GGL BIPLOT ANALYSIS OF DURUM WHEAT (*TRITICUM TURGIDUM* SPP. *DURUM)* YIELD IN MULTI-ENVIRONMENT TRIALS

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Abstract

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Durum wheat (*Triticum turgidum* spp. *durum*) breeders have to determine the new genotypes responsive to the environmental changes for grain yield. Matching durum wheat genotype selection with its production environment is challenged by the occurrence of significant genotype by environment (GE) interaction in multi-environment trials (MET). This investigation was conducted to evaluate 20 durum wheat genotypes for their stability grown in five different locations across three years using randomized completely block design with 4 replications. According to combined analysis of variance, the main effects of genotypes, locations and years, were significant as well as the interactions effects. The first two principal components of the site regression model accounted for 60.3 % of the total variation. Polygon view of genotype plus genotype by location (GGL) biplot indicated that there were three winning genotypes in three mega-environments for durum wheat in rain-fed conditions. Genotype G14 was the most favorable genotype for location Gachsaran and the most favorable genotype of mega-environment Kouhdasht and Ilam was G12 while G10 was the most favorable genotypes for mega-environment Gonbad and Moghan. Ideal environment view of GGL biplot showed that location Gachsaran is more desirable test location than the other locations and genotype evaluation in this location maximizes the observed genotypic variation among genotypes for grain yield of durum wheat. Application of GGL biplots facilitated visual comparison and identification superior durum wheat genotypes for each target locations.

Key words: GGL biplot analysis, yield stability, multi-environment trials, durum wheat, genotype by environment interaction

Introduction

Durum wheat (*Triticum turgidum* spp. *durum*) is one of the most important cereal crops in the world and grown on only 8 to 10% of all the wheat-cultivated area (USDA 2009). Durum wheat is better adapted to semiarid environ than is bread wheat and is a crop adapted to marginal lands. In spite of its low cultivation, durum wheat is an economically important crop because of its unique characteristics (protein content and gluten strength) and food industrial products (Sakin et al., 2011). Iran imports considerable amount of durum wheat due to low quantity and quality of its own produced durum wheat. Durum wheat farmers are interested to new wheat cultivars due to both high mean yield and proper quality. In the improving of new durum wheat genotypes, effects of climate

and soil properties on grain yield are of great importance. Therefore, wheat breeders must attempt to select genotypes responsive to diverse environments for high grain yield because both mean yield and quality of durum wheat is influenced by the environmental factors (Rharrabti et al., 2003).

New improved genotypes are tested in multi-environment trials (MET), to determine genotype performance before recommending them for production in a given location. Research focusing on yield stability, or genotype by environment (GE) interaction, is necessary for plant breeders to develop genotypes that respond consistently across test environments (Yang et al., 2009). Usually, GE interaction occurs and studied genotypes response differently to environmental changes. There are different methods for analyzing and interpreting GE interaction such as univariate (parametric and

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nonparametric) and multivariate procedures (Lin et al., 1986). Among multivariate methods, linear-bilinear models are useful tools for analyzing MET data and GE interaction interpretation (Crossa Cornelius 1997). The additive main effects and multiplicative interactions (AMMI) and genotype plus GE interaction (GGE) biplot models are introduced as powerful tools for effective analysis and interpretation of MET data in plant breeding programs (Zobel et al., 1988; Yan et al., 2000).

Although the measured yield is a combined result of the main effects of the genotype, main effects of the environment and GE interaction, only genotype main effects and GE interaction are relevant to genotypes evaluation and mega-environment identification. Also, Gauch Zobel (1996) emphasized that genotype main effect and GE interaction are the two important sources of grain yield variation and must be considered in MET data for genotypes evaluation. Usually, E explains most (grater than 80%) of the total grain yield variation, while G and GE interaction are usually small (Yan Kang 2003). For introducing a new method, Yan et al. (2000) used a site regression model (SREG), combined both G and GE sources, repartitioned this into an additive GE interaction and a crossover GE interaction, and proposed a graphical procedure biplot (Gabriel, 1971) to use these effects (G and GE) and in exploring yield stability and cultivar recommendation in MET. The GGE biplot model is a multiplicative model that absorbs the genotypes main effects plus the GE interaction, which are the important factors in yield stability (Yan Tinker, 2006). This model uses the primary and secondary effects from GGE biplot analysis and is useful in mega-environment identification (Yan et al., 2007; Yang et al., 2009).

Different crop breeders of Iran interested to using this procedures in their MET data and attempt to apply this tool in GE interaction analysis. Dehghani et al. (2006) in barley (*Hordeum vulgare* L.), Mohammadi et al. (2007) in wheat (*Triticum aestivum* L.), Sabaghnia et al. (2008a) in lentil (Lens culinaris Medik), Dehghani et al. (2009) in maize (*Zea mays* L.), Ebadi-Segherloo et al. (2010) in chickpea (*Cicer arietinum* L.), Mohammadi et al. (2011) in durum wheat (*Triticum turgidum* spp. *durum*) exploited the GGE biplot methodology in mega-environment investigation in Iran. According to the above mentioned studies, three different mega-environments for barley in cold regions, four winter wheat mega-environments, three possible lentil mega-environments in semi-arid regions, three mega-environments for late maize hybrids and four chickpea mega-environments were identified in Iran. Although, the durum wheat breeding in Iran was followed with MET, the uses of linear-bilinear models as well as the pervious statistical analysis (parametric methods) procedures as an effective tool for analyzing MET and interpreting

GE interaction have not been very much documented. This paper therefore tried to apply GGE biplot methodology via GGL biplot procedure to evaluate magnitude of GE interaction on durum wheat grain yield, determine the best performing genotypes for selection locations, the identification of mega-environments and analysis of the ideal genotype and environment.

