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# Yield stability analysis in advanced durum wheat genotypes by using AMMI and GGE biplot models under diverse environment

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## Abstract

**A investigation was carried out to ascertain the GEI, the yield stability and adaptability of 17 advanced durum wheat genotypes (G) in four environments over two crop years (2011-12 and 2012-13) under rainfed and supplementary irrigation (IRR) conditions. Combined analysis of variance showed that environmental factor and GEI explained 70% and 10.71% of total sum squares, respectively. The AMMI and GGE biplot model were used to study the nature of GEI on the grain yield. First and second component of AMMI model totally explained 90.73% of GEI variations. Results of GGEbiplot model similar to the results of AMMI model showed that the G12 with the environment of IRR2, G2 with the environment of RA2 and G17 and G9 with the environment of RA1 and IRR1, respectively showed a special adaptability. G8 and G11 could be recommended for all environments. Considering both graphical analysis models of AMMI and GGEbiplot could be recommended. The ideal environment, according to AMMI model, was RA2, while GGEbiplot model represented IRR2 as ideal environment. The results indicated that AMMI and GGEbiplot are facilitated visual comparison and informative methods to detect genotypes stability and in the preferential genotypes recommendations.**

**Key words:** GEI, AMMI, GGEbiplot, durum wheat, yield stability

## Introduction

Durum wheat (*Triticum durum* Desf.) is the only tetraploid wheat species of commercial importance in the food industry, due to its good grain quality (Rachon et al. 2009). The success of durum wheat in Iran is largely due to its good ability and capacity to yield well under drought prone, marginal and poor management conditions, where other crops would fail (Mohammadi et al. 2011). In Iran, about two-third of crop cultivation areas are located in dryland and rainfed regions. Supplemental irrigation could help in preventing crop failure during droughts and improve yields in cropping seasons with average precipitation (Mohammadi et al. 2011). The ideal genotype should be high yielding under any environmental conditions, but as genetic effects are not independent of environmental effects, most genotypes do not perform satisfactorily in all environments (Carvalho et al. 1983). The development of improved genotypes, which can be adapted to a wide range of environments, is one of the final goals of researchers in plant breeding program. It is complicating to determine genotypes which have desirable performance, whether in the moisture stress conditions or no stress, due to significant GEI (Gauch 2006). The reaction of different genotypes is often resulted from the varied response of genes or their different expression ability in different environments (Brandiej and Meverty 1994). Breeders conduct multi-environmental yield trials (MET) to investigate GEI and according to their results, the compatible and stable genotypes are recommended to the farmers (Najafian et al. 2010; Zali et al. 2011). The varied versions of biplot based on the multivariate statistical methods have been represented and broadly used by plant breeders in order to graphically analyze GEI (Gauch 2006; Yan and Tinker 2006; Yan et al. 2000). The additive main effects and multiplicative interaction (AMMI) and GGE biplot models can be powerful tools for effective analysis and interpretation of multienvironment data structure in breeding programs (Yan et al. 2000; Ebdon and Gauch 2002; Samonte et al. 2005).The utilization of both AMMI and GGE biplot methods simultaneously in confirmation of stable

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genotypes with high yield conducted by many researchers. Mortazavian et al. (2014) evaluated twenty promising barley lines at different environments in Iran, during two cropping seasons. They find out the effects of GEI on grain yield by use of AMMI and GGE biplot analysis. “Which-won-where” pattern revealed G5 and G6 had the general adaptability while G7 and G13 exhibited specific adaptation to conditions. Considering both techniques, genotype G1 revealed high grain yield along with yield stability. They showed that these two methods are effective to identify adaptability and stability pattern of genotypes in the developmental program and introduced genotype. Ahmadi et al. (2012) determined the effects of GEI on yields by use of AMMI and GGE biplot analysis. The AMMI1 model explained up to 88% of the main and interaction effects. They showed that use of AMMI and GGEbiplot facilitates visual comparison and identification of superior bread wheat genotypes. Choukan (2011) conducted MET for 14 maize inbred lines by AMMI and GGE biplot analyses. These genotypes evaluated under diverse climatic conditions during two cropping cycles. The AMMI and GGE biplot graphics revealed the inbred lines that were most responsive to the environment were K3615/2, K166B, K19/1 and K18; the least responsive line was K3547/5. Substantial variation in barley genotypes was reported by kumar et al (2016) by conducting AMMI and GGE model analysis from the data generated at nine environments. The purpose of the present study was to apply GGE biplot and AMMI techniques to study the patterns of GEI in 17 advanced durum wheat genotypes under supplementary irrigation and rainfed conditions; to graphically display means, adaptability and stability of durum wheat genotypes, to identify suitable genotypes for each condition, to the relationship among the test environments and to compare result of GGEbiplot and AMMI models.

