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Additive main effects and multiplicative interaction (AMMI) and GGE-biplot analysis of genotype × environment interactions for grain yield in bread wheat (*Triticum aestivum* L.)

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The combine ANOVA analysis for grain yield of 10 wheat genotypes at 12 environments showed that bread wheat grain yields were significantly affected by E (environment), which explained 75.01% of the total treatment (G+E+GEI) variation, whereas the G (Genotype) and GEI were significant and accounted for 9.48 and 15.5% respectively. Additive main effects and multiplicative interaction (AMMI) analysis indicated that three principal components (PCAs) were significant (P < 0.01). PCA 1, PCA 2, and PCA 3 accounted for 65.49, 17.10 and 10.11% of the GE interaction, respectively. A GGE-biplot based on genotype-focused scaling was depicted in order to detect the locations of genotypes, whereas the wheat genotypes were divided into 4 groups based on their scores of PCA1 and PCA2. The first group included on 3 stable genotypes (G2, G10 and G6) that were highest yielding. As for Group 2 included 2 unstable genotypes (G4 and G1) that were higher yielding, while the Group 3 (G5, G7 and G8) were low yielding and stable genotypes, and Group 4 consist of 2 genotypes (G9 and G3) that were low yielding and genotypic instability. The correlation coefficients among the 12 test environments and the vector view of the GGE-biplot provide a succinct summary of the interrelationship between the environments. Among 67 correlation coefficients, 38 of which were significant. All environments were positively correlated except that environment E5 negatively correlated with E9, E12 and E10.

Key words: Additive main effects and multiplicative interaction (AMMI), additive main effects and multiplicative interaction, bread wheat, genotype-by-environment interaction (GEI), genotype x environment interaction, GGE-biplot, multi environment trials (METs), principal component (PC).

INTRODUCTION

Wheat is the most important cereal crop not only in Egypt but also all over the world, which is receives the most attention of specialists in plant breeding and production. Its production in many regions of the world is below average because of adverse environmental conditions. Genotype-by-environment interaction (GEI) refers to the differential responses of different genotypes across a range of environments (Kang, 2004). This is a universal issue relating to all living organisms, from bacteria to plants to humans (Kang, 1998), and it is important in agricultural, genetic, evolutionary, and statistical research. In breeding program, GEI cause many difficulties, whereas the environmental factors such as temperature and drought stress affect the performance of genotypes change depending on both micro and macro environmental levels. GE interaction reduces the genetic

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progress in plant breeding programs through minimizing the association between phenotypic and genotypic values (Comstock and Moll, 1963). Multi-environment yield trails are essential in estimation of GE interaction and identification of superior genotypes in the final selection cycles (Kaya et al., 2006; Mitrovic et al., 2012).

The use of different planting dates allow for subjecting the plant at different developmental stages to various temperature regimes. However, high temperature during the grain filling period is a major environmental factor which drastically reduces wheat production in Upper Egypt (Kheiralla et al., 2001). Heat stress is a major limitation to wheat (*Triticum aestivum* L.) productivity in arid, semiarid, tropical and subtropical regions of the world (Ashraf and Harris, 2005). Consequently, development of heat-tolerant cultivars is of major concern in wheat breeding programs. A detailed understanding of the genetics and physiology of heat tolerance as well as the use of the proper germplasm and selection methods will facilitate the development of heat tolerant cultivars (Mohammadi et al., 2007).

Selection for high yield potential has frequently led to some yield improvements under stress conditions (Araus et al., 2002, 2008). In these cases the breeders have selected plants characterized by high yield potential and high yield stability, with the latter being attributed to a minimal GEI. This implies that traits maximizing productivity normally expressed in the absence of stress, can still sustain a significant yield improvement under mild to moderate stress (Slafer et al., 2005; Tambussi et al., 2005). Phenotypes are a mixture of genotype (G) and environment (E) components and interactions (GxE) between them. GEI complicate the process of selecting of genotypes with superior performance. Consequently, Multi-environment trails (METs) are widely used by plant breeders to evaluate the relative performance of genotypes for target environments (Delacy et al., 1996).