Materials and Methods

The trials were conducted during three years (2005 to 2007) growing seasons in five different warm locations: Gachsaran, Gonbad, Ilam, Kouhdasht and Moghan. Gachsaran, in southern Iran, is relatively arid, warm climatic, and has silt loam soil. Gonbad in the northeast of Iran are characterized by semi-arid conditions and have sandy loam soil. Ilam in western Iran has moderate rainfall and have silt loam soil. Kouhdasht in the southern-east of Iran are characterized by semi-arid conditions and has silt-loam soil. Moghan in the northern-west of Iran are characterized by arid and warm conditions and has sandy loam soil. These mentioned locations were selected to sample climatic and edaphic conditions in rain-fed and warm durum wheat growing regions. They vary in agro-climatic factors such as latitude, rainfall, soil types, temperature etc. Most of these locations were classified as warm areas in Iran and have good potential for durum wheat production. Location geographical descriptions are given in Table 1.

Twenty durum wheat genotypes, including 19 advanced breeding lines and one local check cultivar (Seimareh), were used as plant material in this investigation (Table 2). The studied genotypes were the advanced breeding lines originated from International Centre for Agricultural Research in the Dry Areas (ICARDA) were determined to be high yielding and resistant to common durum wheat diseases. At each experimental location and each year, all genotypes were sown according to randomized completely block design with four replications. Each experimental plot was consisted of 6 rows (space between rows was 17.5 cm), 7 m each in length. All of the P fertilizer and half of the N fertilizer were applied at sowing, while the rest of the N fertilizer was applied at the stem starting growth stage. Fertilizer application was 30 kg nitrogen ha^{-1} and 70 kg P_2O_5 ha^{-1} at planting and 40 kg nitrogen ha^{-1} at stem elongation stage for all test environments. Plot size was 7.35 m[2] and an area of 4.2 m[2] (4 rows with 6 m long) was harvested to estimate seed per plot and then converted to kg ha^{-1}.

Statistical analysis of variance for linear-bilinear GGE biplot model was performed via the program developed by Burgueno et al. (2001). These analyses were performed using the

SAS release 6.12 (SAS, 1996). In addition, F-Gollob (Gollob 1968) was used to test the significance of PCs for the biplot model. To explore G plus GE variability in grain yield of durum wheat, we used the linear-bilinear GGE biplot model that is given by:

$$Y_{ij} = \mu + \beta_j + \sum_{n=1}^{k} \lambda_n \xi_{in} \eta_{in} + \varepsilon_{ij}$$

where Y_{ij} is the mean of genotype i in environment j; μ is the grand mean; β_j is the environment j main effect; n is the singu-

lar value; λ_{in} and ζ_{in} are, the singular vectors for genotypes and environments for lambda$_n$ = 1, 2, . . . ,k, respectively; and ε_{ij} is the residual effect. The dataset was then subjected to graphic analysis using the GGEbiplot software program (Yan, 2001). The GGE biplots were draw using the first two symmetrically scaled principal components for generating average tester coordinate and polygon view graphs (Yan Kang, 2003). To visualize the associations among locations, a vector view biplot was obtained. The results of this vector view biplot, were compared with Pearson's correlation coefficient (Steel

Table 1
Geographical property of test locations

Location	Longitude Latitude	Altitude, m	Soil Texture	Soil Type¶	Rainfall, mm
Gachsaran	50˚ 50´ E 30˚ 20´ N	710	Silty Clay Loam	Regosols	460.8
Gonbadd	55˚ 12´ E 37˚ 16´ N	45	Silty Clay Loam	Regosols	367.5
Kouhdasht	23˚ 26´ E 48˚ 17´ N	1148	Silt-Loam	Regosols	433.1
Ilam	46˚ 36´ E 33˚ 47´ N	975	Clay-Loam	Regosols	502.6
Moghan	48° 03´E 39° 01´N	1100	Sandy-Loam	Cambisols	271.2

¶ Based on the FAO soil classification system (FAO, 1990).

Table 2
The characterization of 20 durum wheat genotypes studied in multi-environmental trials

No	Code	Name / Pedigree	Origin
1	G1	SRN-1/KILL//2*FOLTA-1	CIMMYT
2	G2	GREEN-14//YAV-10/AUK	CIMMYT
3	G3	GA//2×CHEN/ALTAR84	CIMMYT
4	G4	BCR//MEMO/GOO/3/STJ7	ICARDA
5	G5	SERRATOR-1//SRN-3/AJAIA-15	CIMMYT
6	G6	D68-1-93A-1A//Ruff/Fg/3/Mtl-5/4/Lahn ICD93-0654-C-12AP-0AP-4AP-0AP	ICARDA
7	G7	D68-1-93A-1A//Ruff/Fg/3/Mtl-5/4/Lahn ICD93-0654-C-12AP-0AP-6AP-0AP	ICARDA
8	G8	GREEN-14//YAV-10/AUK	CIMMYT
9	G9	Bisu-1//CHEN-1/TEZ/3/HUI//CIT71/Cll	CIMMYT
10	G10	BCR/3/CH1//GTA/STK/4/BCR/LKS4 ICD92-0150-CABL-11AP-0AP-8AP-0TR-4AP-0AP	ICARDA
11	G11	GSB1-1-4/D68/1/93A-1A//RUFF/FG/3/MTL/5 ICD95-1174-C-2AP-0AP-2AP-0AP	ICARDA
12	G12	ALTAR84/STN/WDZ-2 ICD92-MABL-0238-4AP-0AP-5AP-0TR-15AP-0AP	ICARDA
13	G13	DON-MD 81-36	ICARDA
14	G14	STJ3//BCR/LKS4 ICD94-0994-CABL-10AP-0AP-2AP-0AP	ICARDA
15	G15	STJ3//BCR/LKS4 ICD94-0994-CABL-10AP-0AP-6AP-0AP	ICARDA
16	G16	OUASERL-1 ICD96-0758-C-2AP-0AP-5AP-0AP	ICARDA
17	G17	TRE97/4/GDOVZ5512/CIT/RUFF/FG/3/ENTE/MARIO//CA ICD97-1044-C-0AP-6AP-AP-5AP-OAP	ICARDA
18	G18	MARSYR-6 ICD95-1127-T-0AP-9AP-0AP-7AP-0TR-5AP-AP	ICARDA
19	G19	ETH-LRBRI-133/3*ALTER 84 CDSP91B31-A-1H-030Y-030M-3Y-0M-1Y-0B	CIMMYT
20	G20	Seimareh	Iran

