TURKISH J. OF FIELD CROPS 14(2): 123 – 135 2009

ASSESSMENT OF GENOTYPE X ENVIRONMENT INTERACTIONS FOR GRAIN YIELD IN MAIZE HYBRIDS USING AMMI AND GGE BIPLOT ANALYSES

Emre İLKER* Fatma AYKUT TONK[1] Önder ÇAYLAK[1] Muzaffer TOSUN[1]
İlker ÖZMEN[2]

[1]Ege University, Faculty of Agriculture, Department of Field Crops. 35100 Izmir, TURKEY
[2]MayAgro Seed Corporation. Bursa, TURKEY

*Corresponding Author: emre.ilker@ege.edu.tr

ABSTRACT

Seventeen hybrid maize genotypes were evaluated at four locations (Yenişehir-Marmora Region; Bornova-Aegean Region; Ceyhan-Mediterranean Region; Seyhan-Mediterranean Region) in 2005 and 2006 cropping seasons under irrigated conditions in Turkey. The analysis of variance for grain yield of the 17 hybrid genotypes tested in eight environments showed mean squares of environments, genotypes and GEI (genotype x environment interaction) were highly significant and accounted for 62.1%, 12.5% and 25.4% of treatment combination sum of squares, respectively. To determine the effects of GEI on yields, the data were subjected to additive main effects and multiplicative interaction (AMMI) and the GGE biplot analysis.

Although mean grain yield of the check cultivar G12 was higher than those of experimental hybrids, difference between G12 and G16, which is the most stable genotype according to AMMI and GGE biplot, was insignificant. It is understood that the experimental hybrid maize G16 can be proposed in reliably for growing by the farmers. Also, it was detected that only the test environment E3 (Ceyhan location) may be sufficient for deciding about which experimental hybrids can be recommended, instead of four test locations (Ceyhan, Seyhan, Bornova and Yenişehir) in this study. In addition, it is concluded that there is no difference between the AMMI and GGE biplot analysis in evaluation of experimental maize hybrids and test environments in this research and that both methods can be used successfully in determining suitable locations for maize hybrids in the environments under Mediterranean climate conditions.

Key words: AMMI biplot, genotype x environment interaction, GGE biplot, hybrid maize, mega-environments, superiority of genotypes

INTRODUCTION

Maize cultivars are grown in approximately 500.000 hectares annually in Turkey and national average yield is about 7 ton ha^{-1}. Maize production is carried out mostly in Marmara (Marmora), Ege (Aegean) and Akdeniz (Mediterranean) regions of Turkey. Hybrid maize cultivars are grown mainly under irrigated conditions. Hybrid seeds demanded by maize growers are provided by mostly national or international seed companies in Turkey.

The considerable variation in soil and climate has resulted in large variation in yield performance of maize hybrids annually; thus GEI (genotype x environment interaction) is an important circumstance for plant breeders and agronomists. In evaluation of performance of the maize hybrid genotypes and experimental hybrids which are developed by private companies in Turkey, it is prerequisite that in addition to their yield performance, the yield stability of such hybrids should be identified in order to make specific selections and recommendations to maize growers. Selection of experimental hybrid genotypes is based on the evaluation of their phenotypic value in a number of environments. GEI, which is associated with the differential performance of genetic materials, tested in a number of locations and in different years has long been recognized (Lin et al., 1986). Evaluation of genotypic performance in a number of environments provides useful information to identify their adaptation and stability (Crossa, 1990).

Multi-environment yield trials are used commonly to release superior genotypes for target sites in plant breeding programs. GEI is universal phenomenon when different genotypes are tested in a number of environments. The large GEI variation usually impairs the accuracy of yield estimation and reduces the relationship between genotypic and phenotypic values (Nachit et al., 1992). GEI due to different responses of genotypes in diverse environments makes choosing the superior genotypes difficult in plant breeding programs.