## Material and methods

A total of 17 durum wheat genotypes (Table 1) including three checks, *viz*., Saji, Zardak and Sardari were evaluated under rainfed and supplementary irrigation conditions (twice irrigation at flowering stage to reach each stage up to 25 mm) in the randomized complete blocks design (RCBD) with three replications over 2 crop years (2011-12 and 2012-13). The experiment was conducted in Sararood Dryland Agriculture Research Institute (DARI), Kermanshah, Iran (geographical coordinates are in longitude of 47° 16' 48", latitude of 34° 19' 12" and altitude of 1351 meters above sea level with average rainfall of 425 mm). Each genotype was grown in 6 rows of 6 meters and at 20cm row-row spacing. All the cultural practices were carried out as recommended. Following harvest, grain yield was determined for each line in each test environment.

**Table 1.** Pedigree and mean yield of the investigated genotypes

| Entry code | Pedigree | Mean yield (g/m$^2$) in all environments |
|---|---|---|
| G1 (C) | Saji | 763.13 |
| G2 (C) | Zardak | 569.80 |
| G3 (C) | Sardari | 703.08 |
| G4 | 19E-TOPDY | 611.53 |
| G5 | 19E-RASCON | 560.80 |
| G6 | 19E-M84859 | 557.87 |
| G7 | 19E-M141979 | 661.14 |
| G8 | 19E-M141982 | 713.23 |
| G9 | 19E-M141994 | 685.64 |
| G10 | 19E-M141995 | 798.14 |
| G11 | 18E-M142005 | 678.32 |
| G12 | 19E-M142017 | 818.09 |
| G13 | 19E-M142025 | 608.83 |
| G14 | 19E-M142038 | 730.05 |
| G15 | 19E-M142045 | 662.18 |
| G16 | 19E-M142069 | 710.53 |
| G17 | 19E-M142070 | 669.78 |
| Mean | | 676.59 |

C = Control

Meteorological data of two crop years recorded at for Sararood, Dryland Agriculture Researches together with the different environments used in the experiment are given in Table 2.

Combined analysis of variance was performed for different environment. The PROC GLM procedure available in SAS (Ver. 6, SAS Institute 1996) was used to partition yield variation into environments, genotypes, and genotypes x environment interaction (GEI). The grain yield data were subjected to AMMI and GGE biplots analysis. The results of the AMMI model analysis by Zobel et al. (1988) were interpreted from the AMMI1 graph that showed the main and first multiplicative axis term (PC1) of both genotypes and environments. The GGE biplots were constructed from the first two principal components (PC1 and PC2) derived by subjecting the environment-centered yield

**Table 2.** Different environments used in the experiment and average yield in every environment

| Environment<br>Condition | Year | Av. rainfall (mm) | Temperature ($^oC$) | | | Mean yield |
|---|---|---|---|---|---|---|
| | | | Min. | Max. | Av. | |
| Rainfed1 (RA1) | 2011-12 | 330.63 | 3.3 | 17.98 | 10.6 | 336.14 |
| Irrigation1 (IRRI1) | 2011-12 | 330.63+50 | | | | 588.16 |
| Rainfed2 (RA2) | 2012-13 | 430.87 | 4.5 | 19.17 | 12 | 487.86 |
| Irrigation2 (IRRI2) | 2012-13 | 430.87+50 | | | | 1294.23 |

*9 months (October-June); Min. = Minimum; Max. = maximum; Av = Average

data (which contains G and GE) to singular valued composition (SVD) (Yan et al. 2000; Yan 2002). The GGE biplot software (Yan 2001) was used to generate graphs showing (i) "which-won-where" pattern, (ii) ranking of cultivars on the basis of yield and stability, and (iii) correlation vectors among environments. Angles between environment vectors were used to judge correlations between pairs of environments as per the method described by Yan and Kang (2003).

