual associated with genotype l in environment j .

To generate a biplot that can be used in visual analysis of MET data, the SVs have

to be partitioned into the genotype and environment eigenvectors so that the previous equation could be written in the form of:

$$y_{ij} - \mu - \beta_j = \sum_{t=1}^k g_{it} * e_{tj} + \epsilon_{ij}$$

Where g_{it} and e_{tj} are called PC t scores for genotype i and environment j , respectively. In a biplot graph, genotype i is displayed as a point defined by all g_{it} values, and environment j is displayed as a point defined by all e_{tj} values ($t = 1$ and 2 for a two-dimensional biplot). Singular-value partitioning is implemented as:

$$g_{it} = \lambda_t^{f_t} e_{tj} \text{ and } e_{tj} = \lambda_t^{1-f_t} \eta_{ij}$$

Where f_t is the partition factor for PC t . Yan (2002) presented four ways to partition singular value. In the course of the current study three ways were used *i.e.*, environment-focused scaling, genotype-focused scaling and symmetric scaling where f_t are 0, 1 and 0.5, respectively.

The previous methodology and its interpretation of a GGE biplot was firstly described and discussed in Yan (1999), Yan *et al.* (2000) and Saba (2006). Correlation coefficients between pairs of environments were computed using SAS PROC CORR (SAS Institute, 1996).

RESULTS AND DISCUSSION

Genotype evaluation

Analysis of variance for grain yield revealed significant differences ($P < 0.01$) among the genotypes (G) at each Location (macro-environment E) with homogenous error. The combined analysis also revealed

significant differences among the testing environments and genotypes (Table 2). The GE interaction was significant ($P < 0.01$) indicating the influence of environmental conditions in different locations on the yield performance of the evaluated genotypes.

Table (2): Combined analysis of variance for grain yield for 12 maize crosses tested at 9 environments in 2008 season.

Source of variation	df \ddagger	Sum of Squares	Mean squares
Environments (E)	8, 45	10888.6	1360.6**
Genotype (G)	11, 495	2403.2	217.1**
G \times E	88, 495	2704.1	30.7**

** Significant at the 0.01 probability level.

\ddagger Degrees of freedom for the nominator and denominator, respectively.

The proportional participations of E, G and GE factors of the total sums of squares describing their variation were 68, 15 and 17%, respectively (Table 2). The large yield variation due to E is familiar. Gauch and Zobel (1997) reported that, in normal METs, E accounts for about 80% of the total variation, while G and GE each account only for about 10%. They also stated, the large yield variation due to E, which is irrelevant to genotype evaluation and mega-environment investigation, justified the selection of GGE as the model for analyzing the MET data. Applying singular value decomposition resulted significant principal components PC1 and PC2, explaining 61.7% and 17.8% of GGE sum of squares, respectively. Therefore, any graph depending on them illustrates 79.5% of

data variation (Table 3), so these two components were regarded disrespecting other significant PCs.

However, the analyzed data were presented in Table 4. These results accentuate the superiority of five crosses *i.e.*, G11, G2, G7, G1 and G5 as they significantly surpassed the general average. Nevertheless, their ranks changed from an environment to another, which is one aspect of significant GE interaction. It is common for METs data to find a mixture of both crossover and non-crossover types of GE (Kaya *et al.* 2006). In this study, different genotypes produced the highest grain yield in different environments. Genotypes G5, G1, and G7 showed the highest grain yield at environments E1, E4, and E9,

respectively (Table 4). This differential ranking of the previous genotypes across the testing environments revealed that possible crossover GE was existed. In this regard, Mishra *et al.* (2006) stated that crossover interactions are changes in ranks among cultivars across environments. However, crossover GE is not always the case. Genotypes G2 was the highest yielding at environ-

ments E2, E3, E5, and E6. Similarly, G11 possessed the highest yielding at environments E7 and E8 (Table 4). These results in differential change of yield mean but not of ranking of genotypes showed that GE may also have a non-crossover nature. Previous data indicated that both crossover and non-crossover GE were existed.

