GENOTYPE BY ENVIRONMENT INTERACTION ANALYSIS FOR GRAIN YIELD OF WHEAT IN IRRIGATED AND RAIN-FED MEGA-ENVIRONMENTS USING AMMI AND GGE BIPOLT MODELS

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Romena H. M., A. Najaphy, M. Saeidi, M. Khoramivafa (2022). Genotype by environment interaction analysis for grain yield of wheat in irrigated and rain-fed megaenvironments using AMMI and GGE bipolt models. - Genetika, Vol 54, No.3, 1447-1463. Wheat (Triticum aestivum L.) is the major and strategic cereal crop globally. It is grown worldwide under a wide range of agro-ecological conditions. The performance of quantitative traits, for example grain yield, often varies due to significant effects of the genotype and environment interaction (GEI). Therefore, the integration of higher grain yield with stable performance is one of the common objectives in wheat-breeding programs. The present investigation was carried out to evaluate the GEI through GGE biplot and AMMI analysis over six environments (rain-fed and irrigated conditions during three years) using 29 diverse wheat genotypes. The analysis of variance revealed that the effect of environments (E), genotypes (G) and GEI are significant. The first two AMMI components justified 72.6% of the GEI variation. In the other hands, the first two principal components of the GGE biplot explained 58.3% of the observed variation for the grain yield. The GGE biplot suggested suitability of the tester E6 based on discrimination ability and representativeness, which is ideal for selecting superior genotypes. Based on the similar results of AMMI and GGE-biplot methods, the genotype G6 was the best performing genotypes at the rain-fed mega-environment. In addition, the entries G1 and G29 were suitable for the irrigated mega-environment.

Key words: Adaptability analysis, Multi-environment trials, Stability analysis, Modified AMMI stability values (MASVs), *Triticum aestivum*

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most common grown cultivated crops and one of the widely adapted cereals, which can be cultivated from warm humid to dry cold

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environments (HAKIM et al., 2012; STATISTICS 2018). It stands first in terms of production and acreage among the cereals, while because of the food shortages due to population growth, its importance has been increased day by day (HOSSAIN et al., 2012; HOSSAIN et al., 2012). The global requirements of wheat by 2050 is about 1045 million tons, to achieve food needs imposed by the increasing of population. This could be reached if global wheat productivity is improved by 1.6% per annum (WHEAT INITIATIVE 2013). In Iran, wheat is grown in diverse agro-ecological zones ranging from Zagros hills at West and North-West to the central and Southeastern plains. At all wheat farming zones in Iran, the climate conditions, especially rainfall and final season available water are highly variable, very important and the most challenging issue and have significant impact on crop yield (WFP 2016; MESGARAN et al., 2017). Unfavorable environmental conditions negatively influence on wheat grain yield and quality parameters. The high temperature in combination with water deficiency at the end of growing season deteriorate the grain quality of wheat (MASTILOVIĆ et al., 2018). Selection of superior genotypes in such situations is very difficult (FARSHADFAR et al., 2011). Due to difficulties in selecting genotypes evaluated across diverse agro-climatic conditions, the genotype and environment interactions (GEI) has remained as a challenge to plant breeders to improve grain yield and quality (KUMAR et al., 2014). GEI decreases association between phenotypic and genotypic values and leads to bias in the estimates of gene effects and combining ability for various characters sensitive to environmental fluctuation (RAO et al., 2011). The importance of GEI in breeding programs have been demonstrated in almost all major crops, including wheat genotypes (NAJAFIAN et al., 2010; ZALI et al., 2011). Therefore, development of new varieties which are stable under the various environmental conditions with high grain yield are crucial to meet the food demand of increasing population in the world, under future changing climate such as drought stress conditions (WHEAT INITIATIVE 2013). The performance of cultivar especially in marginal fragile environments of the foothills is strongly influenced by genotype and environment interactions. In this conditions, the multi-environment trials (MET) can effectively be used to accurately evaluate the performance of cultivars across environments, predict the yield level as well as examine the stability of genotypes for target environment and assist the selection of the best genotypes for target environment (MUSTAPHA et al., 2014). To study and reveal the nature and complexity of the genotype and environment interaction, a wide array of statistical techniques has been developed. Among them, two parametric methods are very efficient and common. Additive main effects and multiplicative interaction (AMMI) can effectively assesses the stability and adaptability of genotypes (PACHECO et al., 2005). In the other hand, GGE biplot enables the simplistic graphical visualization for the complex MET data (YAN et al., 2000). This study was aimed to investigate stability and adaptability of 29 diverse wheat genotypes over six environments (i.e. two rain-fed and irrigated conditions over three years) using AMMI analysis and GGE biplot.