Numerous methods have been developed to reveal patterns of GEI, such as joint regression (Finlay and Wilkinson, 1963; Eberhart and Russel, 1966; Perkins and Jinks, 1968), sum of squared deviations from regression (Eberhart and Russel, 1966), stability variance (Shukla, 1972), coefficient of determination (Pinthus, 1973), coefficient of variability (Francis and Kanneberg, 1978), and type B genetic correlation (Burdon, 1977; Yamada, 1962) These methods are commonly used to analyze MET data to reveal patterns of GE interaction. Alternatively, the additive main effects and multiplicative interaction (AMMI) model have led to more insight in the complicated patterns of genotypic responses to the environment (Gauch and Zobel, 1988; Zobel et al., 1988; Gauch 1992, 2006). These patterns have been successfully related to biotic and abiotic factors (Romagosa et al., 1993; Royo et al., 1993).

Yan et al. (2000) proposed another methodology known as GGE-biplot for graphical display of GE interaction pattern of MET data with many advantages. GGE biplot analysis considers both genotype (G) and GE interaction effects and graphically displays GE interaction in a two way table (Yan et al., 2000). GGE biplot is an effective method based on principal component analysis (PCA) to fully explore MET data. It allows visual examination of the relationships among the test environments, genotypes and the GE interactions.

This is done using singular value decomposition to break the data matrix into component matrices. The first two principle components (PC1 and PC2) are used to produce a two-dimensional GGE-biplot. If a large portion of the variation is explained by these components, a rank-two matrix, represented by a GGE-biplot, is appropriate (Yan and Kang, 2003). Using a mixed model analysis may offer superior results when the regression of genotype by environment interaction on environment effect does not explain all the interaction (Piepho, 1997; Yan and Rajcan, 2002).

In this work we have attempted to describe GEI on grain yield by characterizing genotypic responses to a set of contrasting environmental conditions. To provide insight into GEI, external genotypic and environmental information has been incorporated into statistical models that allow a direct interpretation of GEI (Denis, 1988; van Eeuwijk et al., 1996). As a preliminary exploratory tool, AMMI models were used to represent an additive component, and the effect of interaction (Gauch, 1992). GGE-biplots representing mean vs. stability and “ideal” genotype was constructed with genotype focus scaling for comparison the genotypes with the ideal genotype.

MATERIALS AND METHODS

This study carried out in 2010/2011, and 2011/2012 seasons at the Research Farm of Faculty of Agriculture, Sohag University, Egypt. The soil was reclaimed with top layer (25 cm) of clay-loam. Ten genetically diverse wheat cultivars differing in adaptation to heat and drought stress were used in Table 1. Field experiments were carried out in 12 environments (2 years, 2 sowing dates and 3 drought treatments). The experimental layout at each environment was a completely randomized block design with three replicates. In each environment plots size was 10.5 m^2, the drought treatments were (normal Irrigation, withholding water from tillering up to anthesis and from Anthesis to maturity), and two sowing dates were used (15 November and 5 December) in both seasons, all other agricultural practices were applied as recommended. The more information on the environments is given in Table 2. The grain yield (t/ha) was obtained by converting plot grain yield (kg) to productivity tons per hectare.

Statistical analysis

In ANOVA non-additive residue is GE interaction. The multiplication part in AMMI model uses PCA analysis to decompose the interaction into several principal components (PCA axis) from 1 to N and residue which remains if not all possible PCA axis are included. G-1 and E-1 are the possible numbers of Axis, but usually only the first few are of interest. The AMMI model is:

$$Y_{ij} = \mu + g_i + e_j + \sum_{1}^{N} \Lambda_k Y_{ik} \delta_{jk} + \varepsilon_{ij}$$

Table 1. List of Egyptian Bread wheat entries and their pedigree which were evaluated in 12 environments.