Numerous methods for multi-environment trials data have been developed to expose patterns of GxE interaction, for instance type B genetic correlation (Yamada, 1962), joint regression (Finlay and Wilkinson, 1963; Eberhart and Russel,1966; Perkins and Jinks, 1968) and currently AMMI (Gauch, 1992) and GGE biplot (genotype main effect plus genotype-by-environment interaction). AMMI model combines the analysis of variance of genotypes and the environment main effects with principal component analysis of the GEI into a unified approach (Gauch and Zobel, 1996). However GGE biplot method, which is always close to the best AMMI models in most cases (Ma et al., 2004), was recently developed to use some of the functions of these methods jointly. It allows visual examination of the relationships among the test environments, genotypes and the genotype by environment interactions (Ding et al, 2007). The differences of the two methods, GGE biplot analysis is based on environment-centred PCA, whereas AMMI analysis is referred to double centred PCA (Kroonenberg, 1997; Ding et al, 2007). AMMI stands for the additive main effect and multiplicative interaction (Gauch, 1992) and GGE biplot stands for genotype main effect plus GxE interaction (Ma, 2004) even so both methods are based on singular value decomposition (SVD) or principal component analysis and considered to be effective tool to diagnose GEI patterns graphically (Yan and Kang, 2003; Admassu et al., 2008).

Crossa et al. (1990) indicated that the AMMI model can be used to analyze the GEI and to identify the superior hybrid maize genotypes. Also, he pointed out that it can be used in the selection of the best test environments for hybrid maize genotype evaluation. Fan et al. (2007) showed that the GGE biplot methodology was a useful tool for identifying locations that optimized hybrid genotypes performance and for making better use of limited resources available for the maize testing programs.

Annicchiarico (1997) stated that AMMI analysis appears particularly useful for depicting adaptive responses of small grain cereals tested over whole Italy. At the same time, the researcher explained that joint regression and AMMI analysis are more likely to perform alike, and provide similar results, for small grain cereals over coastal and southern areas of Italy, where cold stress is limited.

Nachit et al. (1992) determined that the postdictive AMMI models are superior to the linear regression techniques in accounting for and partitioning GEI in Mediterranean multi-location test trials of durum wheat. In addition, they expressed that predictive assessment is a useful statistical tool in estimating precise yield to make accurate and therefore successful selection in durum wheat breeding programs.

Kaya et al. (2002) suggested that the interaction of the 20 genotypes with six environments was best predicted by the first two principal components of genotypes and environments. Also, they proposed that biplots generated using genotypic and environmental scores of the first two AMMI components can be used by breeders and have an overall picture of the behavior of the genotype, the environment and GEIs. At the same time, Kaya et al. (2006) also evaluated bread wheat genotypes in multi-environment yield trials by using GGE biplot analysis and they determined that there were two proper rain-fed mega-environments in the Central Anatolian Plateau, also they recommended that two mega-environments should be used by rain-fed wheat improvement programs in order to enhance yield-based selection gain in multi-environment yield trials.

Multi-environment trials are widely used for the selection of superior hybrids in public and private sector hybrid maize breeding programs in Turkey. Private sector seed companies willing to market their hybrids in a target region should get them tested in multi-environment trials for two years and recommended by an evaluation board from Turkish Ministry of Agriculture and Rural Affairs. However they are used to evaluate genotypes using F-test based on randomized complete block design

The objectives of this study were to identify the superior experimental hybrids and to select the best location for testing of the hybrids developed in maize breeding program of the private company (MayAgro Seed Corporation) by using and comparing the AMMI and GGE biplot methods.

MATERIALS AND METHODS

Seventeen maize genotypes consisted of 14 experimental hybrids and 3 check hybrids (Table 1) were evaluated at four locations (Yenişehir-Marmora Region; Bornova-Aegean Region; Ceyhan- Mediterranean Region; Seyhan- Mediterranean Region) in 2005 and 2006 cropping seasons under irrigated conditions. Randomized complete block design with three replications was used. Each plot had four rows of 5 m length with spacing of 70 cm between rows and 18 cm between plants within a row. Two seeds were planted per hill and then thinned to one plant per hill to have a final plant density of 79.286 plants ha^{-1}. To reduce border effects, data were recorded from the two central rows of each plot. Fourteen experimental hybrids developed by MayAgro Seed Corporation (Private Company) and three check maize hybrid cultivars were included in this study.