MATERIALS AND METHODS

2.1. Plant materials and experimental design

Twenty-nine bread wheat genotypes (*Triticum aestivum* L.) listed in Table 1 were assessed using randomized complete block designs with three replications under two different irrigation regimes (rain-fed and irrigated conditions) for three consecutive years (2008–2011) at

research farm of College of Agriculture, Razi University, Kermanshah, Iran (47° 20' N latitude, 34° 20' E longitude and 1351.6 m altitude). The climate in the region has classified as semi-arid. The annual rainfall, average, minimum and maximum temperature are presented in Table 2. Each genotype planted in 3×1.25 m plot (3.75 m²) with 25 cm inter-row distances. The soil of the experimental field was clay loam with pH=7.1. The density rate was about 400 seeds per m² for all the plots. The seeds planted in early October and harvested in late July. Due to the time of the cessation of rain, the water deficit stress imposed after anthesis at the rain-fed conditions. The irrigated environment watered three times after anthesis. Irrigation was applied based on 80 mm evaporation from class A evaporation pan. The grain yield measured from two meters of the middle rows of each plot at harvesting time.

Table 1. Twenty-nine bread wheat genotypes used for multi-environment trials (MET) at different environments

	environmenis		
Code	Pedigree	Code	pedigree
G1	F103-L-1-12//PONY/OPATA	G16	Pishtaz
G2	OR F1.158/FDL//BLO/3/SH14414/CROW/4/C ICWH99381-0AP- 0AP-OMAR-6MAR	G17	KAR-1//RMNF12-71/JUP'S'
G3	PYN/BAU//VORONA/HD2402	G18	QAFZAH-25
G4	KATILA-13	G19	Marvdasht
G5	Pishgam (Bkt/Zhong)	G20	Chamran
G6	Zarin	G21	M-81-13
G7	CA8055//KS82W409/STEPHENS	G22	TEVEE'S'//CROW/VEE'S'
G8	Bolani	G23	M-83-17
G9	Shahriar	G24	M-83-6
G10	WS-82-9	G25	M-82-6
G11	SABALAN/4/VRZ/3/OR F1.148/TDL//BLO	G26	Jcam/Emu"s"//dove"S"/3/Alvd/4/MV17/Attila
G12	Karim	G27	Shiraz
G13	Atila2/PBW65	G28	STAR/SHUHA-4
G14	KAUZ'S'/MACHETE	G29	KATILA-1
G15	M-79-7		

Table 2. Agro-climatic properties of the experimental environments

Year	Rainfall (mm)	Average temperature* (°C)	Maximum temperature (°C)	Minimum temperature (°C)	Environment	Code
2008-	337	18.9	41.1	-12.3	Rain-fed	E1
09	337	10.9	41.1	-12.5	Irrigated	E4
2009-	480	20.2	42.6	-8.7	Rain-fed	E2
10	480	20.2	42.0	-0./	Irrigated	E5
2010-	369	19.6	12 6	-9.7	Rain-fed	E3
11	309	19.0	43.6	-9.7	Irrigated	E6

2.2. Statistical analyses

Combined ANOVA was performed on the grain yield data with PROC GLM in SAS using RANDOM and TEST options (SAS INSTITUTE 2003) to determine the interaction of genotypes and environments. In the combined ANOVA, the environmental effect was considered as random, while genotypic effect as fixed. The differences between means compared using least significant difference (LSD) test at the 0.05 probability level. AMMI analysis performed using the model suggested by (GAUCH 1988):

$$y_{ij} = \mu + \alpha_i + \beta_j + \sum_{k=1}^{N} \lambda_k \gamma_{ik} \delta_{jk} + \rho_{ij}$$