Code	Name	Pedigree
G1	Giza 164	Kavkas/Buho "s"//Kal/Bluebird =Veery #5
G2	Sakha 8	Indus/Norteno "s"
G3	Sakha 69	Inia - RL 4220//Siete Cerros/Yaqui 50
G4	Gemmeiza 3	Bb/Siete Cerros//Yaqui 50/Kal*3//Sakha 8/4/Prv/WW/3/3/Bg"s"ON CGM-4024-1-GM-2GM-0GM
G5	Gemmiza 7	CMH74 A. 630/5x//Seri 82/3/Agent
G6	Sids 1	HD2172/Pavon "s"//1158.57/Maya74 "s"
G7	Gemmeiza 1	Maya "s"/On//1160 147/3/Bluebird/Gal 1/4/Chat "s"
G8	Sahel 1	N.S.732/Pim /Vee"s"Sd735-4sd-1sd-)sd
G9	Giza 165	Ciano/ Maris Fundin//Mantaro
G10	Giza 168	MRL/BUC//Seri.z

Table 2. Characterization of the 12 Environments used in this investigation

Code	Sowing date	Drought stress stage	Cropping season
E1	15 November	S_0: Normal Irrigation	2010 - 2011
E2	15 November	S_1: Withholding water from tillering up to anthesis	2010 - 2011
E3	15 November	S_2: Withholding water from anthesis up to maturity	2010 - 2011
E4	5 December	S_0: Normal Irrigation	2011 - 2012
E5	5 December	S_1: Withholding water from tillering up to anthesis	2011 - 2012
E6	5 December	S_2: Withholding water from anthesis up to maturity	2011 - 2012
E7	15 November	S_0: Normal Irrigation	2010 - 2011
E8	15 November	S_1: Withholding water from tillering up to anthesis	2010 - 2011
E9	15 November	S_2: Withholding water from anthesis up to maturity	2010 - 2011
E10	5 December	S_0: Normal Irrigation	2011 - 2012
E11	5 December	S_1: Withholding water from tillering up to anthesis	2011 - 2012
E12	5 December	S_2: Withholding water from anthesis up to maturity	2011 - 2012

Where Y_{ij} is the grain yield of the i-th genotype in the j-th environment, μ is the grand mean, g_i and e_j are the genotype and environment deviation from the grand mean, respectively, λ_k is the eigenvalue of the PCA axis k, γ_{ik} and δ_{jk} are the genotype and environment principal component scores for axis k, N is the number of principal components retained in the model, and ε_{ij} is the residual term.

GGE-biplot methodology, which is composed of 2 concepts, the biplot concept (Gabriel, 1971) and the GGE concept (Yan et al., 2000) was used to visually analyze the METs data. This methodology uses a biplot to show the factors (G and GEI) that are important in genotype evaluation and that are also the source of variation in GEI analysis of METs data (Yan et al., 2000). 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 GGE) to singular value decomposition (Yan et al., 2000). In the current study, genotype-focused scaling was used in visualizing for genotypic comparison, with environment-focused scaling for environmental comparison. The statistical analysis was conducted using GenStat 12th edition (Glaser, 2010).

RESULTS AND DISCUSSION

The combine ANOVA and AMMI analysis (Table 3) for grain yield at 12 environments showed that bread wheat grain yields were significantly affected by E, which explained 75.01% of the total treatment (G+E+GEI) variation, whereas the G and GEI were significant and accounted for 9.48 and 15.5% respectively. Similar results obtained by Kaya et al. (2006) and Farshadfar et al. (2012). In their study, the effects of E, G and GEI account for 81, 7.3 and 11.7% of the total treatments variation respectively. According to Gauch and Zobel (1996, 1997), in standard muti-environment trials (METs), environment effect acts 80% of the total sum of treatments and 10% effect of genotype and interaction. In additive variance, the portioning of GEI ss data matrix by using AMMI analysis indicated that three PCAs were significant ($P < 0.01$). PCA 1, PCA 2, and PCA 3 accounted for 65.49, 17.10 and 10.11% of the GE interaction, respectively. The three PCAs represent a total of 92.70% of the interaction variation (Table 3). Similar results were obtained by Mohammadi and Amri (2009), their found that three principal component (PCA1, PCA 2 and PCA 3) were significant and represented 40.80, 2.71 and 8.25% of the GE interaction respectively.

A wide yield variation explained by environments

Table 3. AMMI analysis of variance for grain yield (t/ha^2) of 10 bread wheat genotypes grown at 12 environments.