Table 1. Hybrid codes and hybrid definitions of 17 maize genotypes used in the study.

No	Hybrid Code	Hybrid Definition
1	SX896	Experimental Hybrid
2	SX897	Experimental Hybrid
3	SX880	Experimental Hybrid
4	RX9292 (C)	Check Hybrid
5	SX825	Experimental Hybrid
6	SX829	Experimental Hybrid
7	SX733	Experimental Hybrid
8	SX731	Experimental Hybrid
9	SX885	Experimental Hybrid
10	SX886	Experimental Hybrid
11	SX883	Experimental Hybrid
12	P31G98 (C)	Check Hybrid
13	SX813	Experimental Hybrid
14	SX847	Experimental Hybrid
15	SHEMAL (C)	Check Hybrid
16	SX891	Experimental Hybrid
17	SX882	Experimental Hybrid

Table 2. Description of the test locations.

Locations	Mean Seasonal Rainfall* (mm)		Soil Type
	2005	2006	
Adana-Seyhan	(**E1**) 28.4	(**E5**) 18.7	Clay loam
İzmir-Bornova	(**E2**) 21.2	(**E6**) 40.2	Silty clay
Adana-Ceyhan	(**E3**) 26.9	(**E7**) 13.3	Clay
Bursa-Yenişehir	(**E4**) 52.9	(**E8**) 27.9	Clay

*: Mean rainfall during April to October

The locations where the experiment was conducted were different in soil type and mean seasonal rainfall (Table 2). Also the years differentiated in terms of mean seasonal rainfall. Therefore, locations in each year were considered as different environments. Besides, temperature and relative humidity didn't vary in both the locations and the years. Several traits were assessed but only data for grain yield (kg ha^{-1}, at 15.0% grain moisture, estimated on the basis of two plot) was reported here.

Combinations of years (2005 and 2006) and four locations were treated as eight environments (E1-E8). To determine the effects of GEI on yields, the data were subjected to AMMI analysis using XLSTAT for MS Excel. The GGE biplot software (Yan, 2001) was used to show graphically the genotypes and environments. Angles between environment vectors were used to judge correlations (similarities/dissimilarities) between pairs of environments (Yan and Kang, 2003). A GGE distance was computed and correlated with yield-stability statistic (YS$_i$).

RESULTS

The analysis of variance for grain yield (kg ha^{-1}) of the 17 hybrid genotypes tested in eight environments showed that mean squares of environments, genotypes and GEI were highly significant (Table 3) and accounted for 62.1%, 12.5% and 25.4% of treatment combination sum of squares, respectively. This case, along with a highly significant GEI, required using of stability analysis.

Table 3. AMMI partition of genotype x environment interaction for grain yield

Source of variation	d.f.	Mean squares	(%) GxE Explained
Treatments	135	133992.76**	
Genotypes (G)	16	141050.47**	12.5
Environments (E)	7	1605371.40**	62.1
G x E	112	41023.35**	25.4
IPCA1	22	116237.90**	55.7
IPCA2	20	39250.67**	17.1
IPCA3	18	34826.81**	13.6
IPCA4	16	13171.19	4.6
IPCA5	14	12059.82	3.7
IPCA6	12	11605.54	3.0
IPCA7	10	8902.19	1.9
IPCA8	8	2202.48	0.4
Pooled Error	256	15634.22	

*, **: Significant at p = 0.01

The AMMI analysis partitioned the sum of squares of GEI into eight interaction principal components axes (IPCA), of which the first three IPCA were significant. Result from AMMI model showed that the first interaction principal component axis (IPCA1) of the interaction captured 55.7% of the interaction sum of squares. Similarly, the second and third interaction principal component axis (IPCA2 and IPCA3) explained a further 17.1% and 13.6% of the genotype-environment interaction sum of squares. At the same time, IPCA1, IPCA2 and IPCA3 had sum of squares greater than that of genotypes. The mean squares for the IPCA1, IPCA2 and IPCA3 were significant at p=0.01 level and cumulatively contributed to 86.4% of the total genotype-environment interaction.