Table (3): Principal component analysis of environment centered yield data of 12 maize crosses evaluated and tested across 9 environments.

Principle component	df	Singular value¥	Eigen value	Proportional sharing	Cumulative sharing%
PC1	19	56.13	3150.22	61.7**	61.7
PC2	17	30.16	909.53	17.8**	79.5
PC3	15	20.37	414.94	8.1	87.6
PC4	13	16.74	280.28	5.5	93.1
Residual (PC5-PC9)	35	18.77	352.28	6.9	100
Total	99‡	71.47	5107.3‡	100	100

** Significant at the 0.01 probability level

¥ Singular value equals square root of eigen value

‡ Total df equal sums df of G and GEI

‡ Total eigen values equal total sum of squares of G and GE

Table (4): Average grain yield (ardabs/feddan) of evaluated 12 maize crosses (G) tested at 9 environments (E) in 2008 season.

Genotype	E1	E2	E3	E4	E5	E6	E7	E8	E9	G Average
G1	32.8	34.5	34.0	27.5	26.1	25.6	25.0	27.9	25.8	28.8
G2	34.0	39.1	35.6	25.6	27.6	28.6	23.0	27.5	25.8	29.6
G3	33.7	35.2	31.3	23.6	25.2	22.7	28.4	28.2	23.7	28.0
G4	31.6	38.7	34.0	23.5	23.5	22.0	26.8	26.5	24.3	27.9
G5	34.4	37.1	34.2	24.3	27.1	23.1	25.4	27.2	25.2	28.7
G6	34.0	31.8	33.6	23.5	24.4	20.2	22.3	25.1	21.6	26.3
G7	33.9	34.8	34.9	24.8	25.4	26.0	26.4	30.1	25.9	29.1
G8	32.8	31.5	28.0	22.3	24.3	24.3	19.0	23.0	24.9	25.6
G9	31.7	35.4	30.7	23.0	24.2	24.3	18.5	21.3	17.2	25.1
G10	31.3	31.4	29.9	24.1	23.6	25.6	24.8	25.1	23.8	26.6
G11	33.2	35.1	29.6	26.9	24.7	26.7	34.1	33.0	24.4	29.7
G12	32.5	25.8	27.3	23.7	20.5	24.4	17.3	22.5	16.0	23.4
E. Average	33.0	34.2	31.9	24.4	24.7	24.5	24.2	26.4	23.2	27.4
Variance §	1.11	13.44	7.92	2.43	3.42	5.12	21.99	10.98	11.03	1.11
LSD _{0.05}	3.1	3.7	3.2	2.6	2.7	2.4	2.6	3.0	3.4	1.0
CV%	8.2	9.3	8.7	9.1	9.4	8.6	9.5	9.8	12.6	9.5

§ the variance due to genotype within each location

On the other hand, the biplot techniques add another approach to analysis METs data. The GGE biplot model indicates

that ideal cultivars should have large PC1 (high mean yield) and near-zero PC2 (more stable) and the ideal environments should

have large PC1 (high power to discriminate cultivars) and small PC2 (more representative of all sites), according to Yan *et al.* (2000). The average environment (AE) is a hypothetical environment with PC1 and PC2 equal to the average PC1 and PC2 scores across all environments. The AE is superimposed on the standard GGE biplot so that all the genotypes can be projected onto the abscissa of the AE such that the average performance of a genotype can be approximated by its projection onto the abscissa of the AE. A genotype with a positive average performance will show its direction toward the positive direction of the abscissa of AE. An ideal Environment will have large PC1 (high power to discriminate lines) and small PC2 (more representative of all Environments) such that the best Environ-

ment will be the one with the largest PC1 value and zero projection on the AE ordinate (Saba 2006).