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Where y_{ij} is the yield of genotype (i=1,..., g) in environment (j=1,...,e). μ is the total yield mean. α_i is the main effect of genotype or the genotype mean deviation (genotype mean minus total yield mean). β_i is the main effect of environment or the environment mean deviation. λ_k is the singular value for the interaction principal component axis N (IPCA) and N is the number of remain IPCA axis in AMMI model. γ_{ik} is the genotype eigenvector value for IPCA axis N and δ_{jk} is the environment eigenvector value for IPCA axis N. ρ_{ij} is the residual or noise. It should be mentioned, eigenvalues and eigenvector are without unit but λ_k has a yield unit (GABRIEL 1978). The AMMI biplots base on the yield vs. IPCA[1] and IPCA[1] vs. IPCA[2] were drawn. The modified AMMI stability values (MASVs) were used to compare the stability of the genotypes as described by ZALI *et al.* (2011):

$$MASV = \sqrt{\sum_{k=1}^{N^{\circ}-1} \left[\frac{SSIPCA_n}{SSIPCA_{n+1}} (IPCA_n)\right]^2 + (IPCA_{N^{\circ}})^2}$$

where SSIPCAs are the sum of squares of IPCAs. The IPCAs scores are the genotypic scores in AMMI model and N° is number of significant IPCAs. The modified AMMI stability value demonstrates the distance of a genotype from origin in a multi-dimensional scatterplot of significant IPCAs scores. Therefore, the lower value represents the more stability of the genotype. In addition, yield data were analyzed by GGE biplot method, which is based on the first two principal components (PC1 and PC2) that is obtained by subjecting environment-centered grain yield means to singular-value decomposition. No transformation, no standardization, and environment centering options were used for the "which-won-where" biplot. The "discriminating power and representativeness" biplot for visualizing the relationships among environments was based on environment-focused singular-value partitioning. The "mean vs. stability" was based on genotype-focused singular-value partitioning when relationships among genotypes is desired. The following GGE biplot model was used (YAN *et al.*, 2003):

$$Y_{ij} - \mu_j = \lambda_1 \gamma_{i1} \delta_{j1} + \lambda_2 \gamma_{i2} \delta_{j2} + e_{ij}$$

Where V_{ij} is the mean yield of the genotype (i=1,..., g) in environment (j=1,...,e). μ is the mean value in environment j. λ_1 and λ_2 is the singular value for PC1 and PC2, respectively. γ_{i1} and γ_{i2} are the PC1 and PC2 scores, respectively, for genotype i. δ_{j1} and δ_{j2} are the PC1 and PC2 scores, respectively, for genotype i. δ_{j1} and δ_{j2} are the PC1 and PC2 scores, respectively, for genotype i. δ_{j1} and δ_{j2} are the PC1 and PC2 scores, respectively, for environment j. e_{ij} is the residual of the model associated with genotype i in environment j. The GenStat 12th edition software was used for AMMI and GGE biplot analysis.

RESULTS

3.1. The mean performance and the stability of the genotypes by AMMI analysis

The AMMI analysis of variance for grain yield revealed highly significant differences among the environments, the genotypes and the interaction of them (P < 0.01) as shown in Table 3. Results showed that the environment, the genotype and the genotype and environment interaction effects accounted for 54%, 7.3% and 16.6% of total sum of squares, respectively (Table 3). AMMI is useful in representing adaptation and stability by delineating the "whichwins-where" pattern, that is, which genotype wins in a specific environment or more (GAUCH 2013). The analysis showed that IPCA[1], IPCA[2] and IPCA[3] were significant and explained 47.6%, 25% and 14% of total GEI variation, respectively (Table 3). The computational assessments indicated that AMMI with the first two IPCAs was sufficient for cross-validation of most variation explained by the most GEI variations. HEIDARI *et al.* (2018) and MORTAZAVIAN *et al.* (2009) stated that the simpler AMMI model is more efficient because it makes possible for evaluation of many mega-environments as practical agricultural considerations. Additionally, using more than two IPCA usually capture the non-predictive variation and merit a noisy predicted validation data set.

Table 3. Combined ANOVA, additive main effects and multiplicative interaction (AMMI) analysis of variance of the wheat genotypes

		Sum aguana (SS)	Mean Squares				
S.O.V	Df	Sum squares (SS)	(MS)	F-test	SS (%)		
Env.	5	9545486	1909097	29.4**	54		
Rep./Env.	12	778908	64909	6.98^{**}	4.4		
Gen.	28	1292847	46173.1	2.20^{**}	7.3		
Env.×Gen.	140	2943984	21028.45	2.26^{**}	16.6		
IPCA[1]	32	1400727	43773	4.70^{**}	47.6		
IPCA[2]	30	734572	24486	2.63**	25.0		
IPCA[3]	28	412360	14727	1.58^{*}	14.0		
IPCA[4]	26	255814	9839	1.06 ^{ns}	8.7		
Residual	24	140510	5855		4.8		
Error	336	3126016	9304				

Env: environment, Gen: genotype, Rep: replication, IPCA: Interaction principal component. * significant at the 5%, ** significant at 1% probability levels, respectively, ns: non-significant.