The criterion of postdictive success of the AMMI model identified the first three IPCA axes in the model and three principal component axes of the interaction were significant for the AMMI model. However Admassu et al. (2008) in accordance with Zobel et al. (1988) proposed that two interaction principal component axes for AMMI model was sufficient for predictive model. Other interaction principal component axes captured mostly non-predictive random variation (noise) and did not fit to predict validation observations. Therefore, the interaction of the 17 hybrid genotypes with eight environments was best predicted by the first two interaction principal components of genotypes and environments. In general, the model chosen by predictive criterion consists of two interaction principal components (Kaya et al., 2002).

A biplot analysis was carried out by using genotypic and environmental scores of the first two AMMI components explaining 72.8% of the GEI variation. A biplot has four sections, depending upon signs of the genotypic and environmental scores (Kaya et al., 2002). The environments took place into the three sections (Figure 1). The best hybrid genotype with respect to environments 1, 5, 6 and 7 was hybrid genotype 12. The hybrid genotype 15 was the best for environments 3 and 8. Hybrid genotypes 10, 11 and 13 were the best for environments 2 and 4.

Genotypes placed near the plot origin were less responsive than genotypes far from it. Genotypes 12 and 15 gave the highest mean yield (largest IPCA1 scores) but genotypes G15 was more stable than genotypes G12, because it has smaller absolute IPCA2 score. Genotypes G3 and G1 appeared to be stable but yielded nearly average at all environments, because they have small IPCA1 scores and relatively small IPCA2 scores.

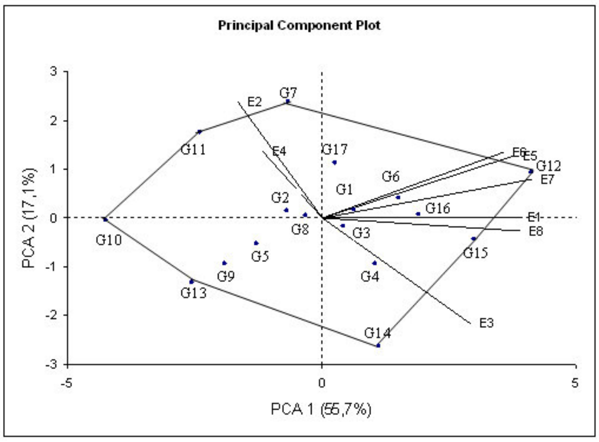

Figure 1. AMMI biplot of 17 maize genotypes and eight environments for grain yield using genotypic and environmental scores.

The IPCA scores of a genotype in the AMMI analysis are an indication of the stability or adaptation over environments. The greater the IPCA scores are, either negative or positive, (as it is a relative value) the more specific adapted is a genotype to certain environments. The more the IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled (Crossa et al., 1990). Since IPCA2 scores also play a significant role (17.1%) in explaining the GEI, the IPCA1 scores were plotted against the IPCA2 scores to more investigate adaptation (Figure 1). Hybrid genotypes 4, 7, 9, 12, 14 and 17 were unstable for all environments. Genotypes 1, 2, 3, 6, 8, 15 and 16 were more stable across environments.

Mean yields of the hybrid genotypes across environments ranged from 12.668-15.605 kg ha^{-1} (Table 4). Reference check hybrid cultivars 12, 15 and 4 yielded 15.605, 14.944 and 13.887 kg ha^{-1}, respectively and experimental hybrids had yields lower than 12 and 15 check cultivars, except 4.

The combined ANOVA indicated that hybrid maize cultivar yields were significantly affected by environment, which explained 62.1% of the total (G+E+GEI) variation. Also, genotype and GEI were found significant and accounted for 12.5% and 25.4% of the total treatment variation, respectively (Table 3). The partitioning of genotype main effect (G) plus genotype by environment (GE) interaction (GGE) via GGE-biplot analysis showed that PC1 and PC2 were significant factors, explaining 55.7% and 17.1% of GGE sum of squares, respectively.

In this study, four different hybrid genotypes gave the highest grain yield in different environments. Genotypes G2 and G17 possessed the highest yield in environments E4 and E2, respectively. Genotype G15 produced the highest yield in environments E3 and E5. On the other hand, hybrid check cultivar G12 exhibited the highest grain yield in environments E1, E6, E7 and E8 (Table 4). These differential and same rankings of hybrids maize genotypes across test environments demonstrated that there exists possible in both crossover and non-crossover GEI. Moreover, these results revealed that GEI may have a non-crossover nature in to a large extent.

