

Interpretation of genotype \times environment interaction for grain yield of barley using the GGE biplot method

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Abstract

The identification of the most favorable cultivar(s) with high yield and stable performance is usually done based on the analysis of the genotype \times environment (GE) interaction. The yield stability of 16 barley lines with two check varieties was studied in a randomized complete block design with four replications across three years at five locations in a multi-environment trial layout. The dataset was analyzed with a GGE (genotype main effect (G) + GE interaction) biplot method. Results indicated that the first two principal components (PCs) explained 81, 78 and 71% of the GGE sum of squares for 2017, 2018 and 2019 growing seasons, respectively. According to the average environment coordinate abscissa, G2, G13 and G18 were the best genotypes in terms of grain yield in years 2017 and 2018 while genotypes G2, G7 and G14 were the highest yielding genotypes in 2019. When both yield performance and stability were considered simultaneously, the G2 and G13 genotypes in 2017 and G2, G8 and G13 in 2018, were closer to the ideal genotype. In 2019, G2, G7 and G14 were the best in terms of grain yield and stability. In the "which-won-where" pattern, the five locations in 2017 fell into four sectors with different winning genotypes as G2, G5, G14 and G13. In 2018, the five locations fell into three sectors in which G2, G4 and G17 were the highest yielding genotypes while in 2019, locations were positioned in four sectors and G2, G7, G10 and G13 were chosen as the winning genotypes. However, for practical use of the "which-won-where" pattern, the mean performance of genotypes over three years in the five test locations was taken into account. Although the results revealed six mega-environments, by neglecting small differences, we can assume only one mega-environment in which G2 (the check variety Khorram) was the best performing genotype.

Keywords: Barley; GGE biplot; Grain yield; Multi-environment trials; Singular value decomposition

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Introduction

Barley (*Hordeum vulgare* L.) is mainly used for animal feed as well as brewing, although it is also considered as food in regions where other cereals cannot be cultivated due to biotic and abiotic

stresses. Barley is grown mainly on rainfed conditions and genotype by environment (GE) interaction limits the progress under these unpredictable climatic conditions, so breeding programs are directed towards the development of

genotypes with wide stability as well as high yield potential. Therefore, the knowledge about GE interaction is of major importance, because it provides useful information about the differential effects of environments on genotypes (Oghan *et al.* 2016). Yield performance is affected by genetic and environmental factors. The considerable variation in growing conditions including climatic conditions and soil constituents causes large variations in yield performance due to the low heritability of yield as a quantitative trait (Le Marié *et al.* 2019). The best way for estimating GE interaction is conducting multi-environment trials to select the most favorable genotypes for the test environments (Roorkiwal *et al.* 2018).

Several statistical techniques are available to interpret the GE interaction such as linear regression, nonparametric statistics and multivariate methods (Bustos-Korts *et al.* 2018). The GGE biplot method was developed for graphical analysis of multi-environment trial data which considers both the genotype main effect and GE interaction effects (Yan 2014). The GGE method with a graphical option is based on principal component analysis (PCA) and can reveal the structure of the genotype by environment interaction, derived by the singular value decomposition of a two-way data matrix (Yan *et al.* 2000). The main objective of this investigation was to evaluate barley genotypes under study using GGE biplot analysis to identify the best performing genotype (s) for practical recommendations.

Materials and Methods

Multi-environment trial

Data sets were obtained from the national barley multi-environment yield trial for three years (2017–2019) at five locations (Ghachsaran, Gonbad, Ilam, Lorestan, Mughan) in Iran. Some properties of test locations are given in Table 1. In each environment (location \times year), 16 advanced breeding lines together with two standard check cultivars (Mahour, Khorram), which had relatively high mean yield and good stability were tested. The code and pedigree of the lines are presented in Table 2. The trial of each environment was a randomized complete block design with four replications. Seeds were planted in 1.05×7.03 m plots (6 rows with 17.5 cm spacing). Thus the sowing rate was about 200 seeds per m^2 and the plot size was about $7.4 m^2$. Agronomic practices were performed optimally in all tested locations based on the local agroecological conditions. At planting $50 kg ha^{-1}$ N and $75 kg ha^{-1} P_2O_5$ were applied. The grain yield ($kg ha^{-1}$) was measured from four middle rows of each plot in all environments and corrected to the 12% moisture basis.