Source	df	SS	MS	F	% SS	Prob.
Block	24	9.24	0.385	1.40		N.S
Treatment	119	611.30	5.14	18.69		**
Genotypes	9	57.95	6.44	23.42	9.48	**
Env.	11	458.57	41.69	151.60	75.01	**
Gen.&Env.	99	94.75	0.96	3.491	15.5	**
IPCA 1	19	62.05	3.26	11.85	65.49	**
IPCA 2	17	16.20	0.95	3.45	17.10	**
IPCA 3	15	9.58	0.64	2.33	10.11	**
IPCA 4	13	5.31	0.41	1.49	5.56	NS
Residual	35	1.51	0.043	0.156	1.59	NS
Error	216	59.40	0.275			
Total	359	679.94	1.71			

**Significant at the 0.01 level of probability

Table 4. Average grain yield (t/ha^2) of 10 bread wheat genotypes tested across 12 environments.

Gen / Env	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	Mean
G1	6.103	*5.235*	3.154	2.99	3.543	5.605	4.980	3.424	*3.441*	6.262	5.276	5.313	4.611
G2	5.789	4.146	3.178	2.575	5.711	5.21	4.369	3.233	2.822	5.722	5.215	5.117	4.424
G3	5.344	3.945	2.711	2.306	3.768	4.664	3.800	2.799	2.663	3.318	4.403	4.44	3.847
G4	6.590	4.349	3.181	1.992	6.322	5.676	4.678	3.384	2.044	6.477	5.784	5.682	4.68
G5	5.486	3.867	2.453	2.346	5.061	4.662	3.777	2.522	2.749	5.531	4.991	4.507	3.996
G6	5.727	3.915	3.676	2.184	4.463	5.202	4.224	3.714	2.209	5.416	4.336	5.091	4.18
G7	6.124	3.143	2.865	1.825	4.153	4.291	2.627	2.785	1.995	5.761	4.175	4.118	3.655
G8	4.604	3.383	3.205	2.284	4.589	4.331	3.613	2.625	2.614	4.533	4.114	4.179	3.628
G9	5.231	2.993	1.842	1.631	4.974	3.943	2.765	1.846	1.992	5.185	4.51	3.821	3.394
G10	*6.509*	4.635	*4.198*	*3.177*	*6.336*	*5.902*	*4.941*	*4.193*	3.307	*6.294*	*5.610*	*5.828*	5.078
Mean	5.751	3.961	2.992	2.331	4.892	4.949	3.977	3.053	2.584	5.65	4.841	4.81	4.1493

indicated that the environments were diverse, with large differences between environmental means causing most of the variation in grain yield. Grain yield of environments ranged from 2.331 t/ha in E4 to 5.751 t/ha in E1. Genotype grain yield ranged from 3.394 t/ha in G9 to 5.087 t/ha in G10 (Table 4).

A GGE-biplot based on genotype-focused scaling was depicted in order to detect the locations of genotypes, where the genotypes that had PC1 scores > 0 were identified as higher yielding, while the genotypes that had PC1 scores < 0 were identified as lower yielding (Figure 1 and Table 4). In contrast PC2, which was related to genotypic stability or instability, divided the genotypes of interest into 4 groups based on their scores. The first group included on 3 stable genotypes (G2, G10 and G6) that were highest yielding, since near-zero PC2 scores showed genotypic stability. As for Group 2 included 2 unstable genotypes (G4 and G1) that were higher yielding, as absolute larger PC2 scores were associated with genotypic stability, while the Group 3 (G5, G7 and G8) were low yielding and stable genotypes, and Group 4 consist of 2 genotypes (G9 and G3) that were low yielding and genotypic instability, these results agreements with those obtained by Kaya et al. (2006).