## Results and discussion

### *Analysis of variance*

Analysis of Variance for grain yield measured per condition showed a significant genotype effect in all environment except irrigation (2012-13) condition (Table 3), suggesting the presence of exploitable genotypic differences.

**Table 3.** Mean squares of grain yield analysis of variation per condition

| Source of variation | df | Rainfed 1 | Irrigation1 | Rainfed 2 | Irrigation 2 |
|---|---|---|---|---|---|
| Total | 50 | 19950.109 | 44190.409 | 44065.318 | 127206.687 |
| Block | 2 | 145368.110 | 111624.034 | 48640.994 | 105749.618 |
| Genotype | 16 | 28496.396** | 73691.964** | 71086.217* | 162731.760$^{ns}$ |
| Error | 32 | 7838.341 | 25225.031 | 30268.889 | 110785.218 |

Rainfed 1 and 2 represented rainfed condition in 2011-12 and 2012-13 crop seasons, respectively. Irrigation1 and 2 represented irrigation condition in 2011-12 and 2012-13 crop seasons, respectively; **Genotypic effect significant at 1% probability

In the combined analysis of variance for grain yield, the main effects of year (Y), environment (E) was significant (P<0.05) and the main effect of genotype was non-significant. The effect of genotype × environment interaction (GE) is shown to be significant at 0.05 level of probability which indicates that the genotypes had differential yields in rainfed and irrigated conditions (Table 4). The GEI was significant ($p$<0.01) and explained 10.71% of total sum squares, which is indicating that the studied genotypes exhibited complicated GEI (Table 5). Grain yield is a quantitative trait, and the performance is the result of genotype, environmental factors and GEI. The large GEI results in to different genetic nature of genotypes and control the diverse processes bringing in the yield stability under different environments (Cooper et al. 2001). The relative contribution of GEI effects for grain yield found in this study are similar to those found in other studies in multi environments trials. Adjabi et al. (2014) studied the stability analysis of 15 durum wheat grain yield during 6 consecutive cropping seasons under semi-arid conditions and they showed despite significant GEI but genotype effect was not significant. So they investigated GEI by use of AMMI method. Chandra et al. (1974) reported that GEI with condition is more important than GEI with year. Since GEI was significant, we therefore move further to estimate stability by AMMI and GGE biplot models to identify the most stable genotype in different environments and attribute special genotypes to special environments.

### *AMMI biplot analysis*

About 70% of total sum squares are due to environment. GEI also explained 10.71% of total sum of squares that implies importance of GEI and its

**Table 4.** Combined analysis of variance for grain yield in durum wheat

| Source | df | Sum of squares | Mean square | F |
|---|---|---|---|---|
| Year (Y) | 1 | 1128410.063 | 1128410.063 | $21.399^{**}$ |
| Environment (E) | 1 | 1.428E7 | 1.428E7 | $270.844^{**}$ |
| Y × E | 1 | 775495.357 | 775495.357 | $14.706^{**}$ |
| Replication/YE | 8 | 1.222E7 | 1527314.428 | $28.964^{**}$ |
| Genotype (G) | 16 | 1159754.379 | 72484.649 | $1.375^{ns}$ |
| G × Y | 16 | 954991.992 | 59687.000 | $1.132^{ns}$ |
| G × E | 16 | 1458272.335 | 91142.021 | $1.728^{*}$ |
| G × Y × E | 16 | 625102.841 | 39068.928 | $0.741^{ns}$ |
| R × G/YE | 128 | 6749739.172 | 52732.337 | |
| Corrected total | 203 | 3.935E7 | | |

**, *significant at the 0.01 and 0.05 probability level, respectively and ns = non-significant

evaluation (Table 5). Only a small portion (2.94%) of the total sum of squares was attributed to genotype effect. Thus, these results gave an overall description of the relative magnitudes of the variance components. The grain yield variation due to conditions term, consents using of the multivariate methods as one possible approach for GEI evaluation and MET data analysis (Yan et al. 2000). The multiplicative GEI component is very complex to be summarized by one or two parameters in univariate stability analysis methods while multivariate methods such as AMMI and GGE biplot can detect multi-directionality aspect and try to extract more information out of this component (Sabaghnia et al. 2008). Gauch (1988) and Zobel et al. (1988) proposed the additive main effects and the multiplicative interaction (AMMI) model for analyzing multi-environment trials. The AMMI model is comprised of additive main effects of genotype and environment, and the multiplicative effect of GE interaction, and thus can explain more information compared to other methods. In the present study the AMMI analysis captured a sizeable part of the interaction sum of squares, the first two components of AMMI as significant and explained 90.73% of the interaction sum of squares.