Statistical analysis

The GGE biplot analysis was performed on the yearly basis for the yield data from the 2017-2019 barley trials. The grain yield data were standardized (P_{ij}) and subjected to singular value decomposition (SVD) according to Yan (2019). After SVD, the biplots were drawn, using the first two principal components (PCs). SVD

Table 1. Code and pedigree of studied barley genotypes

Code	Pedigree
G1	Mahour (check cultivar)
G2	Khorram (check cultivar)
G3	Arbayan-01//As46/Aths/3/Barjouj ICB02-0406-0AP-8AP-0AP
G4	Avt/Attiki//MAtt733371/3/Aths/Lignee686/4/Kabaa ICB98-0796-0AP-15AP-0AP-14AP-0AP-8AP-0AP
G5	Lignee527/NK1272/4/Avt/Attiki//Aths/3/Giza121/Pue ICB95-0279-0AP-8AP-0AP-14AP-0AP
G6	Rhn03/3/Mr2584/Att/Mari/Aths*302/4/Rhn03/Lignee527 ICB05-0272-3AP-0AP
G7	Rhn03/3/Mr2584/Att/Mari/Aths*302/4/Ssn/Badia//Arar/3/Gloria'S'/Copal'S' ICB05-0292-7AP-0AP
G8	Aths/Lignee686//Mari/Aths*2/3/Lignee527/NK1272//Alanda/6/JLB7001/5/DeirAlla106//DL70/Pyo/3/RM150 8/4/Arizona5908/Aths//Avt/Attiki/3/Ager ICB05-0238-0AP-5AP-0AP
G9	AwBlack/Aths//Arar/3/9Cr27907/Roho/4/CompCr229//As46/Pro/3/DeirAlla106//DL71/Strain205 ICB97- 0605-0AP-10AP-0AP-5AP-0AP-1AP-0AP
G10	E. ACACIA/DEFRA//PENCO/CHEVRON-BAR CBSS02Y00319S-0M-0M-5Y-1M-0Y
G11	SHENMAI NO.3/MSEL//CANELA CBSS04Y00367T-I-2Y-2M-0Y-0M-0Y
G12	SHENMAI NO.3/MSEL//CANELA CBSS04Y00367T-D-3Y-1M-0Y-0M-0Y
G13	ATAH92/2*M81//TOCTE/3/PENCO/CHEVRON-BAR CBSS01M00733T-0TOPY-7M-2M-2Y-1M-0Y
G14	DEFRA/CL128//PFC 88209 CBSS02Y00326S-0M-0M-4Y-1M-0Y
G15	FRESA/LEGACYCBSS05Y00125S-7Y-0M-0Y-0M-1AP
G16	MoB1337/Wi2291//Mooroco9-75/3/Hml
G17	TRADITION/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA1/7/LEGACY//PENCO/CHEV RON-BARCBSS04M00295T-2M-0Y-0M-0Y-1M-0AP
G18	LIMON/BICHY2000//NE167/CLE176 CBSS05Y00064S-29Y-0M-0Y-0M-3AP

Table 2. Geographical and climatic properties of test locations.

Location	Gachsaran	Gonbad	Ilam	Lorestan	Mugan
Longitude	30°18'N	37°16'N	39°39'N	33°39'N	33°44'N
Latitude	50°59'E	55°12'E	47°88'E	48°28'E	46°36'E
Altitude (m)	668	45	100	1125	975
Soil Texture	Silty Clay	Loam Silty	Loam Clay	Loam	Clay Loam
Soil pH	7.3	7.8	7.6	7.3	7.5
Rainfall (mm) 2017	236.8	401.1	178.2	306.7	408.9
Rainfall (mm) 2018	176.8	341.4	250.1	488.4	496.4
Rainfall (mm) 2019	764.4	627.7	181.1	953	900.9
Rainfall (mm) 30 Years	443	466	312	520	550

decomposes the data of the standardized genotype-by-environment table into genotype

eigenvalues, environment eigenvalues and singular values:

$$P_{ij} = (d\lambda_1^\alpha \zeta_{i1}) \left(\frac{\lambda_1^{1-\alpha} \tau_{1j}}{d} \right) + (d\lambda_2^\alpha \zeta_{i2}) \left(\frac{\lambda_2^{1-\alpha} \tau_{2j}}{d} \right) + \varepsilon_{ij}$$

where the scalar d is the length of the longest vector among genotypes equals to that among environments; λ_1 and λ_2 are the singular values for PC1 and PC2, respectively; ζ_{i1} and ζ_{i2} are the

eigenvalues for PC1 and PC2, respectively for the genotype i ; α is the singular value partitioning (SVP) factor; τ_{1j} and τ_{2j} are the eigenvalues of for PC1 and PC2, respectively, for environment j , and

ε_{ij} is the residual after fitting PC1 and PC2 for genotype i in environment j . With $SVP=1$, the biplot is a genotype-focused type, and is useful for comparison of the genotypes. The data were graphically analyzed via generating biplot figures to interpret stability and adaptability using the GGEbiplot software (Yan 2001).

Results and discussion

Analysis of variance

Analysis of variance indicated that the effects of genotype, environment and genotype by environment interaction were significant and the environment was the most important source of variation for the grain yield (Table 3). Dehghani *et al.* (2006) and Ahmadi *et al.* (2012) also found significant GE interaction in multi-environment trials of barley and indicted the relatively large effect of the environment on the grain yield as compared to other sources (genotype and GE interaction). Thus, they indicated that it was essential to use the site regression model as the best statistical model for analyzing their dataset. In our study, the first two PCs explained 81% of the total variation for grain yield (53 and 28% for PC1 and PC2, respectively) in the first year, 78% of the total variation (49 and 29% for PC1 and PC2, respectively) in the second year and 71% of the total variation (43 and 28% for PC1 and PC2, respectively) in the third year (Figure 1). The GGE biplot integrates some features of the multivariate methods and allows visual interpretation of the GE interaction, especially the crossover type which is usually essential to any breeding program (Yan and Wu 2008).

Yield and stability

The average environment coordination (AEC) axis was drawn to visualize the mean grain yield and stability of the barley genotypes under investigation (Yan and Kang 2003). G2, G13 and G18 were the best genotypes followed by G1, G5, G15 and G16 in the 2017 growing season (Figure 1). Accordingly, G2, G13 and G18 were the best performing genotypes followed by G5 and G17 in 2018, while G2, G7 and G14 were the best performing genotypes followed by G5 and G16 in 2019 (Figure 1). Regarding all three years, it can be concluded that the genotype G2 had the best performance in the tested environments. In all three years, genotypes G6 and G10 had the poorest yield and the lowest stability with higher projection from the AEC axis (Figure 1). According to Dia *et al.* (2016), stability alone is not useful and should be associated with a high mean yield. Therefore, a genotype is ideal when it is featured with both high mean yield and stability.

Ideal Genotype

The head of the arrow in the small circle in Figure 2 represents the ideal genotype and is located on the AEC abscissa. The ideal genotype has the highest yield and is absolutely stable by being located in the AEC abscissa (Yan and Kang 2003). Among the genotypes, G2 and G13 were close to the ideal genotype and had the highest yield and highest stability that were qualified as the best genotypes in 2017 (Figure 2). In 2018, G2, G8 and G13 were closer to the ideal genotype position while G2, G7 and G14 had the highest

Table 3. Analysis of variance of the studied barley genotypes

Sources of variation	df	MS
Environment (E)	14	40602382**
Replicates within E	45	354779
Genotype (G)	17	568591**
GE interaction	238	211314**
Error	765	83910

**Significant at the 0.01 level of probability.

yield and stability in 2019 (Figure 2). Therefore, regarding the ideal entry view of the GGE biplot in three years, genotype G2 showed the best performance in the tested locations.