Figure 2 showed that, estimation of yield and stability of genotypes was done by using so-called average coordinates of the environment (AEC) methods (Yan, 2001; Yan and Hunt, 2001). The average environment is defined by the average values of PC1 and PC2 for the all environments and it is presented with a circle. The average ordinate environment (AOE) defined by the line which is perpendicular to the average environment axis (AEA) line and pass through the origin. This line divides the genotypes in to those with higher yield than average and in to those lower yield than average. By projecting the genotypes on AEA axis, the genotypes are ranked by yield, where the yield increases in the direction of arrow. In this study the highest yield had genotypes G10, G4, G1, G2, G6 and the lowers had G9, G7, G8, G3 and G5. Stability of the genotypes depends on their distance from

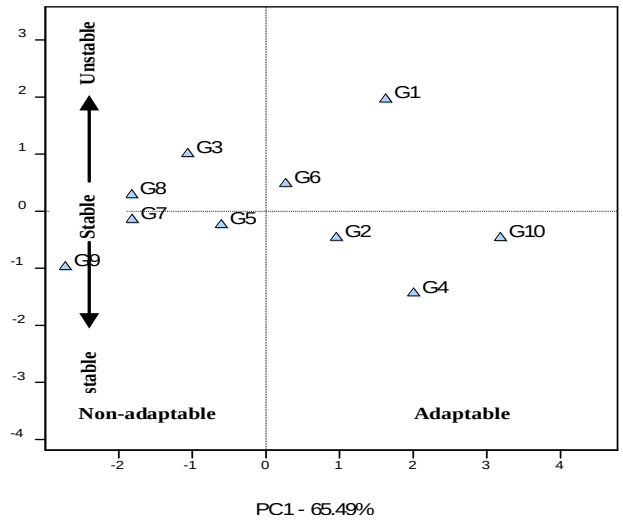

Figure 1. GGE-biplot based on genotype-focused scaling for genotype. PC and G stand for principal component and genotypes, respectively.

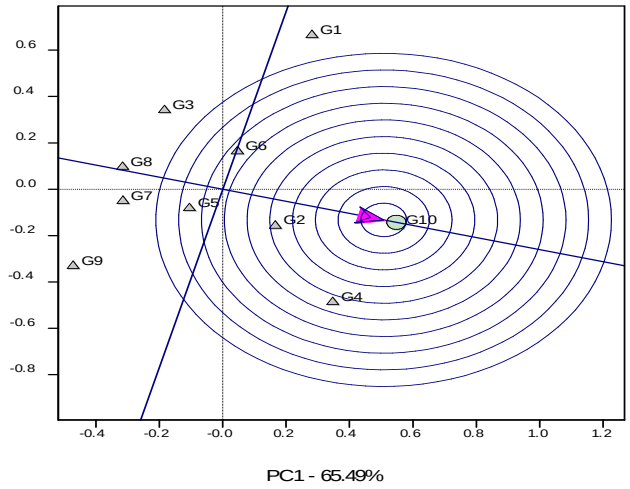

Figure 3. GGE-bioplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype. PC and G stand for principal component and genotypes, respectively.

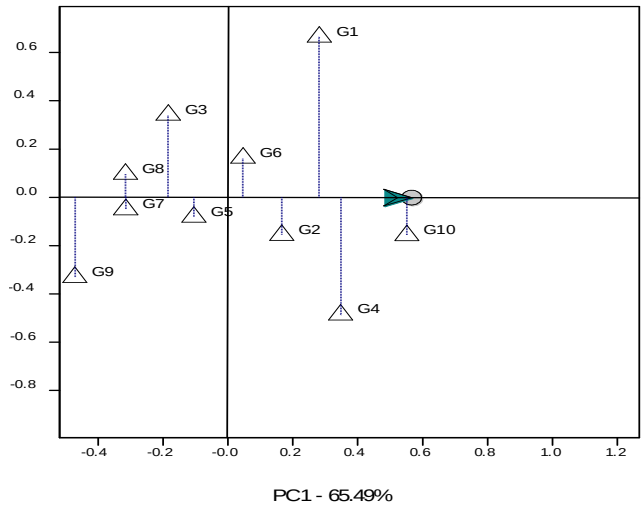

Figure 2. The "mean *vs.* stability" view of the GGE-biplot of 10 bread wheat genotypes across 12 environments.