Table 4. Mean grain yield (kg ha^{-1}) of 17 maize genotypes tested in 8 environments.

No	E1	E2	E3	E4	E5	E6	E7	E8	Mean
G1	14125	10721	16034	14231	15360	11620	15472	13865	13929
G2	13974	9781	15748	**15948**	13882	10341	14235	14279	13524
G3	14640	10047	16403	15441	14980	10713	14255	14656	13892
G4	14398	9409	16738	14669	14933	10478	15368	15101	13887
G5	14103	10457	16490	15888	13124	10146	12726	13708	13330
G6	14202	13504	16246	13790	14766	11483	15938	16640	14571
G7	13786	14839	15331	15287	15191	12330	14126	13625	14314
G8	14068	12207	16418	15187	12857	11501	13783	14918	13867
G9	12871	12122	16433	14359	12946	9424	12781	13707	13080
G10	11338	14277	15676	15044	11929	8211	11674	13191	12668
G11	12654	14531	14747	15075	13932	10240	13539	13484	13525
G12	**15761**	11919	17343	15011	17125	**13720**	**17143**	**16816**	15605
G13	13674	12569	16427	14641	12046	8047	11609	13833	12856
G14	14045	9190	17724	13331	13286	11089	14334	15357	13544
G15	14460	10580	**18073**	14960	**17309**	11779	16510	15881	14944
G16	15462	12111	16436	14267	16368	10542	14926	16338	14556
G17	14239	**14924**	16243	14622	15240	10594	15134	14888	14486
Mean	13988	11952	16383	14809	14428	10721	14327	14723	13916

A GGE biplot is constructed by plotting the first principal component (PC1) score (55.7%) of the genotypes and the environments against their respective score (17.1%) for the second principal component (PC2) that result from singular value decomposition of the environment-centered or environment- standardized genotype by environment data (Yan et al. 2007). GGE biplot analysis is based on genotype-focused scaling to obtain the location of genotypes. Kaya et al. (2006) expressed that genotypes having PC1 scores > 0 were recognized as high yielding and that those genotypes having PC1 scores < 0 were identified as low yielding. PC2 components of genotypes are related to genotypic stability or instability. The hybrid genotypes having high yield divided into two groups based on their PC2 scores. Groups 1 consisted of 5 stable genotypes (G1, G4, G12, G15 and G16) that were higher yielding, because their near-zero PC2 scores showed genotypic stability. Group 2 contains 4 unstable genotypes (G3, G6, G14 and G17) that were higher yielding since their larger PC2 scores correlated with genotypic instability (Figure 2).

A GGE biplot which was based on environment-focused scaling was described to estimate the pattern of environments (Figure 3). Environmental PC1 scores were obtained in both positive and negative scores. This case exhibited that PC1 scores represent proportional genotype yield differences across environments which were caused by both crossover and non-crossover GEI. Similar to PC1, environmental PC2 scores had both positive and negative scores (Figure 3). To make a decision about hybrid genotypes for evaluation, environments E7 and E5 may be better test environments. Favorable test environments should have larger PC1 scores (more discriminative or powerful) and near-zero PC2 scores (more representative). Test environments with larger vectors (like E3 and E7) are more discriminative for the genotypes. The correlation coefficients among the 8 environments are presented in Table 5. The vector view of the GGE biplot (Figure 3) illustrated a summary of the interrelationships among the environments. The line that connects the biplot origin and markers of the test environment are called environment vectors. The angle between the vectors of 2 environments is related to their correlation coefficient (Kaya et al., 2006).

The 28 correlation coefficients were calculated, 13 of which were significant (Table 5). Six environments were positively correlated because their angles among them were smaller than 90°, except environments E2 and E4. The angles between environments E2, E4 and other six environments (E1, E3, E5, E6, E7 and E8) was larger than 90° and therefore, the correlation between them should be close to zero. In fact, the correlation coefficients were well reflected except environment E3.