Figure (1) displays environment ordination view of GGE biplot that indicates seven maize crosses have average yield more than the general mean with positive PC1 values and can be arranged in descending manner as G11, G7, G2, G5, G4, G1 and G3. The latter rank is closely associated with that derived from convenient methods but this rank derived from analyzing all collected data. However, the near-perfect correlation ($r = 0.98$; $P < 0.01$) between the genotypic PC1 scores and genotypic average yields, subscribes this clear association between resulted superior genotypes.

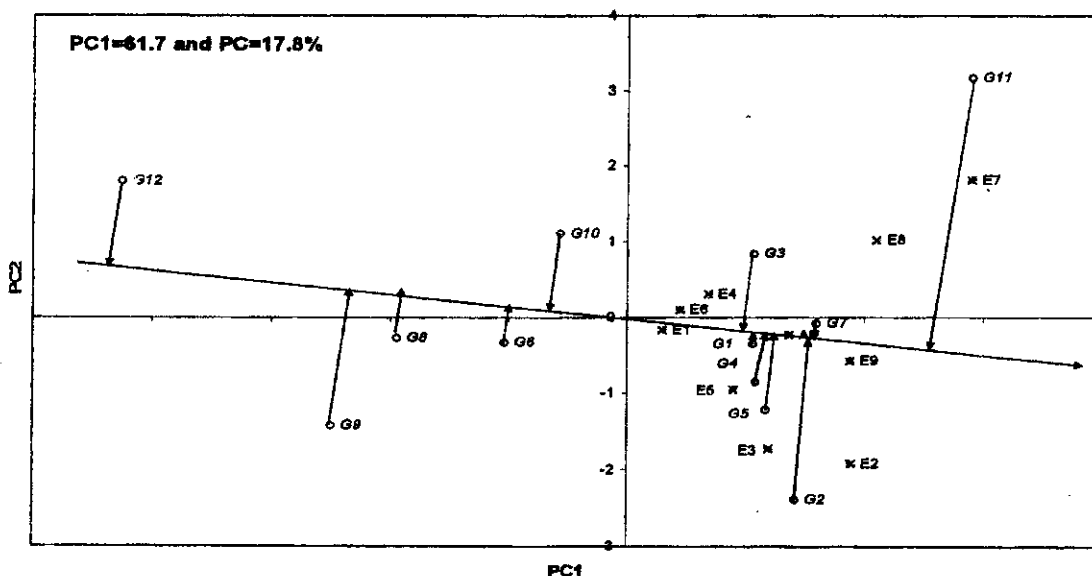


Figure (1): Average Environment ordination view of GGE biplot of 12 maize crosses yield evaluated over 9 environments; the parallel perpendicular lines onto its abscissa express average productivity.

However, focusing on genotypes as in Figure (2) displays the distribution of genotype markers so their stability and their response for environmental changes can be detected. Genotypes G7, G8, G6 and G1 are the most staple genotypes in the target region as their markers are concentrated beside the abscissa. On the other hand, the genotypes G11, G12 and G10 are the more unstable in the upper half of the abscissa and have positive PC2 and the genotypes G2, G9 and G5 are unstable genotype having negative

PC2 values. These two groups show different responses to environmental productivity. It is wisely to note that in the first group The G11 is the most productive genotype and G10 and G12 produce yield less than the average mean. The second group shows two productive genotypes G3 and G5 and one of the worst productive genotypes in the MET. The GGE biplot mode enables researchers to easily identify more productive and stable genotypes.