Torrie 1980). To estimate the standard error of correlation coefficients, bootstrap analysis was performed using the S-Plus (Mathsoft 1999) statistical package. The biplot graphs were generated through GGEbiplot (Yan 2001) software, which as an excellent graphical tool has many applications other than determining stability of performance.

Results and Discussion

In the combined analysis of variance, the effects of genotype × location (GL) and G × Y× L were significant (Table 3). The main effect of year (Y) was significant ($P < 0.05$), the main effect of location (L) effects was not significant ($P > 0.05$) and their interaction (Y × L) was highly significant ($P < 0.01$). The main effect of genotypes was significant ($P < 0.05$), the genotype by year interaction (G × Y) was significant ($P < 0.05$), the genotype by location interaction (G × L) was not significant ($P > 0.05$). It is indicating that there is at least one durum wheat genotype with a different behavior in at least one of the location and environment (year × location combinations). Differential grain yield ranking

across environments indicates the presence of crossover GE interaction. In this investigation, different genotypes produced the highest grain yields at different environments. Genotype G13 was the highest yielding genotype at two locations (Gachsaran and Gonbad), genotype G12 was highest at location Kouhdasht, genotype G10 was highest at location Moghan, and genotype G14 was highest at location Ilam (data are not shown). The GGE biplot analysis based on biplot model should be applied to MET data when GE interaction is significant, its use should not be precluded when it is not significant.

It is clear that 39% of G+E+GE variation is due to year, 35% is due to location and 26% is due to GE interaction. Thus, the importance of years and locations are relatively equal. According to analysis of variance for the yearly data (Table 4), location was always the most important source of grain yield variation, accounting for 63 to 95% of the total variation (L + G + GL). These results gave an overall picture of the relative magnitudes of the G, L, and GL variance components. The considerable grain yield variation due to location term, permits using of the multivariate methods as one possible approach for GE interaction investigation and MET data analysis (Yan et al., 2000). According to Fox Rosielle (1982), Gauch Zobel (1996) and Yan et al. (2007) the unpredictable variance components such as year and location are irrelevant to genotype evaluation in MET data analysis. In addition, the multiplicative GE interaction component is far more complex to be summarized by one or two parameters in conventional stability analysis methods while multivariate methods can explore multi-directionality aspect and attempt to extract more information out of this component (Sabaghnia et al., 2008b). Therefore, it can be concluded that using of GGE biplot as the appropriate model for analyzing the MET data is logical.

Based on the results of Table 4, the GL interaction is larger than G term and so there are different mega-environments in durum wheat producing areas of Iran (Yan et al., 2000). Iden-

Table 3
Combined analysis of variance of durum wheat performance trial yield data

Source	DF	MS
Year (Y)	2	206213572.0[*]
Location (L)	4	94220057.1[ns]
Y × L	8	34610128.9[**]
Replication/ YL	45	618760.2
Genotype (G)	19	680166.4[*]
G × Y	76	341113.3[*]
G × L	38	314535.9[ns]
G × Y× L	152	248317.9[**]
R × G / YL	855	102927.8

[**], [*] and [ns] significant at the 0.01 and 0.05 probability level, respectively and non-significant.

Table 4
Analysis of variance for GGE biplot model in durum wheat performance trial yield data

Source	DF	MS	F	% of GE
Location (L)	4	31406644.1	1979.7[**]	
Genotype (G)	19	226723.8	14.2[**]	
G × L	76	113704.6	7.1[**]	
Model GGE biplot				
PC1	22	221671.4	13.9[**]	35.6
PC2	20	177949.5	11.2[**]	27.4
PC3	18	111665.3	7.0[**]	15.5
Residual GGE biplot	30	164843.7	10.3[**]	21.5

[**] Significant at the 0.01 probability level

tification of mega-environments has been an important target in MET data investigation. Gauch Zobel (1997) declared that growing different genotypes in different locations results in presence of GE interaction. Gauch Zobel (1996) defined a mega-environment as a portion of a plant species' growing site with homogeneous conditions that causes similar yield performance of some genotypes. Regarding multi-directionality aspect of GE interaction, relative magnitudes of the L to the G and GL components and mega-environment identification for durum wheat in Iran, genotype plus genotype by location (GGL) biplot methodology was employed to analysis of the preset MET dataset.