**Table 5.** Analysis of variance for AMMI model in grain yield of durum wheat genotypes

| Source | df | Sum of squares | Mean square | F | ss(%) |
|---|---|---|---|---|---|
| Genotype | 16 | 1159754.38 | 72484.65 | $1.58^{ns}$ | 2.94 |
| Environment | 3 | 27581916.59 | 9193972.20 | 200.47 | 70.08 |
| E × G | 48 | 4216347.00 | 87840.56 | 1.92 | 10.71 |
| IPCA$_1$ | 18 | 2266215.92 | 125900.88 | $2.745^{*}$ | |
| IPCA$_2$ | 16 | 1559556.79 | 97472.30 | $2.12^{*}$ | |
| Noise (Residual) | 14 | 390574.29 | 27898.16 | $0.60^{ns}$ | |
| REP | 2 | 248957.60 | 481260.52 | $10.49^{ns}$ | |
| Error | 134 | 6145567.25 | 45862.44 | | 15.62 |
| Corrected total | 203 | 39352542.82 | | | |

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

To display yield stability, the main and IPCA1 effects of both G and E on grain yield are shown in Fig. 1. Displacement along the vertical axis indicated interaction difference between genotypes and between environments indicating the response pattern of genotypes across environments (stability), and displacement along the horizontal axis indicated difference in genotype and environment main effects (yield). The genotypes with IPC1 scores close to zero display general adaptation, while the higher scores demonstrate specific adaptation to environments (Gauch et al. 2008). The best genotype should be high-yielding and stable across environments. G5, G12, G14, G13, G6, G16, G8, G15 and G11 with the least interaction (low IPCA1), respectively, were specified as the most stable genotypes. Therefore, the four high yielding (averaged over environments) G11 with higher yield (678.32 g/m$^2$) and low IPCA1 (–1.52) and G8 (average of 713.23 g/m$^2$ and IPAC1 of –3.52) and G16 (average of 710.53 g/m$^2$ and IPCA1 of –3.73) and G14 (average of 730.05 and IPCA1 of –5.12) were stable. While G2 and G9 were specified as the most unstable genotypes. In another experiment by Sivapalan et al.

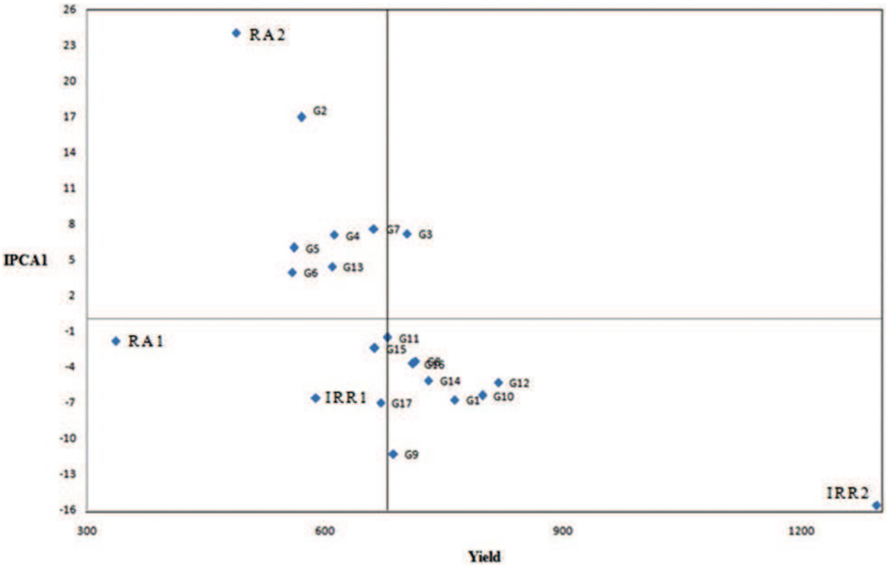

**Fig. 1. AMMI1 biplot showing IPCA1 *vs.* main effect**

(2000) the main effects of genotypes accounted for merely 2 per cent of the total difference whereas the environment's sum of squares was responsible for 87% of the total sum of squares and the remaining 11% was the effect of GEI. These results, regardless of the percentages, were similar to those obtained by Zali et al. (2009).