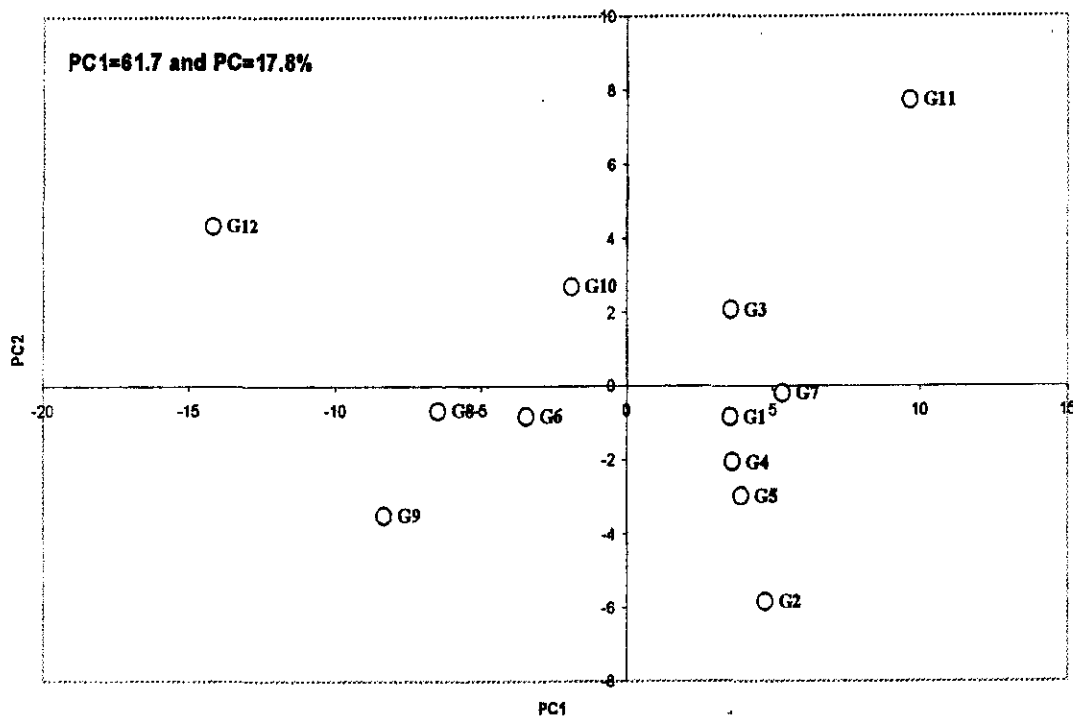


Figure (2): GGE-biplot based on genotype-focused scaling for genotypes. PC and G stand for principal component and genotypes, respectively.

Environment attributes and interrelationships

The vector view of a GGE biplot provides a sufficient brief summary of the interrelationships among the environments (Yan, 2002). This view of the biplot aids understanding of the interrelationships among the environments. The cosine of the angle between the vectors of two environments approximates the correlation coefficient between them. Another useful property of the vector view of the biplot is that the length of the environment vectors approximates the standard deviation within each environment, which is a measure of their discriminating ability.

Figure 3 is biplot, in which the environment markers are connected with the biplot origin point via lines. In the current investigation, the location E7 (El-Menia governorate) is apparently the most discriminative environment as having the longest vector; this result is also supported by the estimated variance among tested genotypes inside E (see Table 4). Four locations (E3, E2, E9 and E8) displayed discriminating capability but less

than E7. On contrast, other four locations didn't display this capability as they had the shortest vectors on the vector view of the GGE biplot. Aiming to clarify this point, the comparison between E7 and E1 was done regarding estimates of the range between the most productive genotype with the worst one and LSD. The range was 3.1 with LSD about 3.1 in E1, while these estimates in E7 (the most discriminating environment) were 16.8 and 2.6. Nevertheless, the recommendation limiting trials at discriminating environments only arise if this result repeated either over years or with other genotype sets.

Obviously, all environments were positively correlated because all angles among them were smaller than 90° that ensuring that all these tested locations locate in one Mega-environment. Obviously, some pairs of vectors displayed approximately identical directions, on other words display angles near zero meaning that these pairs are closely correlated. These pairs are (E2-E5), (E9-E1) and (E8-E4). It is believed that each pair gives similar information so the vector view of a biplot helps identify redundant testing environments.