GGE biplot analyses of variance for grain yield of 20 durum wheat genotypes across five locations are given in Table 5. The fitted GGL biplot model indicated that, the first two PCs explained 60.3% of variation for durum wheat MET. According to the PCA theory, the first two principal component scores are the most important ones to explain the data. Considering 60.3% (PC1 = 35.6% and PC2 = 27.4%) of explanation, the GE interaction SS decomposition into PC's would be useful to understand and explore the relationship among genotypes, GE, and the mega-environment identification. In present investigation F-Gollob (Gollob 1968) was used to test significance of PCs for the GGE biplot model and showed that all PCs were significant but, the magnitudes of the first two PCs are relatively high and GGL biplots can reflect data variations (Table 5). The relative contributions of the first two PCs to the total variation for grain yield of durum wheat found in this investigation are similar to those found in other crop adaptation studies in rain-fed regions of Iran (Sabaghnia et al., 2008a; Ebadi-Segherloo et al., 2010). The GE interaction makes it difficult to select the most stable genotypes and so it is an important consideration in plant breeding programs because it reduces the progress from selection in any one environment (Yau, 1995).

The graphic presentation through the first two PCs indicated that this biplot explained 60.3% (PC1 = 35.6% and PC2 = 24.7%) of the GGL, implying that the GL for grain yield in

this dataset was complex. A biplot of PC3 versus PC4 cannot reveal any discernible patterns due to low explanation of G+GL variation (lower than 22%). According to Yan and Tinker (2005) GGE biplot of PC1 vs. PC2 adequately display the GGE patterns instead of GGE biplot of PC3 vs. PC4. Polygon view of biplot has been used to identify "which-wins-where" patterns in MET data analysis. In this graph, lines are drawn to connect the furthest genotypes in the biplot and then a line is drawn perpendicular to that side of the polygon to pass through the origin. The furthest genotype is the best performer in the location included in that sector. There are 6 rays in Figure 1 which divide the biplot into 6 sectors, and the locations fall into 3 of them. An interesting property of the GGL biplot polygon view is that each vertex genotype has higher yield than the other genotypes in all locations that fall in the related sector (Yan, 2002). Thus, 2 locations (Gonbad and Moghan) fell into sector 1 and the vertex genotype for this sector was G10, suggesting that high yielding genotype for these 2 locations was G10. This genotype was better than the other genotypes, which fell into sector 1 (genotypes G4, G6, G16 and G20).

Similar to the above conclusion, 2 locations, Kouhdasht and Ilam, fell into sector 5, and the vertex genotype for this sector was G12, suggesting that the higher-yielding genotype for these 2 locations was G12. This genotype was better than the genotypes G15 and G19, which fell into sector 5. A single environment, Gachsaran, fell into sector 6 and the vertex genotype for this sector was G14. Genotype G14 was better than the other genotypes, which fell into sector 6 (genotypes G9, G8 and G13). It could be mentioned that the locations are not represented by genotypes. Furthermore, the observed pattern of Figure 1 indicated that relationship among locations, which is the way to define possible mega-environments. Polygon view of biplot has been used to identify polygon view of biplot (Figure 1) suggests that there exist 3 possible durum wheat mega-environments in the Iran: (i) Gonbad and Moghan in northern Iran represented by genotype G10, (ii) Kouhdasht in southwestern and Ilam in western Iran represented by geno-

Table 5
Genotype (G), location (L), and genotype × location (GL) variance terms for durum wheat multi-environmental trials, 2005 to 2007

Source of variation	DF	Year 2005		Year 2006		Year 2007	
		MS	%GL	MS	%GL	MS	%GL
Location (L)	4	16971440.2**	0.63	478845985.5**	0.95	26757379.1**	0.82
Rep. within L	15	379291.2		712689		764300.3	
Genotype (G)	19	678821.8*	0.12	297942.3ns	0.01	332474.3ns	0.05
G × L	76	347439.2**	0.25	257396.3**	0.04	232913.6**	0.14
Error	285	119681.3		107006.9		82095.3	

type G12, and (iii) Gachsaran in southern Iran represented by genotype G14. It is clear that identification of mega-environments through "which wins where" methodology based on polygon view of GGL biplot is in agreement with geographical properties of test locations in durum wheat in Iran.

In GGE biplot methodology, the yield and stability of the genotypes were examined by an average tester coordinate (ATC). The mean yield of the genotypes is estimated by their projections on the ATC x axis. The average location, as the virtual location, is showed by a circle and indicates the positive end of the ATC x axis (Figure 2). According to the ATC figure, the length of the average location vector was adequate to select genotypes based on mean yield. Genotypes with above average were selected means (G7, G8, G9, G13, G14 and G16), whereas the remained genotypes were discarded (Figure 2). In contrast, G10 was the least stable genotype which has variable performance across test locations, while was as the one of the high yielding genotypes. The performance of all genotypes like G5 and G18 close to ATC axe was stable ones, whereas some of them showed low mean yields (Figure 2). Therefore, it seems that genotypes G7, G8, G9, G13, G14 and G16 are good candidates for recommending as the most favorable genotypes from both mean yield and stability aspects. Considering G and L performance in Figure 2, genotypes adapted specifically to Moghan and Gonbad were G4, G9, G10, G16 and G20; and those adapted specifically to Ilam and Kouhdasht were G8, G14, G15 and G19.
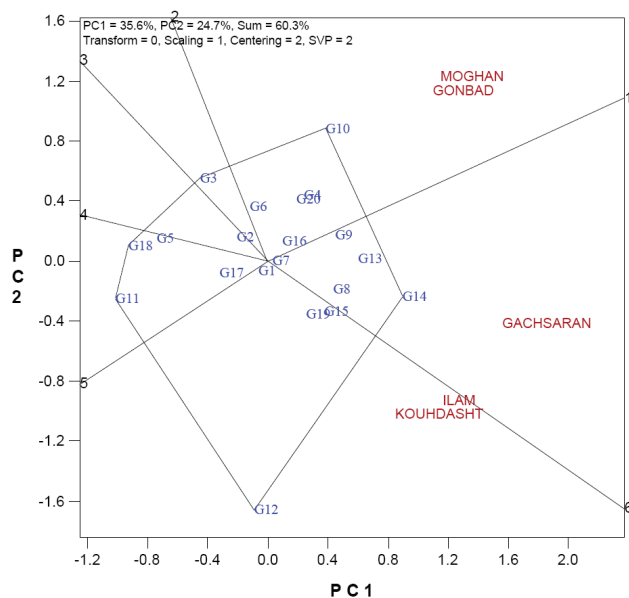
Simultaneous selection for both mean yield and stability of genotypes performance is an important consideration in breeding programs (Yan and Kang, 2003). Kang and Pham (1991) have studied several stability methods for simultaneous selection for yield and stability and reported that a greater emphasis on stable performance would not necessarily be harmful to farmers because they would expect high mean yield from the cultivated genotypes on their farms. According to Crossa et al. (2002) using of GGE biplots in the identification of superior genotypes, facilitates the identification of such genotypes. Our study has clearly indicates that the GGE biplot model can analyze patterns and relationships of genotypes and locations successfully as well as provide a valuable prediction. Finally, ATC view of GGE biplot methodology can be regarded as a suitable tool for simultaneous selection of both mean yield and stability in MET data analysis.