AMMI analysis helps to identify superior genotypes for specific environmental conditions and it permits estimation of interaction effect of a genotype in each environment. The genotypes that are closer to the origin are more adaptive to all the studied environments. The genotypes and environments that fall into the same sector interact positively and conversely or negatively if they fall into opposite sectors (GABRIEL 2002; GAUCH 1988). Obviously, a genotype with high positive interaction to an environment has the ability to exploit the agro-ecological or agro-management conditions of the specific environment, thus, is best suited to that environment (GAUCH 2013). Figure 1 shows the value of the first interaction principal component axis (IPCA1) versus mean yields, which is very useful for simultaneous selection of stable and high yielding genotypes. TOLESSA (2015) stated that the IPCA[1] vs. mean biplot provided an effective tool for illustrating the GEI pattern. The testers E1, E2 and E3 (the rain-fed conditions) had obtuse angles with the testers E4, E5 and E6 (the irrigated conditions), showing different responses of genotypes to these two different irrigation regimes. The results (Table 4 and Figure 1) indicated that the genotype G6 with highest performance (483 g/m²) was more stable in the rain-fed mega-environment (E1, E2 and E3 cluster). In addition, A high performance and degree of stability was observed for the entries G1 (729 g/m²) and G29 (713 g/m²) in the irrigated megaenvironment (E4, E5 and E6 cluster). The magnitude of each genotype and environment interaction illustrated in the IPCA 1 versus IPCA 2 biplot (Figure 2). From the biplot of Figure 2, it is clear that the points for genotype are less scattered than the points for environment, indicated that the variability due to the environments is higher than the variability due to the genotypes, which is in complete agreement of ANOVA table (Table 3).

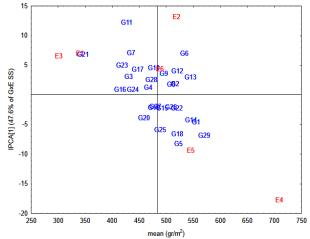


Fig1. Biplot analysis of GE interaction based on AMMI model for the first interaction principal component axis (IPCA1) versus mean yields. See Tables 1 and 2 for the legends.

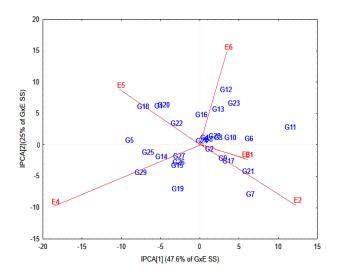


Fig2. Biplot analysis of G-E interaction based on AMMI model for the first two interactions principal component axis. See Tables 1 and 2 for the legends.

Table 4. Mean values for grain yield (gr/m ²	²) of the wheat genotypes (G1 to G29) tested at six

e	nvironmen	ts (El to El	5)							
	Ra	Rain-fed condition			Irrigated condition					
Genotype	2008- 2009 (E1)	2009- 2010 (E2)	2010- 2011 (E3)	Mean(R)	2008- 2009 (E4)	2009- 2010 (E5)	2010- 2011 (E6)	Mean(I)	Mean(G)	MASV
G1	347	500	297	381	833	711	644	729	555	14.33
G2	400	569	339	436	737	541	513	597	516	3.32
G3	294	486	286	355	594	492	430	505	430	4.94
G4	283	524	319	375	653	574	449	559	467	1.91
G5	300	446	327	358	889	712	460	687	522	17.19
G6	447	644	357	483	657	506	593	585	534	12.14
G7	351	640	290	427	632	346	350	443	435	19.57
G8	400	527	351	426	709	555	512	592	509	2.92
G9	290	660	337	429	675	559	454	563	496	7.73
G10	327	626	202	385	669	453	585	569	477	11.57
G11	393	557	303	418	427	363	516	435	426	22.45
G12	381	511	359	417	595	631	644	623	520	15.96
G13	389	597	305	430	699	601	676	659	544	11.05
G14	361	586	270	406	913	601	545	686	546	11.65
G15	337	514	346	399	789	578	393	587	493	9.44
G16	320	356	263	313	590	499	462	517	415	8.40
G17	352	515	367	411	607	478	364	483	447	10.67
G18	368	375	284	342	835	672	587	698	520	16.95
G19	443	447	348	413	827	463	336	542	477	16.01
G20	293	345	295	311	692	640	491	608	459	14.14
G21	271	491	210	324	509	291	304	368	346	14.61
G22	329	546	224	366	806	594	618	673	519	10.04
G23	302	427	283	337	492	502	503	499	418	13.78
G24	295	475	264	345	655	502	438	532	438	0.71
G25	340	431	281	351	855	585	440	627	489	13.05
G26	264	627	286	392	812	606	461	626	509	9.12
G27	312	523	272	369	781	545	448	591	480	6.76
G28	277	550	351	393	619	592	444	552	472	4.43
G29	403	568	311	427	1005	629	506	713	570	17.22
Mean	340	519	301	387	709	546	488	581	484	