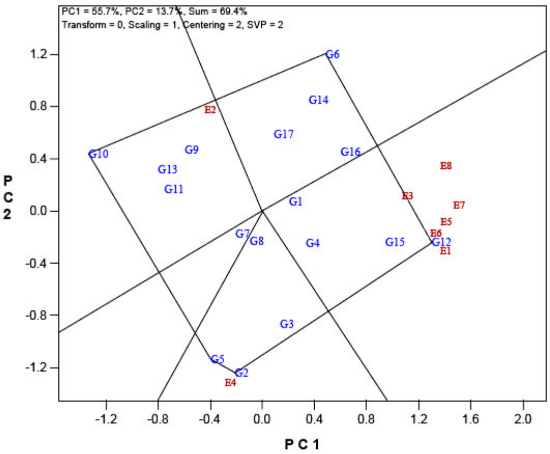

Figure 2. Polygon views of the GGE biplot based on symmetrical scaling for which-won-where pattern for genotypes and environments.

Figure 3 demonstrated that E3 and E7 were the most closely correlated environments, but insignificant correlation coefficient was obtained between them. Some researchers found same inconsistencies and they implied that the biplot analysis did not explain 100% of the GGE variation (Kaya et al., 2006).

The "which-won-where" view of the GGE biplot is an effective visual tool in mega- environment analysis (Yan et al., 2007). The term mega-environment analysis defines the partition of a crop growing region into different target zones (Gauch and Zobel, 1997). It consists of an irregular polygon and lines drawn from the biplot origin. The rays in Figure 2 are lines that intersect perpendicularly sides of the polygon or their extensions. Ray 1 is perpendicular to the side that connects genotypes G6 and G12; Ray 2 is perpendicular to side G12 and G2; Ray 3 is perpendicular to side G2 and G5 extention; Ray 4 is perpendicular to side G5 and G10 and Ray 5 is perpendicular to side G10 and G6. These 5 rays divide the biplot into 5 sectors, and most of the environments fall into 1st of the sectors. If all environments fall into single sector, this indicates that a single genotype has the highest yield in all environments. If environments fall into different sectors, it means that different genotypes win in different sectors (Yan et al., 2007). Six environments, E1, E3, E5, E6, E7 and E8 fell into sector 1 drawn by Rays 1 and 2, indicating that the highest yielding genotype for these six environments was hybrid maize cultivar G12. Environments E2 and E4 fell into sector 4 and sector 2, respectively. Figure 3 indicates that there is one appropriate test environment for evaluation of hybrid maize genotypes in our region. This mega-environment is represented by genotype 12. However, it may be required that the identified mega-environment is verified with multi-year experiments.

Table 5. Phenotypic correlation coefficients among test environments.

	E1	E2	E3	E4	E5	E6	E7
E2	-0.403						
E3	0.525*	-0.588*					
E4	-0.074	-0.002	-0.331				
E5	0.727**	-0.099	0.354	-0.059			
E6	0.665**	-0.109	0.308	-0.039	0.749**		
E7	0.728**	-0.212	0.449	-0.227	0.897**	0.839**	
E8	0.764**	-0.211	0.624**	-0.387	0.664**	0.595*	0.788**

*, **: Significant at P = 0.05 and P = 0.01 respectively.

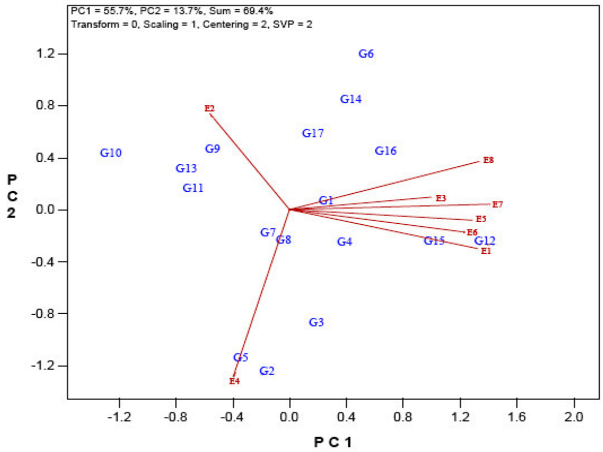

Figure 3. GGE biplot based on environment focused scaling for environments

DISCUSSION

Many statistical methods have been developed for cultivar evaluation in multi-environment trials, including AMMI analysis (Gauch, 1992). The biplot tool has become increasingly popular among plant breeders and agricultural researchers since its use in cultivar evaluation and mega-environment investigation (Yan et al., 2000). AMMI model, GGE model and principal component analysis (PCA) are singular value decomposition (SVD) based statistical analyses often applied to yield-trial data (Gauch, 2006).