Performance of G2

The G2 was identified as the most favorable genotype for three years in all test locations. The locations were ranked in the direction of the entry axis, and the ranking of the locations in terms of the relative performance of G2 was visualized. Therefore, G2 performed the best in Lorestan followed by Gonbad, Mugan, Ghachsaran and Ilam in 2017 (Figure 3). The perpendicular line separates locations in which G2 performed above average from those in which G2 performed below average. Thus, the grain yield of G2 was above average in Lorestan, Gonbad, Mugan, Ghachsaran and below average in Ilam in 2017 (Figure 3). The G2 genotype performed the best in Lorestan as well as Gonbad followed by Mugan, Ilam and Ghachsaran in 2018. This genotype also performed above average in all of the test locations in 2018 (Figure 3). Finally, G2 was the best in Lorestan followed by Ghachsaran, Gonbad, Mugan and Ilam in 2019 and also performed above average in all locations except

Ilam in 2019 (Figure 3). Thus, G2 was the most favorable genotype (high mean yield and high stability) in all locations, except Ilam, and it can be recommended for stable production of barley in rainfed areas of Iran.

Yearly mega-environments

The “which-won-where” pattern is a characteristic of the GGE biplot (Yan and Kang 2003; Yan 2014). In the “which-won-where” view of the GGE biplot (Figure 4), the five locations fell into four sectors with different winning genotypes. G2 was the highest yielding genotype in Lorestan and Mugan, G5 was the highest yielding genotype in Ghachsaran, G14 was the highest yielding genotype in Ilam, and G13 was the highest yielding genotype in Gonbad. However, only slight differences existed between positions of Ghachsaran, Ilam and Gonbad and the other locations and we can assume only one mega-environment in 2017 with G2 as the best performing genotype (Figure 4). In 2018, the locations fell into three sectors and G2, G4 and G17 were the highest yielding genotypes (Figure 4). The five test locations in 2019 fell into four sectors and G2 was the highest yielding genotype in Lorestan, G7 was the highest yielding genotype

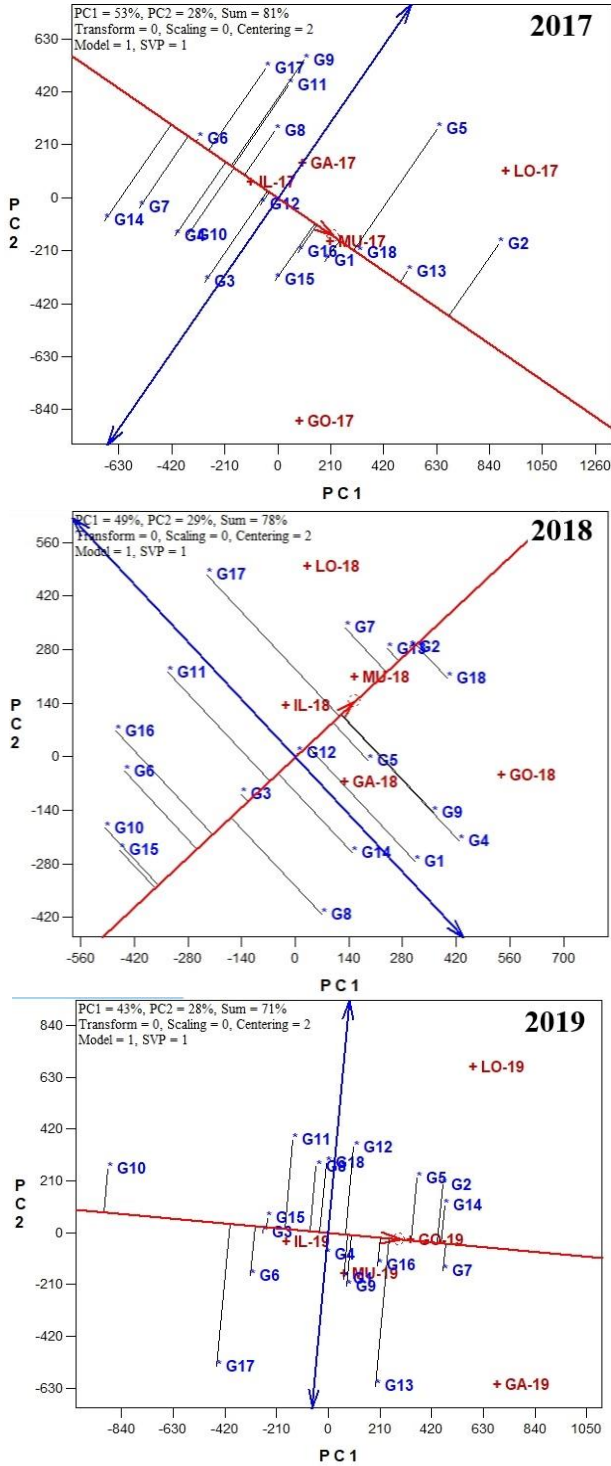


Figure 1. Average environment coordinate (AEC) view of the GGE biplot across 2017-2019 years. The biplot was based on the genotype-focused scale. The test locations were Ghachsaran (GA), Gonbad (GO), Ilam (IL), Lorestan (LO) and Mughan (MU).