Obtaining accurate information by using fewer test environments should reduce the cost of testing and increase breeding efficiency. Again the results suggest using less discriminating locations. Comparable results

can be deduced from normal statistical methods like simple correlation (Table 5), but in biplot procedure dislike correlation, all data use to induce information.

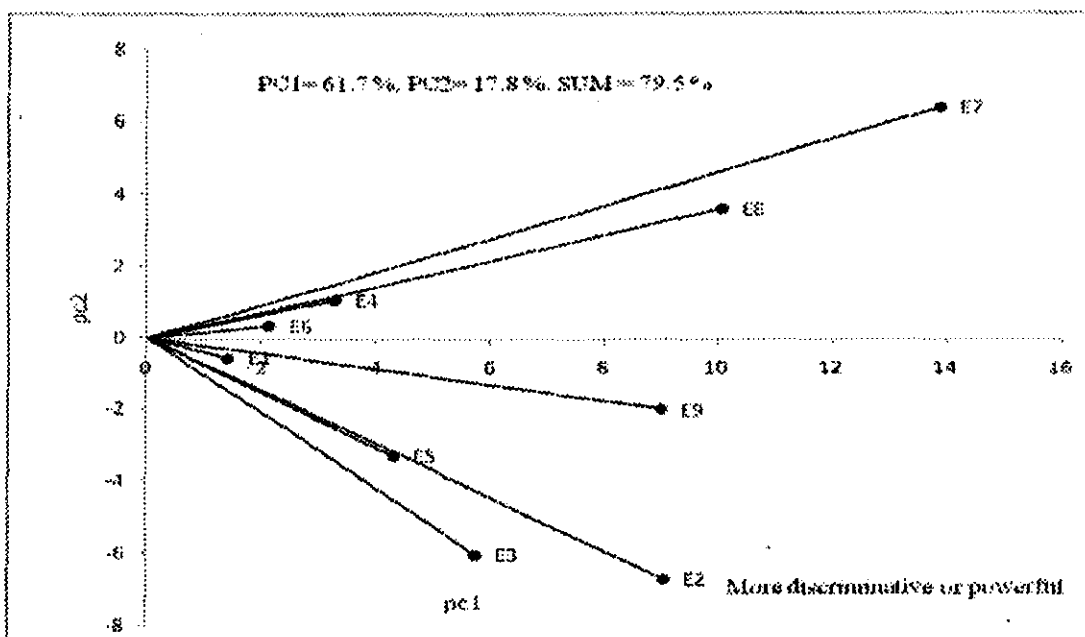


Figure (2): GGE-biplot based on environment-focused scaling for environments. PC and E stand for principal component and environments, respectively.

Table (5): Correlation coefficients among testing environments.

Environments	E1	E2	E3	E4	E5	E6	E7	E8	E9
Behaira (E1)	1.00								
Kafr El Sheikh (E2)	0.82**	1.00							
Dakahlia (E3)	0.62*	0.73**	1.00						
Monofia (E4)	0.21	0.27	0.35	1.00					
Sharkia (E5)	0.85**	0.76**	0.73**	0.43	1.00				
Beni Suef (E6)	0.01	0.16	0.02	0.58*	0.31	1.00			
Minia (E7)	0.50	0.49	0.28	0.58*	0.37	0.15	1.00		
Assuit (E8)	0.50	0.46	0.41	0.72**	0.49	0.34	0.92**	1.00	
Sohag (E9)	0.74**	0.59*	0.55	0.44	0.73**	0.28	0.60*	0.67*	1.00

* indicate significance at $P < 0.05$ and $P < 0.01$, respectively.

However, some inconsistencies may observe because the biplot does not explain 100% of the GGE variation (Yan, 2002). The correlation coefficients among the 9 testing environments are showed and presented in Table 5.