New hybrid maize genotypes improved by public or private companies are released for growers after they are registrated in evaluation board of the Ministry of Agriculture and Rural Affairs in Turkey. New experimental hybrids or hybrid maize genotypes introduced from abroad have been tested in multi-environment trials for target maize production environments in Turkey, before they are released for farmers.

On the other hand, all seed companies in Turkey always compete with each other to sell more hybrid seeds for maize growers. Therefore, each company consider more quickly preparing of their new hybrid genotypes for maize farmers after multi-environment trials are completed. If they decide correctly for releasing of which hybrid cultivars are to be grown by farmers, it is presented rapidly their new hybrids to the maize seed markets by the companies. At this point, it is important to decide of which statistical method is used to evaluate multi-location trials data. Public or private companies usually prefer to test their promising genotypes with only F-test and results are accepted for registration by an evaluation board from Ministry of Agriculture and Rural Affairs in Turkey. However researchers from all over the world have been used AMMI and GGE biplot or at least a stability parameter for a long time to analyze GEI. It is of great importance to be proposed true variety to farmers from different environments. We exploited the AMMI and GGE biplot analysis as statistical methods for evaluating experimental maize hybrids using the performance data. AMMI biplot

(Figure 1) and GGE biplot (Figure 3) analysis revealed similar results in identifying the highest yielding hybrid genotypes and in identifying the best test environments. Although the highest yielding genotype was the check cultivar G12, difference for mean grain yield between G12 and G16 was insignificant according to t-test result. Besides, G16 was the best stable genotype in both of AMMI and GGE biplot statistical analyses in this study. When we consider the test environments in experiments, six similar test environments (E1, E3, E5, E6, E7, E8) were determined as target growing environments in both AMMI biplot and GGE biplot analysis. Environment E3 was found to be the highest yielding location among the target environments in both statistical methods. Also, Kaya et al. (2006) determined that one test environment (Çumra) was the best representative of overall environments and the most powerful to discriminate bread wheat genotypes. According to the results of the AMMI and GGE biplot analysis obtained the similar findings from our multi-environment trials data, both of statistical methods can be used reliably by the plant breeders to evaluate maize experimental hybrids and to identify proper test environments.

CONCLUSION

There is a severe competition among the private seed companies in hybrid seed production. New hybrid genotypes have been developed by each private company to market their hybrid seeds in target regions. One hybrid genotype G16 is to be registrated by evaluation board, which has the highest yield among experimental hybrids.

It is understood that the experimental maize hybrid G16 can be proposed safely to be grown by the farmers. Also, it was detected that only the test environment E3 (Ceyhan location) can be sufficient for deciding about which experimental hybrids is recommended, instead of four test locations (Ceyhan, Seyhan, Bornova and Yenişehir) in these trials. This information should be useful for plant breeders of private companies in performance trials by targeting appropriate experimental hybrids to different regions and by identifying the best test environments to use economically limited resources such as time and money. In addition, it was concluded that there is no difference between the AMMI and GGE biplot analysis in evaluation experimental maize hybrids and test environments in this study and that both methods can be used successfully in determining suitable locations for maize hybrids in the environments under Mediterranean climate conditions.

ACKNOWLEDGEMENTS

We are grateful to Dr. Weikai Yan from Eastern Cereal and Oilseed Research Centre, Canada for analyzing our data with GGE biplot software and we gratefully acknowledge the collaboration of MayAgro Seed Corporation.

LITERATURE CITED

Annicchiarico, P., 1997. Joint regression vs. AMMI analysis of genotype-environment interactions for cereals in Italy. Euphytica 94: 53-62.