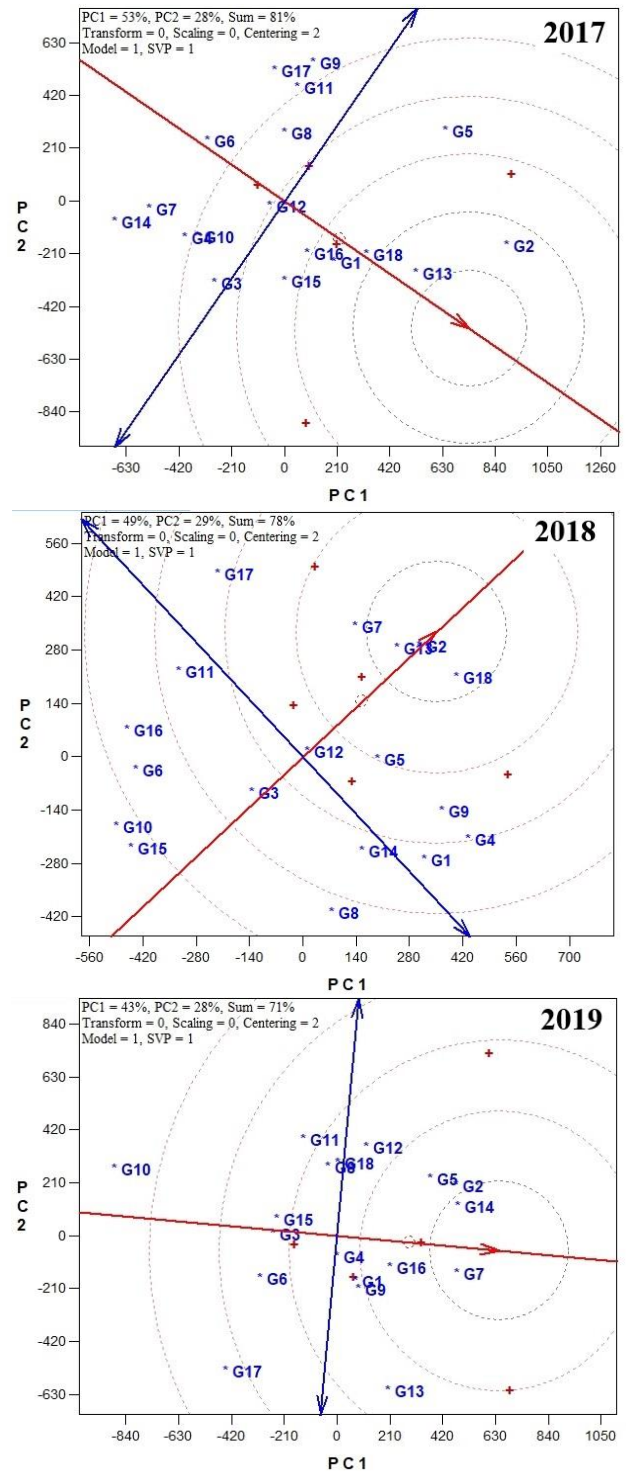


Figure 2. The "Ideal Genotype" view of the GGE biplot across 2017-2019 years. The biplot was based on the genotype-focused scale..