The correlation coefficients among the five test locations are presented in Table 6. The vector view of a GGL biplot provides a summary of the interrelationships among the locations (Yan, 2002). If the biplot explained an adequate amount (≥50%) of the total variation, the correlation coefficient between any two locations is reliable. The biplot in Figure 3 explained 60.3 % of the total variation and so this biplot can be used for extracting interrelationships among the locations. The correlation coefficient between any two locations is estimated by the cosine of the angle between their vectors. Two
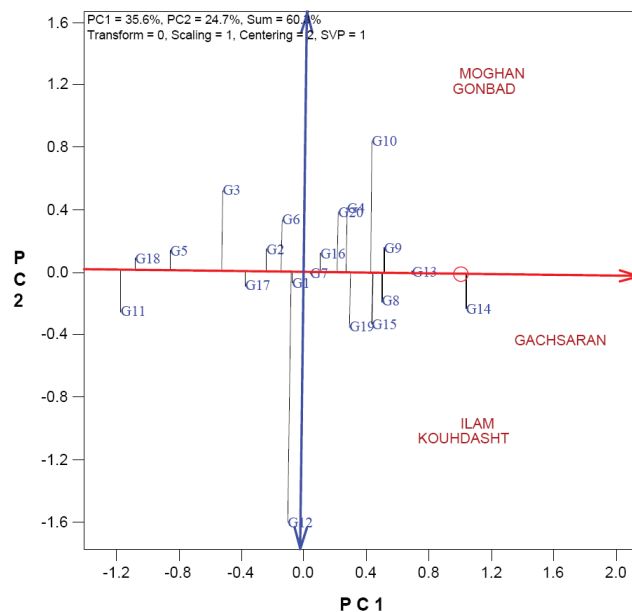

Fig. 1. GGE biplot identification of winning genotypes and their mega-environments. Twenty durum wheat genotypes grown in five locations

Fig. 2. GGE biplot of mean and stability of 20 durum wheat genotypes for yield and specific genotype × environment interactions

locations are positively correlated if the angle between their vectors is <90°, negatively correlated if the angle is >90°, independent if the angle is 90°. In addition, locations with longer vectors are more responsive to the genotypes; locations with shorter vectors are less responsive to the genotypes; and those located at the biplot origin are not responsive at all (Yan and Kang, 2003).

The most prominent relations based on Figure 3 were: (i) positive associations between Moghan and Gonbad and between Ilam and Kouhdasht locations and (ii) a low positive or near-zero correlations between Gachsaran with the other locations. Pearson's correlation coefficients and output of the bootstrap resampling technique (mean, bias and standard error) are given in Table 6. The low standard error of all the correlation coefficients and the low bias also indicated the robustness of correlation analysis. Although some of the above predictions can be verified from the Pearson's correlation coefficients and bootstrap analysis (Table 4) but some others are not consistent with the original coefficients of correlation. Such discrepancies are seen because the GGL biplot method explained only 60.3% rather than 100% of the total variation. Although, all above conclusions have some error but GGL biplot shows predictions on the general pattern of the whole dataset, the predictions are probably more reliable than the individual observations (Yan and Hunt 2002).

The biplot vector view can be used to identify test environments which have large angles or low or negative correlations. Locations with small angles between them were highly positively correlated, and they provided similar information on genotypes. In the MET data of durum wheat in all 3 years, two locations Ilam and Kouhdasht besides two locations Moghan and Gonbad were closely correlated (Figure 3),

suggesting that these locations provide redundant information about genotypes. Obtaining similar information by using fewer test environments should reduce the cost of testing and increase breeding efficiency. Therefore, we can suggest that one of the two locations in each set be dropped to reduce the cost of testing. In addition, in the vector view of the biplot, the length of the location vectors estimates the standard deviation within each location, which is a measure of their discriminating ability. Thus, all five-test locations were most discriminating locations for durum wheat yield performance (Figure 3).
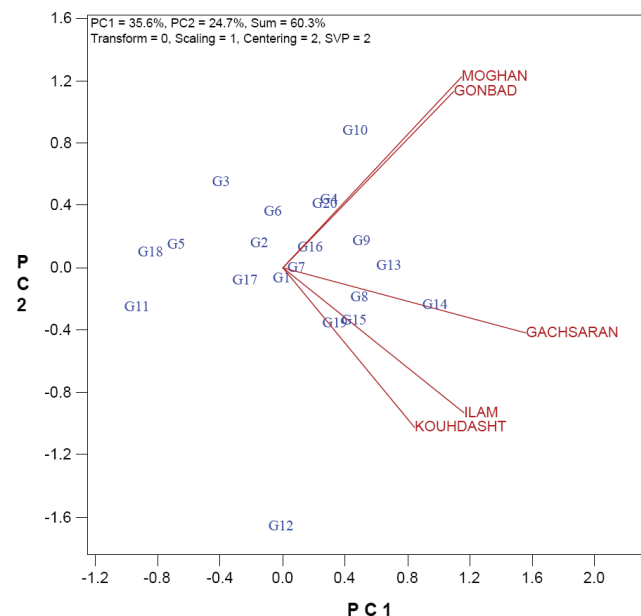