Mean_(B): average grain yield across all rain-fed conditions, Mean_{(D}: average grain yield across all irrigated conditions, Mean_(G): average grain yield across all the environments, MASV: The modified AMMI stability value.

GAUCH (2013) stated that in the general case, it is preferable to select the simpler AMMI model, particularly if IPCA[1] is agriculturally interpretable but IPCA[2] is not. The distribution of the genotype points in the biplot of IPCA[1] vs. IPCA[2] (Figure 2) and also the modified AMMI stability values (Table 4) revealed that the entries G24, G4 and G8 scattered close to the origin indicating the minimal interaction of these genotypes with the environments. Stable genotypes have MASV values close to zero (ZALI *et al.*, 2011). Thus, G24, with the lowest MASV (0.71), could harbor genes for adaptability to the various irrigation regimes. The other remaining genotypes, which scatter away from the origin, were more sensitive to the environmental conditions. The entries G7 and G21 displayed acute angle with the vectors of the testers E1, E2 and E3 (rain-fed mega-environment), while showed obtuse angle with the testers E4, E5 and E6 (irrigated mega-environment) which illustrate positive interactions of these entries on other hand, the entries G1, G18 and G20 demonstrated positive interactions with the irrigated mega-environment and negative interaction with the rain-fed mega-environment, according to display acute angle with the vectors of the testers E4, E5 and E6 (with the vectors of the testers E4, E5 and E6, while showed obtuse angle with the irrigated mega-environments and negative interaction with irrigated mega-environments.

with the testers E1, E2 and E3 (Figure 2). The relationships between the environments indicated that there were large differences among genotypes in response to the irrigation regimes.

3.2. GGE Biplot Analysis of the grain yield and the stability of the wheat genotypes

In the GGE biplot, the PC1 explained 34.68% of total variation, whereas PC2 explained 23.61% of the variation, thus, the two axes together accounted for 58.29% of the total variation (Figure. 3-5). The polygon view of the biplot depicts which genotype shows best performance in which environment(s) (Figure 3). The polygon (Fig. 3) divided by the rays into nine sectors. The genotypes fell into most of these sectors but the environments fell only in three of them. This shows that the environments comprised of three different mega environments (I, II, and III). The mega-environments (ME) I consisted of E1, E2 and E3. It can be called rain-fed megaenvironment because of all these environments were under rain-fed conditions in different years. The mega-environment II had E6 while E4 and E5 appeared in the mega-environment III. The mega-environments II and III are the irrigated mega-environments. The repeatable crossover GE pattern across years indicated that the genotypes can be exploited by selecting in and for each mega-environment. Given that information, the vertex genotype in the mega-environment I was the genotype G6. The accession G29 was the suitable genotype in tester E6 (ME II). In addition, the genotype G1 was the vertex genotype in the mega-environment III (Irrigated ME). No environment fell into the sector where the entries G5, G7, G11, G18, G20 and G21 were the vertex genotypes, indicating that these genotypes were the lowest-yielding genotypes in some or all the studied environments. The entries G28, G10, G15 located close to the origin of the polygon were more adapted to low-yielding environments than the vertex genotypes. ADU et al. (2013) stated that the vertex genotypes are the most responsive compared to those located within the polygon. In the other hand, the genotypes, which are closer to origin of biplot, show average response across all environmets (YAN et al., 2006).