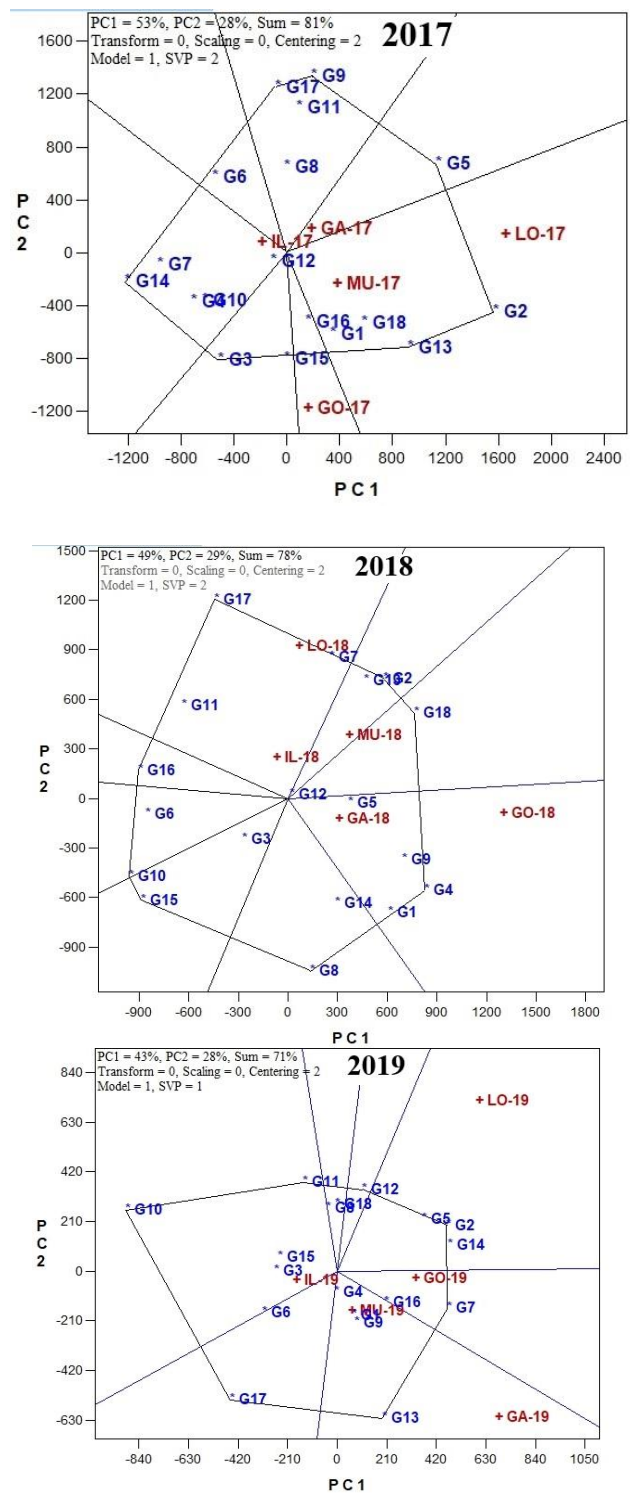
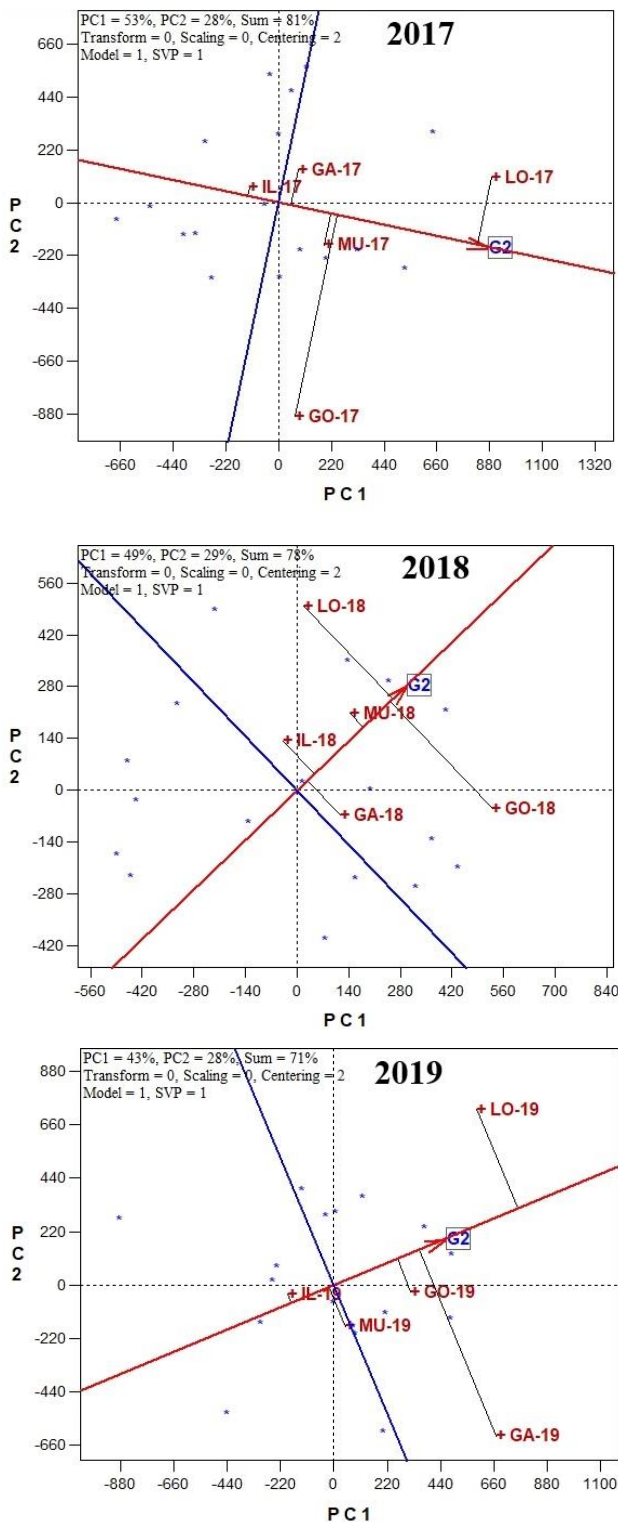