According to the IPC1 *vs* IPC2 scores of genotypes and environments, when a genotype is near an environment, this indicates that the genotype is specifically adapted to that environment (Shafii and Price 1998; Kumar et al. 2016). G15, G16 and G17 were recognized as superior genotypes for IRR1 and RA1 environments. Therefore in the first crop year, reaction of these three genotypes in the rainfed environments was similar to their reaction in the supplementary irrigation conditions. That is because of similar genetic performance of three mentioned genotypes in the first year. In the second crop year, reaction of genotypes was different from their reaction in supplementary irrigation conditions. G2, G3 and G4 are represented as selected genotypes for RA2 environment (rainfed conditions). G1, G12, G11, G8 and G14 are represented as selected genotypes for IRR2 environment (supplementary irrigation). In order to select appropriate environments with high ability for separating genotypes, environments should have a high IPCA1 and low IPCA2 (Mohammadi et al. 2008). According to IPCA1, IRR1 and RA1 environments had the most stability and the least contribution of interaction, and RA2 and IRR2 with the most IPCA1 had the most contribution to produce GEI. It observed the least environmental IPCA2 for RA1 and RA2 environments and the most for IRR1 and IRR2. Ideal environment based on the more IPCA1 and the less IPCA2, was RA2. Since drought resistantce is a complicated trait, where the performance of gneotypes depend on reaction between relevant morphological, physiological and genetic traits. Therefore the present study is able to deduce under rainfed condition, that the resistant genotypes gain maximum yield potential and discriminated from genotypes which could not show their potential. AMMI stable parameters for environments have been used by several researchers (Yan 1999; Yan et al. 2000;Yan and Rajcan 2002; Mohammadi et al. 2008) in order to preferential analyze GEI, and additionally they introduced stable and compatible genotypes to environments. They were also able to distinguish environments with high genotype separating ability from the others.

### *GGE biplot analysis*

The numerous researches reveal that the main environmental effect is of the majore magnitude in stability analysis experiments, while the explained variations by the main genotype effect and GEI, which is interpretable, are low. Since the environment is not a factor that can be controlled, hence GGE biplot graphically virtualizes G plus GE of a MET in a way that facilitates visual genotypes evaluation and mega-environment identification (Yan et al. 2000). GGE biplot has an objective shape that results from the data and the singular value partitioning (SVP) method, it shows the relative importance of G *vs* GE in the data. GGE biplot was constructed by plotting first two principal components (PC2 and PC1) derived from subjecting the environment centered data to singular-value decomposition (SDV) (Farshadfar et al. 2011). In the GGEbiplot only two PC (PC1 and PC2) are retained in the model because such a model tends to be the best model for extracting patterns and rejecting noise from the data (Yan and Hunt 2002). Results of GGE biplot showed that the first two principal components (PC1