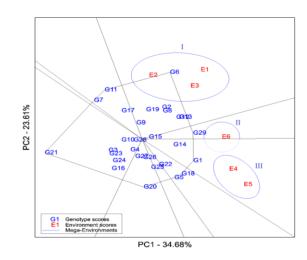


Fig3. A "which-won-where" or "which-is-best-at-what" based on yield data of 29 wheat genotypes evaluated across six environments. See tables 1 and 2 for the legends. PC, principal component.

Figure 4 represents interrelationship among environments. The angle between the vectors of two environments is related to the correlation coefficient between them. Environments with acute angle between their vectors are positively correlated while those with obtuse angle show negative correlation. The purpose of evaluation of interrelationship among environments is to identify test environments that effectively identify superior genotypes for a megaenvironment. An effective test environment should be both discriminating for the genotypes under the evaluation and representative of the mega-environment. In this plot, the AEC can be referred to the effective test environment or "Ideal" test environment (YAN et al., 2000, 2006). Based on Figure 4, the test environments classified into three types: (I) The testers E1, E2 and E3 had acute angels that indicated a high correlation between themselves. In addition, the tester E1 with longer vector was more discriminative, which provided more information about the genotypes in rain-fed environment, so it should be used as test environment for developing genotypes for the rain-fed conditions. (II) The testers E4 and E5 with long vectors and larger angle with the AEC abscissa were ideal for selecting superior genotypes for the irrigated condition. (III) The tester E6 with acute angle with the AEC abscissa was useful in culling unstable genotypes. The tester E5 from irrigated conditions and the tester E1 from rain-fed conditions were found to have high discriminative ability. Thus, these environments might be sufficient for making genotypes recommendation for their irrigation regimes. In Figure 5, the genotypes ranked along the average environment axis (A line) with the arrow pointing to the average environment coordination (AEC). The B line, which is perpendicular to the AEC abscissa, separated entries with below-average grain yield from those with above-average grain yield. The mean yield of the genotypes are measured by the projections of their markers on the A line and the stability of the genotypes are approximated by their distance from the A line. An ideal genotype characterized as the absolute stable with highest mean performance, has the greatest vector length of the high-yielding genotypes and with zero GE (YAN et al., 2006).

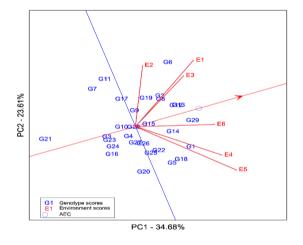


Fig4. The "discriminating power and representativeness" view of the genotype main effects plus GE interactions (GGE) biplot based on yield data of 29 wheat genotypes evaluated across six environments. See tables 1 and 2 for the legends. PC, principal component.

According to the average environment coordination (AEC), the ideal genotype is associated with greatest vector length of the high-yielding genotypes. Although, in reality, the ideal genotype may not exist but a genotype is more desirable if it is located closer to the ideal genotype definition (HORN *et al.*, 2018). Figure 5 indicated that the genotype G21 was the low yielding genotype and the entries G6 and G29 were the high yielding genotypes among all the studied environments due to the projections of genotypes markers on the A line. In addition, based on the above-mentioned concepts, the entries G5, G6, G7, G11, G18, G20 and G21 were the least stable genotypes as indicated by longer vectors/distance from the A line. The entries G12, and G13 were the most stable genotype, as they were located almost on the AEC abscissa and had a near zero projection onto the AEC ordinate. This shows that their rank was highly consistent across the environments.

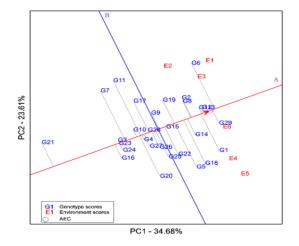


Fig5. The "mean vs. stability" view of the genotype main effects plus G-E interactions (GGE) biplot based on yield data of 29 wheat genotypes evaluated across six environments. See Tables 1 and 2 for the legends. PC, principal component.