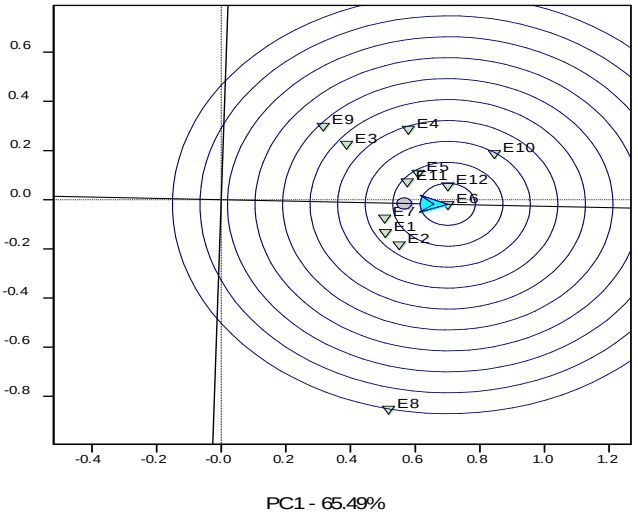

Figure 4. GGE-biplot based on the ranking of environments relative to an ideal environment. PC and E stand for principal component and environments, respectively.

the AE abscissa. Genotypes closer to abscissa are more stable than others. In this study, the greatest stability in the high yielding group had genotypes G10, G2 and G6, while the most stable of all was G10, these results agrees with those obtained by Mitrovic et al. (2012) and Asfaw et al. (2012) in their studies on maize hybrids and Mung Bean respectively.

The genotype ranking is shown on the graph of genotype so-called "ideal" genotype (Figure 3). An ideal genotype is defined as on that is the highest yielding across test environments and it's absolutely stable in performance (that ranks the highest in all test environments) (Yan and Kang, 2003; Farshadfar et al., 2012). Although, such an "ideal" genotype may not exist in reality, it can be used as a reference for genotype evaluation (Mitrovic et al., 2012). A genotype is more desirable if it is located closer to "ideal" genotype (Kaya et al., 2006; Mitrovic et al., 2012). The closer to the "ideal" genotype was G10 (Giza168).

The ideal test environment should have large PC1 scores (more power to discriminate genotypes in terms of the genotypic main effect) and small (absolute) PC2 scores (more representative of the overall environments). Such an ideal environment is represented by an arrow pointing to it (Figure 4). Although such an ideal environment may not exist in reality, it can be used as a reference for genotype selection in the METs. An

Table 5. Correlation coefficients among 12 test environments

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12
E1	1											
E2	0.534	1										
E3	0.640**	0.582*	1									
E4	0.342	0.742**	0.659**	1								
E5	0.415	0.082	0.330	0.105	1							
E6	0.734**	0.653**	0.823**	0.805**	0.408	1						
E7	0.831**	0.884**	0.732**	0.792**	0.331	0.796**	1					
E8	0.864**	0.675**	0.367	0.432	0.294	0.464	0.808**	1				
E9	0.164	0.710**	0.4267	0.410	*-0.248*	0.324	0.462	0.436	1			
E10	0.435	0.459	0.449	0.815**	*- 0.085*	0.735**	0.628*	0.499	0.782**	1		
E11	0.705**	0.837**	0.853**	0.723**	0.379	0.962**	0.876**	0.657**	0.388	0.767**	1	
E12	0.733**	0.632**	0.608*	0.632**	*- 0.131*	0.770**	0.749**	0.416	0.752**	0.874**	0.743**	1

*Significant at the 0.05 level of probability; **Significant at the 0.01 level of probability.

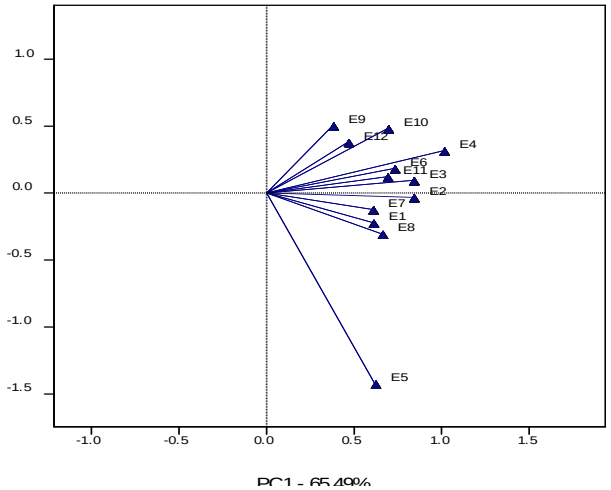

Figure 5. GGE-biplot based on environment-focused scaling for environments. PC and E stand for principal component and environments, respectively. Details of environments are given in Table 2.