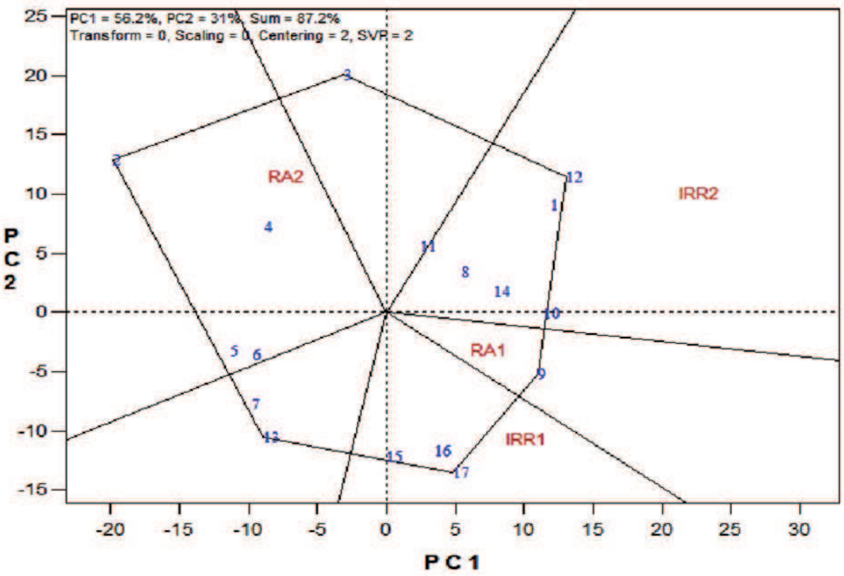

**Fig. 2.** **The polygon for determining mega-environments and the best genotypes for each environment**

and PC2) explained 87.2% of the sum of squares with PC1 = 56.2% and PC2 = 31% of the GGE sum of squares. Illustration of the "which-won-where" biplot as polygon (Fig. 2) is the best way to interpret the interaction patterns between genotypes and environments and give comprehensive information (Yan and Kang 2003). According to this analysis, ideal genotype are those that should have high PC1 scores (high mean yield) and low PC2 scores (high stability). Also, ideal environments should have high PC1 scores (more power to discriminate genotypes in terms of the genotypic main effect) and low PC2 scores (more representative of the overall environments) (Yan et al. 2000; Yan and Rajcan 2002). This polygon is generated by joining the farthest genotypes from the biplot origin in a way that all other genotypes are within the polygon. The perpendicular lines to the sides of the polygon create parts of genotypes and environments (Hernandez and Crossa 2000). According to Fig. 2 the G2, G3, G12, G13, G17 and G9 are situated in the apex of this polygon and indicated superior genotypes and six lines divided the biplot into six parts and the environments fall into four of them and they considered as four mega environments. Irrigation environment in the second year (IRR2) is situated in a part, where G12 is located at its apexes i.e., G12 is the best performer under irrigation in the second year (IRR2). Rainfed environment in the first year (RA1) has situated in a part, where G9 located at its apexes. Irrigation environment in the first year (IRR1) situated in a part where G17 is located at its apexes, and rainfed environment in the second year (RA2) has situated in a part where G2 is located at its apexes. The most important point is that there is no any environment within the parts, where G13 and G3 are located at its apex, which shows G13 and G3 are not superior in mega environment. The length of an environmental vector is an estimation of discriminating ability of the environment (Yan et al. 2007). Environments with longer vectors (IRR2 in Fig. 2) are more discriminating of the genotypes. If an environment is near to the biplot origin (RA1 in Fig. 2), it means that it exhibited low interaction and all genotypes performed similarly and, therefore, it provided little or no information about the genotypic differences and therefore it is considered as non discriminative environment. Another important characteristic of an environment is that how much it represents the target environment? To measure representativeness using a biplot, an average environment has to be determined and used as a criterion. The angle between the vector of an environment and the average environment axis is a measure of the representativeness of the environment. Ideal test environment, should be both discriminative and representativeness (Yan and Tinker 2005). IRR2 is the nearest environment to the test ideal environment. Thus, it is the most favorable environment which is most effective environment in identification of superior genotypes from other environments (Yan and Kang 2003). Correlation between environments is determined by an angle between them. In fact, the angle between vectors which are smaller than $90^o$ shows positive correlation between them and angle $90^o$ between vectors shows independent environments. Larger angle than $90^o$ means that there is a negative correlation between environments (Yan and Kang 2003). Because of a low angle, there is a positive and relatively high correlation between rainfed conditions in the first year (RA1) and irrigation environments of the first year (IRR1) indicates same response of genotypes in this environments. In other words, genotypes which have the first yield rank in IRR1 also show the first rank in RA1. IRR2 and RA2 environments possessed of close correlation to zero caused to an independent yield of genotypes in these environments. Similarly, information obtained from genotypes in RA2 and IRR2 is different due to negative correlation. In this research considering that RA1 and IRR1 environments have a close correlation and with respect to these results are equally replicated during a year, can use one of these environments in order to save and reduce costs.

The mean yield and stability of genotypes are evaluated by defining an average tester coordinate (ATC) (Yan 2001; Yan and Hunt 2002; Yan 2002). ATC X-axis or the performance of genotype passes through the biplot origin with an arrow indicating the positive end of the axis and the average environment is indicated by a circle. The ATC Y-axis or the stability axis passes through the plot origin with double arrow head and is perpendicular to the ATC X-axis (Fig. 3). The average yield of genotypes is estimated by the projections of their markers to the ATC X-axis. Thus, according to the Fig. 3, yield average of genotypes is in the order of G12> G1> G10> G9> G14> G8> G11> G3> G17> G16> G15> G4> G6> G13> G7> G5> G2.