Fig. 3. GGE biplot for relationships between test locations

Table 6
Pearson's correlation coefficients and Bootstrap resampling technique statistics (Bias, Mean and standards error) among five test locations environments

Location 1	Location 2	Observed	Bootstrap statistics		
			Bias	Mean	SE
Gachsaran	Gonbad	0.189	0.0131	0.202	0.2049
	Kouhdasht	0.265	0.0073	0.273	0.1542
	Moghan	0.278	0.0143	0.292	0.2159
	Ilam	0.402	0.0101	0.412	0.1679
Gonbad	Kouhdasht	0.064	-0.0568	0.007	0.4209
	Moghan	0.385	-0.0426	0.342	0.2378
	Ilam	0.059	0.0054	0.064	0.1714
Kouhdasht	Moghan	-0.028	0.0274	-0.001	0.2958
	Ilam	0.180	0.0030	0.183	0.1722
Moghan	Ilam	0.057	-0.0096	0.047	0.2349

[*] Critical values of correlation P<0.05 and P<0.01 (D.F. 18) are 0.44 and 0.56, respectively.

Another interesting application of GGEbiplot software is to evaluateof genotype relative to an ideal genotype. The ideal genotype as virtual genotypes is one that has both high mean yield and high stability (Yan Rajcan 2002). This genotype has large PC1 scores (high mean yield) and small (absolute) PC2 scores (high stability). A genotype is more favorable if it is closer to the ideal genotype position. Therefore, genotypes G13 and G14 following to G8, G9 and G15 were more desirable than other durum wheat genotypes (Figure 4). It seems that Ideal genotype procedure of GGE biplot methodology is a proper tool for identifying high yielding genotypes as the most stable ones. This method can be regarded as the same as AMMI parameters which try to facilitate identifying more stable genotypes using AMMI procedure (Sabaghnia et al., 2008a). In other word, Ideal genotype procedure attempts to define the GE interactions by one parameter (distance from Ideal genotype) and summarize complex aspect of GE interaction using only one parameter.

According to Yan (2001), discriminating ability and representative-ness are the important properties of a test location. An ideal location should be highly differentiating of the tested genotypes and at the same time representative of the target location (Yan and Kang, 2003). Similar to ideal genotype, an ideal environment or location is defined and showed by the small circle with an arrow pointing to it. According to Figure 5, location Gachsaran is more desirable test location than the other test locations. Thus, genotype

evaluation in Gachsaran maximizes the observed genotypic variation among genotypes for grain yield of durum wheat. The discriminating ability of a location is comprised of genotypes, but the presence of GE interaction complicates the identification of an ideal test location (Yan et al., 2000). Usually non-additive or crossover GE interaction was observed in the most MET and it is essential to reveal the nature of GE interaction. GGE methodology is suitable tool to analyze this kind of interactions partitioning them into their PCs. The test location should has large PC1 scores in order to discriminate genotypes in terms of the genotypic main effect and absolute small PC2 scores in order to more representative of the overall locations (Yan Rajcan, 2002).

There is no doubt that multivariate methods for MET data analysis are useful tools for plant breeders. In addition, visualization techniques such as biplot are useful to quickly explore patterns of genotypes or locations, and can be extract useful information from complex MET dataset. Recently there has been an ongoing debate on advantages and disadvantages of biplots in AMMI versus GGE models for MET data analysis and GE interaction studies (Gauch, 2006; Yan et al., 2007; Gauch et al., 2008; Yang et al., 2009). An important disadvantage of the GGE biplot methodology is lack of measure of uncertainty. Yan Hunt (2002) proposes that the significance of the difference between two genotypes can be visually assessed from their plot distance relative to the plot size. Simultaneous selection for both mean yield and stability of genotypes per-
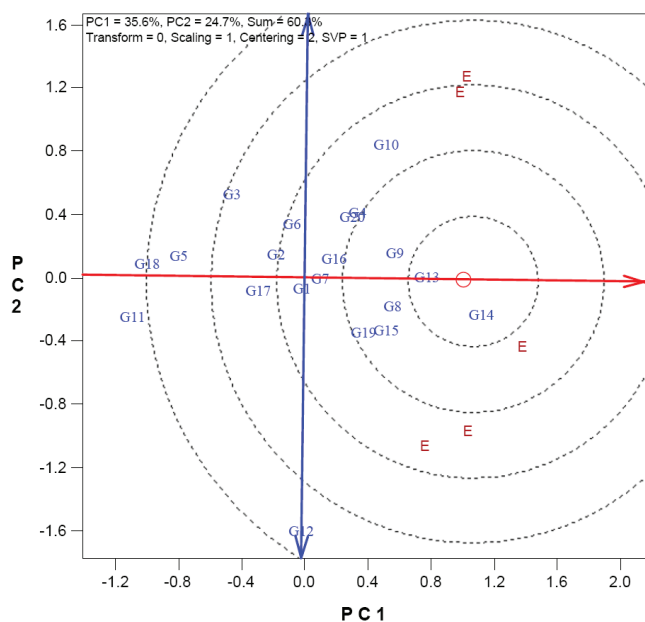