DISCUSSION

Changes in environmental factors like pattern of seasonal precipitation, soil quality and ... are important during crop growth and development. Lack of sufficient moisture in the soil during flowering, pollination and grain-filling causes yield reduction in wheat (HABASH *et al.*, 2009; BÁNYAI *et al.*, 2020). Producing stable and satisfactory grain yield in different environmental conditions is one of the important breeding aims. Stability is the ability of a genotype to evade sizeable variation in grain yield over and array of the environments (BÁNYAI *et al.*, 2020). Desirable genotypes, which could be candidate as cultivars or as parents in crosses, have higher and stable yield in variable environments (MOTZO *et al.*, 2015). However, the genotype-environment interaction hinder selection gain as GEI could reduce genotypic and phenotypic correlations and make selection of genotypes, which have high yield and be more stable in

different environments, so complicate (SHUKLA et al., 2015). In this study, the results showed that the environmental effect was greater than the genotype and the GEI effects. Pronounced influences of environment on the grain yield compared with that of the genotype or the GE interaction effects have been documented in many studies (AMIRI et al., 2013; RASHIDI et al., 2013; HAIDER et al., 2017; MOHAMMED 2020). This may indicate a significant response among the genotypes to the environment variations and the discriminant capability of the test environments (TOLESSA 2015). Cooper et al. (1995) told that the magnitude of the GEI caused by dissimilarity in genetic systems of genotypes, which are controlling physiological processes, can affect the yield stability in the variant environments. Generally, a genotype with high a genotypic main effect (i.e. average over the different environments) and with a low fluctuation in the yield or yield components (stable genotype) is plant breeders' favorite (HAIDER et al., 2017). Due to significant effect of the genotype and environment interaction, selection of genotypes can't be made just based on the overall mean of grain yield. Rather, the genotypes specifically adapted to an environment or at least mega-environment must be identified (MOHAMMADI et al., 2018). Such selections are very difficult to be made. Both yield and stability should be considered simultaneously to reduce the effect of GEI (BOSE et al., 2014). The genotype and environment interactions refer to the differential ranking of genotypes across environments. Only the genotype and the genotype and environment interactions are relevant to cultivar evaluation particularly when GEI is determined as repeatable (COOPER et al., 1996). The genotype and environment interactions may complicate the process of selecting superior genotypes (EBDON et al., 2002; GAUCH 2006). There are three possible strategies for dealing with GEI in a breeding program: (i) ignoring, i.e. using genotypic means across environments even when GEI is significant, (ii) avoiding and (iii) exploiting. The second way i.e. avoiding, is to classify diverse environments into fewer but homogeneous mega-environments and to change the methodology of breeding programs to select specific genotypes for each mega-environment. Genotypes evaluated in a mega-environment would not be expected to show crossover interactions. The third approach i.e. exploiting, is to identify the stable genotypes across the diverse environments by analyzing and interpreting genotypic and environmental differences. This strategy allows the breeders to select genotypes with consistent performance and identify the causes of GEI and provide the opportunity to cope with the problem, of course, if it is possible (KANG 2002). The mega-environments study aims to identify reliable genotype for the specific conditions. Different methodologies have been developed to illustrate the effect of genotype, environment or interaction and have common used in breeding studies and programs. The additive main effects and multiplicative interaction (AMMI) and genotype plus genotype and environment interaction (GGE) biplot techniques have been used by many researchers to elucidate the effect of genotype, environment and genotype-environment interaction based on multi-environment trials (MET) data (YAN et al., 2006; FARSHADFAR et al., 2012; KENDAL et al., 2015; ORAL 2018; KHAN et al., 2020). The AMMI model was exerted to identify the stability and superiority of genotypes, and also desirable and high yielding environment (TEKDAL et al., 2018). In this study, AMMI analysis revealed that G6 was high yielding and stable genotype in the rain-fed megaenvironment, while G1 and G29 were the most stable and high yielding genotypes in the irrigated mega-environment. By using this approach, MARIE et al. (2020) in coffee, MEKONNEN et al. (2020) in barley, MOHAMMADI et al. (2018) in durum wheat, RASHIDI et al. (2013) in chickpea and FARSHADFAR et al. (2012) in bread wheat identified the major environmental or genotypic causes of the genotype-environment interaction in the different crop species. Some researchers reported that AMMI model could be used to illustrate a two-way table of GE means. If the genotype and environment means are homoscedastic and independent, ordinary least squares (OLS) gives optional estimates of the model (GAUCH et al., 2008), AMMI model could be used to appraise genotypes at different conditions (SADEGHZADEH et al., 2017). RAD et al. (2013) reported that the magnitude of the genotype effect was lower than the environment effect, which was also observed in this study. Generally, the environments that are descriptive and representative are the best environment for the selection of adapted genotypes (BILGIN et al., 2018). Based on GGE biplot, it is possible to select the genotypes for specific and general goals. YAN and TINKER (2006) stated that the "which-won-where" view of the GGE biplot is an effective visual tool in mega-environment analysis. The interesting feature of this view of a GGE biplot is that the vertex genotype in each sector could have the highest yield for all the environments which are in the same sector (YAN et al., 2006). In this study, the tested environments could be classified in two mega-environments. G6 was the high yielding accession in the rain-fed mega-environment and G1 in irrigated mega environment, while G12 and G13 were stable in the both mega-environments. YAN and TINKER (2006) declared that one ideal genotype should have highest yield and be stable at least in one mega-environment. It is recommended to use selected genotypes in future breeding program compared with other advanced genotypes. The presence of the two different mega-environments i.e. irrigated and rain-fed mega-environments in the present study suggested that the six environments differed significantly in terms of irrigation regimes, so that deploying genotypes in each of megaenvironments would give different results (YAN et al., 2006). It should be noted that the high annual precipitation with a warmer crop season in 2009/10 season compared to 2008/09 and 2010/11 could be attributed to highly conducive climatic conditions, which has led to an increase in grain yield under the rain-fed conditions (E2) at this year (Tables 2 and 4). GAUCH (2013) and HONGYU et al. (2015) declared that two mega-environments are often sufficient to allow GE to capture a sizeable portion of the interaction signal. Based on the results, AMMI and GGE biplot model showed similar results in view of specific adaptability to the environmental conditions. Both AMMI and GGE biplot models were able to assess the variability present in MET data due to significant GEI. In addition, the two methodologies may provide approximately equivalent conclusion about the stable and high yielding genotypes (KHAN et al., 2020; NEISSE et al., 2018).