environment is more desirable if it is located closer to the ideal environment. Thus, using the ideal environment as the center, concentric circles were drawn to help visualize the distance between each environment and the ideal environment (Yan et al., 2000; Yan and Rajcan, 2002). Figure 4 indicated that E6, which fell into the center of concentric circles, was an ideal test environment in terms of being the most representative of the overall environments and the most powerful to discriminate genotypes. Favorable environments were E12, E7, E1, E2, E11, E5 and E10. On the other hand, the unfavorable ones were E8, E9, E3, and E4. The favorable environments, together with E6, showed high yield potential (> 4.00 t ha-1, except E2 and E7), and the unfavorable ones low yield potential (< 3.00 t ha-1 except E8) (Table 4). Similar results were obtained by Kaya et al. (2006).

Table 5 represents correlation coefficients among the 12 test environments and the vector view of the GGE-biplot (Figure 5) provides a succinct summary of the interrelationship between the environments. The lines that connect the biplot origin and labels of the environments are called environment vectors. The angle between 2 environment vectors is related to the correlation coefficient between them (Kroonenberg, 1995; Yan, 2002). Acute angles indicate a positive correlation, obtuse angles a negative correlation and right angles no correlation (Yan and Kang, 2003). Table 5 contains 67 correlation coefficients, 38 of which were significant. All environments were positively correlated because all angles among them were smaller than 90°. Except that environment E5 negatively correlated with E9, E12 and E10, whereas the angles between them more than 90° (Figure 5). Farshadfar et al. (2012) in their study found that, the environments ER3 and EI3 which represent for rainfed and irrigated conditions in 2011 cropping seasons, respectively, made an obtuse angle with each other, which indicates a negative correlation between the response of genotypes to rainfed and irrigated conditions in 2011 cropping season. Similar results were obtained by Kaya et al. (2006).

Indirect selection can be applied in the case where the same character is measured on the same genotypes in different environments. Where there are no correlations of error effects among environments, the phenotypic correlation between environments maybe used to investigate indirect response to selection (Cooper and Delacy, 1994). Indirect selection for grain yield can be partial across the tested environments for instance, the genotypes adaptable or higher productivity in E3 may also show similar responses to E4, E6, and E7 as well. However, indirect selection from one environment to another may not be sufficiently successful, considering that 38 out of 67 environmental pairwise correlations

were significant.

In our research both of AMMI and GGE-biplot models were successful in assessing the performance of genotypes and the selection of best genotypes was identical in both of them. Mitrovic et al., 2012 used both models to analyze 19 maize hybrids in 12 environments and reported that, the AMMI and GGE-biplot models were very useful in estimation the performance of maize genotypes, and there is no difference in the results obtained by both models. Similar results were obtained by Stojakovic et al. (2010) who analyze a set of 15 commercial maize hybrids in 30 environments.

Conclusion

The magnitude of genotype-by-environment interaction (GEI) for grain yield of 10 bread wheat genotypes tested across 12 environments (2 years, 3 drought treatments and 2 sowing dates) at the Research Farm of Faculty of Agriculture, Sohag University. Based on the two analysis AMMI and GGE-biplot models, G10 (Giza 168), G2 (Sakha 8) and G6 (Sids 1) characterized by high yield and stability, therefore the G10 (Giza 168) close to ideal genotype, so this variety is adaptable for a wide range for drought and heat stress conditions. In contrast G3 (Sakha 69) and G9 (Giza 165) were exhibited a lower score for both yield and stability.

Abbreviations: PC, principal component; **GEI,** genotype by environment interaction; **METs,** multi environment trials; **t,** ton; **ha,** hectare; **AEC,** average coordinates of the environment; **AOE,** average ordinate environment; **AEA**, average environment axis; **G,** genotype; **E,** environment.

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