Admassu, S., Nigussie, M., Zelleke, H., 2008. Genotype x environment interaction and stability analysis for grain yield (*Zea mays* L.) in Ethiopia. Asian J. Plant Sci., **7** (2): 163-169.

Crossa, J., 1990. Statistical analysis of multilocation trials. Adv. Agron., 44: 55-85.

Crossa, J., Gauch, H.G., Zobel, R.W., 1990. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. Crop Sci., 30: 493-500.

Ding, M., B. Tier, W. Yan, 2007. Application of GGE biplot analysis to evaluate Genotype (G), Environment (E) and GxE interaction on *P. radiata*: a case study. Paper presented to Australasian Forest Genetics Conference Breeding for Wood Quality, 11-14 April 2007, Hobart, Tasmania, Australia.

Eberhart, S.A., and W. A. Russel. 1966. Stability parameters for comparing varieties. Crop Science, 6:36-40.

Fan, X.M., Kang, M.S., Chen, H., Zhang, Y., Tan, J., Xu, C., 2007. Yield stability of maize hybrids evaluated in multi-environment trials in Yunnan, China. Agron. J., 99: 220–228.

Finlay, K.W., and G. N. Wilkinson. 1963. The analysis of adaptation in a plant breeding programme. Aust. J. Agri. Res. 14: 742-754.

Gauch, H.G., 1992. Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Elsevier, Amsterdam, 278 pp.

Gauch, H.G. and Zobel, R.W., 1996. AMMI analysis of yield trials. In: Genotype by Environment Interaction (Kang, M.S., Gauch, H.G., ed.). CRC Press, Boca Raton, FL, pp.85-122.

Gauch, H.G. and Zobel, R.W., 1997. Identifying mega-environment and targeting genotypes. Crop Sci., 37: 311-326.

Gauch, H.G., 2006. Statistical analysis of yield trials by AMMI and GGE. Crop Sci., 46: 1488-1500.

Kaya, Y., Palta, C., Taner, S., 2002. Additive main effects and multiplicative interactions analysis of yield performance in bread wheat genotypes a cross environments. Turk. J. Agric. For., 26: 275-279.

Kaya, Y., Akcura, M., Taner, S., 2006. GGE-biplot analysis of multi-environment yield trials in bread wheat. Turk. J. Agric. For., 30: 325-337.

Kroonenberg, P.M., 1997. Introduction to biplots for GxE Tables, University of Queensland, Brisbane. http://www.ggebiplot.com/Kroonenberg1997.pdf Access date: 07.08.2009.

Lin, C.S., Binns, M.R., Lefkovitch L.P., 1986. Stability analysis: Where do we stand? Crop Sci., 26: 894-900.

Ma, B. L., W. Yan, L. M. Dwyer, J. Frégeau-Reid, H. D. Voldeng, Y. Dion, and H. Nass. 2004. Graphic analysis of genotype, environment, Nitrogen fertilizer, and their interaction on Spring Wheat yield. Agron. J., 96: 169-180.

Nachit, M.N., Sorrells, M.E., Zobel, R.W., Gauch, H.G., Fischer, R.A., Coffman, W.R., 1992. Association of environmental variables with sites'mean grain yield and components of genotype-environment interaction in durum wheat. J. Genet. Breed., 46: 369-372.

Yamada, Y. 1962. GEI and genetic correlation of the same trait under different environments. Jap. J. Genetics, 37:498-509.

Yan, W., Hunt, L.A., Sheng, Q., Szlavnics, Z., 2000. Cultivar evaluation and mega-environment investigation based on GGE biplot. Crop Sci., 40: 596-605.

Yan, W., 2001. GGE biplot: A windows application for graphical analysis of multi-environment trial data and other types of two-way data. Agron. J., 93: 1111-1118.

Yan, W., Kang, M.S., 2003. GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, FL, 288 pp.

Yan, W., Kang, M.S., Ma, B., Woods, S., Cornelius, P.L., 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci., 47: 643-655.

Zobel, R.W., Wright, M.J., Gauch, J.H.G., 1988. Statistical analysis of a yield trial. Agron. J., 80: 388-393.