A longer projection to the AEC ordinate, regardless of the direction, represents a greater tendency of the GEI of a genotype, which means it is more variable and less stable across environments. (Crossa et al. 2002). G17, G16, G15, G2 and G3 have most instability and fluctuation of yield, because they have been perpendicular to horizontal axis by the longest line compared to the other genotypes. On the contrary, G 8, G14 and G1 with the shortest line (the least variance) and higher yield than total average are the most stable genotypes in all environments.

An ideal genotype would be that, which has high yield average and high stability. Thus, G1 and G12 are as ideal and G10, G14, G9 and G8 are in the following ranks. Sabaghnia et al. (2013) evaluated yield stability of 20 durum wheat genotypes in five different environments across three years used GGE biplot model. The first two principal components accounted for 60.3 % of the total variation. Polygon view of biplot indicated that there were three winning genotypes in three mega-environments for durum wheat in rainfed conditions. The most favorable genotype was determined for each environment and ideal environment was identified. GGE biplot analysis was also carried out by Kendal and Șener (2015) considering 10 durum genotypes evaluated at environments under dry and wet conditions. The study identified (eight) Zenit is the best genotype in terms of yield and quality parameters. Mohammadi and Amri (2012) studied yield data of 13 durum wheat genotypes grown in 16 diversified environments (differing in winter temperatures and water regimes) to analyze genotype by environment (GE) interactions in rainfed durum MET data in Iran by using GGEbiplot analysis. The results indicated that the grain yield of different genotypes was significantly influenced by environmental effect. The greater GE interaction relative to genotype effect suggested significant environmental groups with different top-yielding genotypes. Warm environments differed from cold environments in the ranking of genotypes. Cold and warm environments were better than moderate environments in both discriminating and representativeness, suggesting the efficiency and accuracy of genotype selection would be greatly enhanced in such environments. They suggested the GGEbiplot methods were useful to average yield and stability of the genotypes ranking. The results from present study indicate that GE interaction is a significant source of variation in the durum wheat MET data. This observed pattern of GE interaction for yield of durum wheat suggests that genotypes respond differently in different environments, hence the need for stability analysis based on different statistics methods and compare their results. It seems that it is not possible to advice a unique method for assessing GEI and yield stability. However, the multiplicative GE interaction component is far too complex to be summarized by one parameter, whereas biplot analysis allows visual interpretation of GE interaction and facilitate genotype recommendations in MET (Dehghani et al. 2008; Vargas 1998).

In the present study, two of the well used models AMMI and GGEbiplot were employed. With respect to results of AMMI model, G11, G8, G16 and G14 were the most stable genotypes with high mean yield. Regarding the two graphical analysis models of AMMI and GGEbiplot, G8 and G11 can be recommended to all environments as the most stable genotypes with high mean yield. Thus they are recommended for commercial release as cultivars to contribute for enhancing durum wheat production in these environments. Results obtained by GGEbiplot model according to the results of AMMI model showed that G12 has a special adaptability to IRR2, and G2 to RA2, G17 and G9 to RA1 and IRR1. GGEbiplot analysis combines G and GE directly but the AMMI analysis separates G from GE first and then puts them together again. The AMMI1 graph for mega-environment analysis and genotype evaluation virtually