According to multiplicative nature of the principal component analysis, all environments (location markers above the abscissa)

having $PC2 > 0$ interact positively with genotypes (their markers above abscissa) having $PC2 > 0$ similarly, all environments (location markers beneath the abscissa) having $PC2 < 0$ interact positively with genotypes (their markers beneath abscissa) having $PC2 < 0$. On contrast, all environments (location markers above the abscissa) having $PC2 > 0$ interact negatively with genotypes (their markers beneath abscissa) having

PC2<0 and vice versa. Therefore, two location groups, (E1, E2, E3, E5 and E9) and (E4, E6, E7 and E8) are differently interacting with maize genotypes. All the first group locations are northern Cairo except E9 (Sohag) while the second group belonging to Upper-Egypt except E4 (Monofia), however, their specification are displayed on Table (1). Generally, the locations in the second group heater and less relative moisture than the first location group; in addition, they frequently encounter drought weather spells.

Which-Won-Where

The polygon view of a biplot is the best way to visualize the interaction patterns between genotypes and environments and to effectively interpret a biplot (Yan and Kang, 2003). Visualization of the “which-won-

where” pattern of MET data is important for studying the possible existence of different mega-environments in a region (Gauch and Zobel, 1997; Yan *et al.*, 2000, 2001).

The polygon is formed by connecting the markers of the genotypes that are further away from the biplot origin such that all other genotypes are contained in the polygon. The rays in Figure 3 are lines that are perpendicular to the sides of the polygon or their extensions. The number of rays in Figure 4 is 4 rays (equals to the number of winning genotypes). For example, Ray 1 is perpendicular to the side that connects genotypes G2 and G1, Ray 2 is perpendicular to side G11-G12, similarly, Ray 3 is perpendicular to side G12-G9, and Ray 4 to side G9-G2.