Fig. 4. GGE biplot of ideal genotype and comparison of the genotypes with the ideal genotype for the twenty durum wheat genotypes which grown in five locations
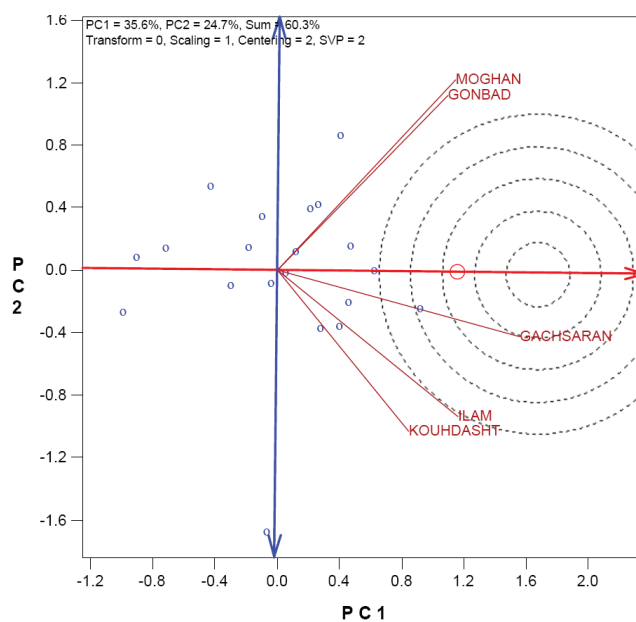

Fig. 5. GGE biplot of ideal environment and comparison of the locations with the ideal environment. Twenty durum wheat genotypes grown in five locations

formance is an important consideration in breeding programs (Yan Kang, 2003). At first time, Kang (1988) proposed a non-parametric stability statistic as named as rank-sum using stability variance of Shukla (1972) and genotype mean rank for simultaneous selection for mean yield and stability. A greater emphasis on stable performance (static concept) would not necessarily be harmful to farmers because they would expect high mean yield from the cultivated genotypes on their farms. Therefore, it seems that GGE model for MET data analysis is a suitable tool for achieve high mean yield genotypes which have acceptable stability (dynamic concept of stability). An inconsistent genotype performance across environments can provide additional information for the breeder and can help predict the variability expected among different regions (Busey, 1983). GGE biplot methodology thus provides a lot of flexibility in the hands of plant breeders for simultaneous selection for yield and stability.

The magnitude of GE interaction for grain yield of 20 durum wheat genotypes tested across 15 rain-fed environments sampled from the arid and semi-arid regions of Iran was larger than that of G effect, but smaller than that of E effect. The genotypes studied indicated additive and crossover of GE interaction and this phenomenon led to differential rankings of genotypes across test environments (location by year combinations), thereby making genotypic selection difficult for the rain-fed conditions of Iran. In general and according to all GGL biplot figures of the present investigation genotypes G14 was the most favorable genotype from both mean yield and stability properties. Also following to this genotype, two other genotypes (G8 and G13) could be considered. Of course, from mega-environment aspect and specific adaptation problems, G14 was the most favorable genotype for location Gachsaran and the most favorable genotypes of mega-environment Kouhdasht and Ilam was G12 and the most favorable genotypes of mega-environment Gonbad and Moghan was G10.

Conclusion

In present investigation, GGE biplot methodology, as has been shown to be very useful for analysing MET dataset of durum wheat (Mohammadi et al., 2010; Mohammadi et al., 2011), permitted a meaningful grasp of GE interaction and exploring the relationships among genotypes and test environments. Cooper et al. (1997) suggest that yield under low-stress conditions was an effective predictor of yield under similar low-stress target environments. Grain yield in the abiotic stress conditions was a poor predictor of yield in the target environments. Our findings are in agreement with those reported by Cooper et al. (1997), given that favorable location

(Gachsaran) was more representative of the overall locations and more powerful to discriminate genotypes than the unfavorable ones. Cooper et al. (1997) also proposed that grain yield breeding can best be done by selection for a combination of yield potential in favorable environments and yield in on-farm trials that sample the range of water-limited environments of the target population of environments. Our results indicate that the GGE biplot model is an excellent tool for visual MET data analysis. It has some advantages: graphical presentation, be interpretative and facility of mega-environments identification.

References

Burgueno, J., Crossa, J. and M. Vargas, 2001. SAS programs for graphing GE and GGE biplots. Biometrics and Statistics Unit, CIMMYT.

Busey, P., 1983. Management of crop breeding, p. 31–54. In: D.R Wood, K.M. Rawal, and M.N. Wood (Eds.), Crop breeding, American Society of Agronomy, Crop Science Society of America, Madison, WI.

Cooper, M., Stucker R. E., DeLacy I. H. and B. D. Harch, 1997. Wheat breeding nurseries, target environments, and indirect selection for grain yield. *Crop Sci.,* **37:** 1168–1176.

Crossa, J., Cornelius P. L. and W. Yan, W. 2002. Biplots linear-bilinear model for studying cross over genotype × environment interaction. *Crop Sci.*, **42**: 619–633.

Crossa, J. and P. L. Cornelius, 1997. Site regression and shifted multiplicative model clustering of cultivar trials sites under heterogeneity of error variances. *Crop Sci.*, **37**: 406–415.

Dehghani, H., Ebadi A. and A. Yousefi, 2006. Biplot analysis of genotype by environment interaction for barley yield in Iran. *Agron. J.*, **98**: 388–393.