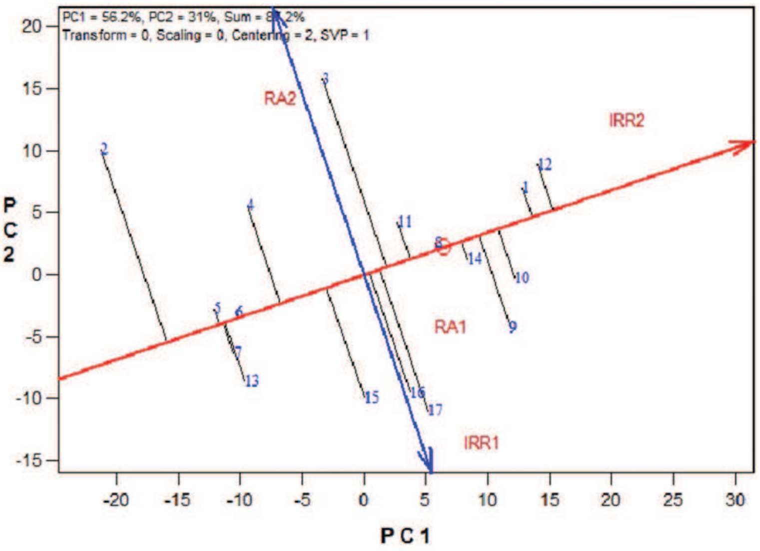

**Fig. 3. Yield average and stability of genotypes**

contain both G and GE same as that based on a GGEbiplot, so they might as well be called GGE graphs but not literally (Ebdon and Gauch 2002); consequently AMMI model differ from the GGEbiplot as described earlier (Yan et al 2007) and also mentioned (Yan et al. 2007) below.

AMMI contain less G+GE, a less accurate presentation of the GGE of the data (because the axes are in different units; original unit for the abscissa and square root of the original unit for the ordinate) and have less functionality than the GGEbiplot to visualize which- won- where pattern (does not have the most important property of a true biplot that called inner-product property that means the performance a given genotype in a given environment cannot be accurately visualized even if it fully displays data). Even according to Yan and Tinker (2006), AMMI could be misleading if used for the purpose of "which-won-where" i.e. identification of mega-environments as well as their wining genotypes. Gauch (2006) argued that AMMI analysis was superior to other methods because it clearly separated G and GE and that G and GE have different agricultural implications, with G representing wide adaptation and GE representing specific adaptation. If specific adaptation is with high performance in specific environments, however, it is determined by G+GE and not by GE alone. The G and GE can be regarded as representing different biological interpretations only if it is shown that G and GE are under the control of distinct genes or genetic interactions, whereas there is little evidence that G and GE are controlled by distinct genes and thereby can be subjected to selection separately. Therefore, explicit separation of G from GE in AMMI analysis does not lead to the conclusion that it is superior to GGEbiplot analysis (Yan et al. 2007).

The results finally indicated that AMMI and GGEbiplot are informative methods to detect stability and adaptation pattern of genotypes and in preferential genotypes recommendations. Application of AMMI and GGEbiplots facilitated visual comparison and identification of superior genotypes for each environment (Freeman 1990). Ideal environment, based on the AMMI, was RA2 (rainfed of the second year), while GGEbiplot model represented IRR2 (irrigation of the second year) as ideal environment. The AMMI1 biplot displays the test environments by their main effects E and IPC1 scores which is irrelevant to environment evaluation and it provides no information on the environment's ability in identifying superior genotypes, while GGEbiplot is an effective tool for test-environment evaluation, which can lead to the identification of discriminating and representative test environments (Zobel et al. 1988). In general, AMMI is a model family rather than a single model (combines two methods: i.e, analysis of variance and PCA). Consequently, model diagnosis is required to detect which member of this model family is the best for a given dataset and research goal (Gauch 2006; Gauch 2013). Model diagnosis is essential because as the selected member of the AMMI model family changes, the mega-environments also change, with higher order models tending to define a larger number of mega-environments. As a consequence, mega-environments cannot be meaningfully or reliably delineated without first performing a model diagnosis to select the best member of the AMMI model family for a given dataset. Model diagnosis enables researchers to distinguish between GE causing actual specific adaptations and GE generating spurious complexity (Gauch 2013). Furthermore in the AMMI model increasing accuracy of yield evaluation is equal to increase the number of replication from 2 to 5 (Zobel et al. 1988; Crossa et al. 1990). The present study thus identified G8 (19E-M141982) and G11(18E-M142005) as stable genotypes. However, the ideal environment were different as per both the models AMMI and GGE biplot analysis.

## Authors' Contribution

Conceptualization of research (RA,SH); Designing of the experiments (RA,RH,SH);Contribution of experimental materials (RA,RH ); Execution of field/ lab experiments and data collection (RH,SH); Analysis of data and interpretation (SH,RA,RH); Preparation of the manuscript (SH,RA).

## Declaration

The authors declare no conflict of interest.

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