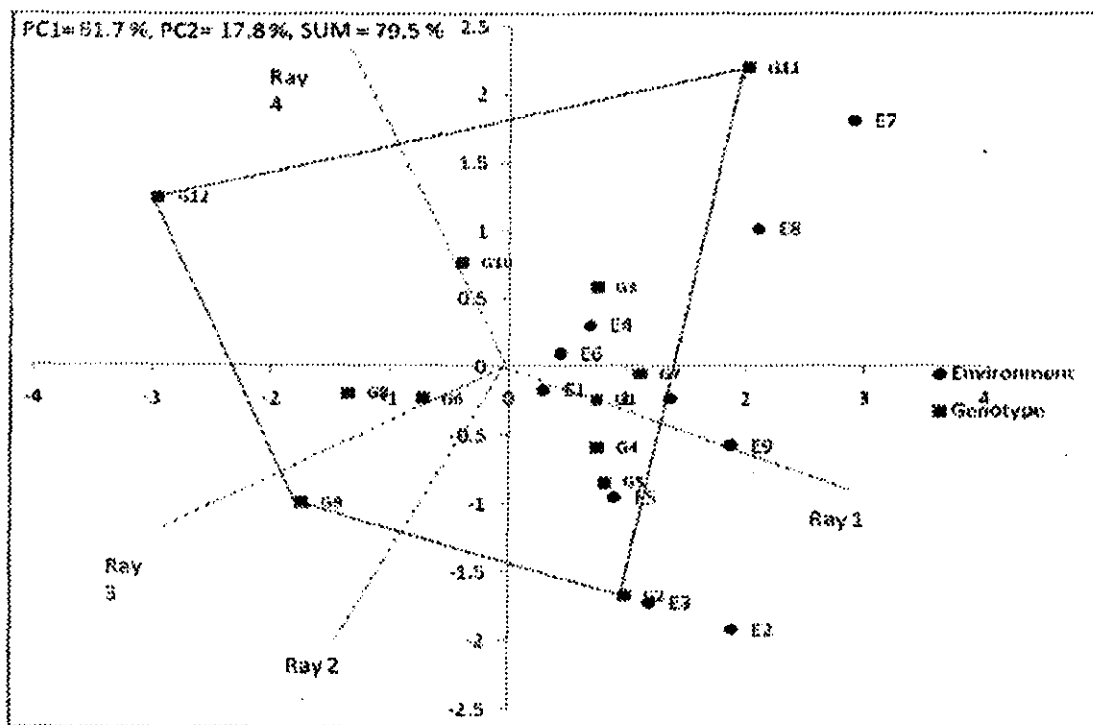


Figure (4):. Polygon views of the GGE-biplot based on symmetrical scaling for the which-won-where pattern for genotypes and environments. PC, G and E stand for principal component, genotypes and environments, respectively.

These 4 rays divided the biplot into 4 sectors, and the testing environments fall into only 2 of them (two environmental groups). An interesting feature of Visualization of the “which-won-where” pattern of MET data is that the vertex genotype(s) for each sector has higher (some times the highest) yield than the

others in all environments that fall in the sector (Yan, 2002). Thus, based on the view of the “which-won-where” polygon, two groups of environments are suggested in Figure 4. The first location group contains environments E2, E3, E5, and E1, with genotype G2 being the winner; the second location group

contains environments E7, E8, E4, E6, and E9, with genotype G11 as the winner one. These results were also confirmed in Table 3, where the winner G2 the highest yielding at environments E2, E3, and E5 and ranked the second at E1. Similarly, G11 was the highest yielding genotype at environments E7 and E8, and was the second at environments E4 and E6. These results suggest that G2 and its partners in first location group are responsive to favorable environmental conditions; and G11 and its partners in the second group are

more withstanding to heater and dryer weather but this aspect needs more investigations.

In brief, this study indicates the possibility of improving progress from selection under different environments conditions via GGE biplot analysis. GGE biplot also allowed visualizing the interrelationship among tested genotypes (including the ranking of tested genotypes based on both mean grain yield and stability), interrelationship among testing environments, and interaction between genotypes and environments.

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استخدام طريقة المحاور الثنائية لتحليل تفاعل التراكيب الوراثية في البيئات
لمحصول الحبوب للذرة الشامية

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استخدم في هذه الدراسة ١٢ هجين ذرة شامية تم استنباطها في محطة بحوث الجيزة - مركز البحوث الزراعية ووزعت من G1 الى G12 وتم زراعتها في ٩ محافظات هم البحيرة - كفر الشيخ - الدقهلية - المنوفية - الشرقية - بنى سويف - المنيا - اسيوط - سوهاج. وتم استخدام تصميم القطاعات الكاملة العشوائية في كل المحافظات في ٦ مكررات.

أعطى تحليل التباين معنوية للتفاعل بين التراكيب الوراثية والبيئات وأظهر تغير في البيئات للمحصول المقدر لكل التراكيب الوراثية. كما أظهرت البيئة ٦٨% من التباين لكل من التراكيب الوراثية والبيئة والتفاعل بينهم. وقد مثلت التراكيب الوراثية ١٥% بينما مثل التفاعل بين التراكيب الوراثية والبيئة ١٧%. ووجد ان هناك ارتباط كامل بين التراكيب الوراثية G1, G5, G4, G7, G3 والبيئات E1, E2, E5, E9. وكذلك البيئات E7 و E8 بينهم ارتباط كامل حيث وجد ان الزاوية المحصورة بينهم صغيرة جداً، وقسمت المحاور الموصلة من نقط المنشأ المحاور الثنائية الى اربع قطاعات ووقعت كل البيئات في اثنين منهم. والتراكيب الوراثية التي وجدت فيهم هم G2, G11, G12, G9 وضحت هذه الدراسة امكانية تطوير برنامج الانتخاب تحت الظروف البيئة المختلفة باستخدام طريقة المحاور الثنائية GGE .