CONCLUSION

Genotype and environment interaction (GEI) has important role in the performance of genotypes in the environments. Development of cultivars needs time, resource, and labor-intensive task. The present study was aimed to identify high yield and stable genotypes by analyzing multienvironment data by using AMMI and GGE biplot analyses. The both methods could be used successfully in determining suitable wheat genotypes in different mega-environments. Analysis of variance indicated that 54, 7.3 and 16.6 percent of total sum of squares related to the environment, the genotype and the genotype and environment interaction effects, respectively. Results of this research revealed that the environmental conditions and the GEI play major roles in controlling wheat genotypes performance. Based on the both AMMI and GGE-biplot methods, the genotype G6 (483 g/m²) was suitable for the rain-fed mega environment, while the entries G1 (729 g/m²) and G29 (713 g/m²) were suitable for the irrigated mega environment. The tester E6 was "ideal" environments for selecting superior genotypes. This study also emphasizes on the importance of evaluating GEI for assessing adaptability and stability.

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ANALIZA INTERAKCIJE GENOTIP ŽIVOTNA SREDINA ZA PRINOS ZRNA PŠENICE U MEGA SREDINAMA UNAVODNJAVANIM I KIŠNIM SREDINAMA POMOĆU AMMI I GGE BIPLOT MODELA

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Izvod

Pšenica (*Triticum aestivum* L.) je glavna i strateška žitarica u svetu. Uzgaja se širom sveta u širokom spektru agroekoloških uslova. Performanse kvantitativnih osobina, na primer prinos zrna, često variraju zbog značajnih efekata interakcije genotipa i životne sredine (GEI). Stoga je integracija većeg prinosa zrna sa stabilnim performansama jedan od zajedničkih ciljeva u programima oplemenjivanja pšenice. Ovo istraživanje je sprovedeno da bi se procenio GEI kroz GGE biplot i AMMI analizu u šest okruženja (kišni uslovi i navodnjavanje tokom tri godine) korišćenjem 29 različitih genotipova pšenice. Analiza varijanse je pokazala da je uticaj okruženja (E), genotipova (G) i GEI značajan. Prve dve komponente AMMI opravdale su 72,6% GEI varijacije. S druge strane, prve dve glavne komponente GGE biplota objasnile su 58,3% uočene varijacije za prinos zrna. GGE biplot je sugerisao prikladnost testera E6 na osnovu sposobnosti diskriminacije i reprezentativnosti, što je idealno za odabir superiornih genotipova. Na osnovu sličnih rezultata AMMI i GGE-biplot metoda, genotip G6 je bio genotip sa najboljim učinkom u mega okruženju sa kišom. Pored toga, unosi G1 i G29 bili su pogodni za navodnjavano mega-okruženje.

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