Dehghani, H., Sabaghnia N. and M. Moghaddam, 2009. Interpretation of Genotype-by-Environment Interaction for Late Maize Hybrids' Grain Yield Using a Biplot Method. *Turk. J. Agric. Fores.*, **33**: 139–148.

Ebadi-Segherloo, A., Sabaghpour, S. H., Dehghani, H. and M. Kamrani, 2010. Screening of superior chickpea genotypes for various environments of Iran using genotype plus genotype × environment (GGE) biplot analysis. *J. Plant Breed. Crop Sci.*, **2**: 286–292.

Fox, P. N. and A. A. Rosielle, 1982. Reducing the influence of environmental main-effects on pattern analysis of plant breeding environments. *Euphytica*, **31:**645–656.

Gabriel, K. R., 1971. The biplot graphic display of matrices with application to principal component analysis. *Biometrika,* **58:** 453-467.

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

Gauch, H. G. and R. W. Zobel, 1996. AMMI analysis of yield trials. p. 85–122. *In* M.S. Kang and H.G. Gauch (ed.) Genotype-by-environment interaction. *CRC Press,* Boca Raton, FL.

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

Gauch, H. G., Piepho, H. P. and P. Annicchiaricoc, 2008. Statistical analysis of yield trials by AMMI and GGE. Further considerations. *Crop Sci.,* **48**: 866–889.

Gollob, H. F., 1968. A statistical model, which combines, features of factor analytic and analysis of variance techniques. *Psychometrika,* **33**: 73–115.

Kang, M. S. and H. N. Pham, 1991. Simultaneous selection for high yielding and stable crop genotypes. *Agron. J.,* **83**: 161–165.

Kang, M. S., 1988. A rank–sum method for selecting high-yielding, stable corn genotypes. *Cereal Res. Comun.*, **16**: 113–115.

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

MATHSOFT, 1999. MathSoft, S-Plus 2000. Guide to Statistics, Volume 1. Data Analysis Products Division, Math-Soft Inc, Seattle, WA.

Mohammadi, R., Armion, M. Sadeghzadeh, D. Amri, A. and M. Nachit, 2011. Analysis of genotype-by-environment interaction for agronomic traits of durum wheat in Iran. *Plant Prod Sci.,* **14**: 15—21.

Mohammadi, R., Haghparast, R. Amri and A. Ceccarelli, 2010. Yield stability of rainfed durum wheat and GGE biplot analysis of multi-environment trials. *Crop and Pasture Sci.*, **61**: 92–101.

Mohammadi, R., Haghparast, R. Aghaee, M. Rostaee, M. and S. S. Pourdad, 2007. Biplot analysis of multi-environment trials for identification of winter wheat mega-environments in Iran. *World J. Agric. Sci.*, **3**: 475–480.

Rharrabti, Y., Garcia del Moral, Villegas, L. F. D. and C. Royo, 2003. Durum wheat quality in Mediterranean environments III. Stability and comparative methods in analyzing G x E interaction. *Field Crop. Res.*, **80**: 141–146.

Sabaghnia, N., Dehghani, H. and S. H. Sabaghpour, 2008a. Graphic analysis of genotype × environment interaction of lentil yield in Iran. *Agron. J.,* **100**: 760-764.

Sabaghnia, N., Sabaghpour, S. H. and H. Dehghani, 2008b. The use of an AMMI model and its parameters to analyze yield stability in multi-environment trials. *J. Agric. Sci.*, **146**: 571–581.

Sakin, M. A., C. Akinci, O. Duzdemir and E. Donmez, 2011. Assessment of genotype x environment interaction on yield and yield components of durum wheat genotypes by multivariate analyses. *African J. Biotech*. **10**: 2875–2885.

SAS Institute. 1996. SAS/STAT user's guide. Version 6.12. SAS Inst., Cary, NC.

Shukla, G. K., 1972. Some statistical aspects of partitioning genotype- environmental components of variability. *Heredity,* **29**: 237–245.

Steel, R. G. D. and J. H. Torrie, 1980. Principles and procedures of statistics. McGraw-Hill Book Co., New York.

USDA, 2009. Global Durum Wheat production, www.fas.usda.gov, http://www.ers.usda.gov/data/wheat/WheatYearbook.aspx

Yan, W., 2001. GGEbiplot–A Windows application for graphical analysis of multienvironment trial data and other types of two-way data. *Agron. J.*, **93**: 1111–1118.

Yan, W., 2002. Singular value partitioning in biplot analysis of multievironment trial data. *Agron. J.*, **94**: 990–996.

Yan, W. and I. Rajcan, 2002. Biplot evaluation of test sites and trait relations of soybean in Ontario. *Crop Sci.,* **42**: 11–20.

Yan, W. and L. A. Hunt, 2002. Biplot analysis of diallel data. *Crop Sci.,* **42**: 21–30.

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

Yan, W. and N. A. Tinker, 2005. An integrated system of biplot analysis for displaying, interpreting, and exploring genotype by-environment interactions. *Crop Sci.*, **45:** 1004–1016.

Yan, W. and N. A. Tinker, 2006. Biplot analysis of multi-environment trial data: Principles and applications. *Can. J. Plant Sci.*, **86**: 623–645.

Yan, W., L. A. Hunt, Q. Sheng and Z. Szlavnics, 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Sci.*, **40**:597–605.

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

Yang, R. C., Crossa, J. Cornelius, P. L. and J. Burgueño, 2009. Biplot analysis of genotype × environment interaction: proceed with caution. *Crop Sci.*, **49**: 1564–1576.

Yau, S. K., 1995. Regression and AMMI analyses of genotype × environment interactions: An empirical comparison. *Agron. J.,* **87**: 121–126.

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