Figure 3. The relative performance of genotype G2 in different locations across 2017-2019 years. The biplot was based on the genotype-focused scale. The test locations were Ghachsaran (GA), Gonbad (GO), Ilam (IL), Lorestan (LO) and Mughan (MU).

Figure 4. The convex-hull view of the GGE biplot across 2017-2019 years. The biplot was based on the genotype-focused scale. The test locations were Ghachsaran (GA), Gonbad (GO), Ilam (IL), Lorestan (LO) and Mughan (MU).

in Gonbad, G10 was the highest yielding genotype in Ilam and G13 was the highest yielding genotype in Ghachsaran and Mugan. The GE interaction and especially the crossover type of interaction in 2019 was more complicated which cannot be ignored completely. So, we may assume at least three mega-environments as follows: Gonbad and Lorestan with G2 as the best performing genotype, Ilam with G10 as the best performing genotype and Ghachsaran and Mugan with G13 as the best performing genotype (Figure 4). If the crossover interaction structure is the GGE biplot model, the mean performance of the genotypes over the three years was analyzed in the five test locations. The first two PCs explained 80% of the variation for grain yield (56 and 24% for PC1 and PC2, respectively). Although, the results revealed six mega-environments, by ignoring small differences we can assume only one mega-environment in which G2 was the best performing genotype in terms of the grain yield and stability (Figure 5). Karimzadeh *et al.* (2013) and Mattos *et al.* (2013) also used the GGE biplot approach to select simultaneously for high yield and stability.

Conclusions

This study demonstrated the usefulness of GGE biplot analysis in the interpretation of $G \times E$ interaction for the grain yield data of barley from

repeatable over years, the target environment can be divided into mega-environments, and if it is not repeatable across years, the GE cannot be exploited and selecting high yielding and stable genotypes in mega-environments must be avoided (Yan and Tinker 2005).

General mega-environment

A mega-environment is a group of locations that invariably share the best set of genotypes over years (Yan and Rajcan 2002). However, for practical use of the “which-won-where” view of the multi-environment trials. We identified one mega-environment with one favorable genotype (G2) which was the check cultivar (Khorram). Our results showed that on the whole, the new promising lines were not better than the Khorram cultivar in terms of yield and stability in the five tested locations over three years. Therefore, it seems that some refinement is needed in the breeding methods and other strategies for producing new barley varieties to be planted in the rainfed areas of Iran, however, it is a difficult task because rainfed conditions in the semi-arid areas limit the gain from selection due to irregular precipitation and heat and drought stress occurrence.

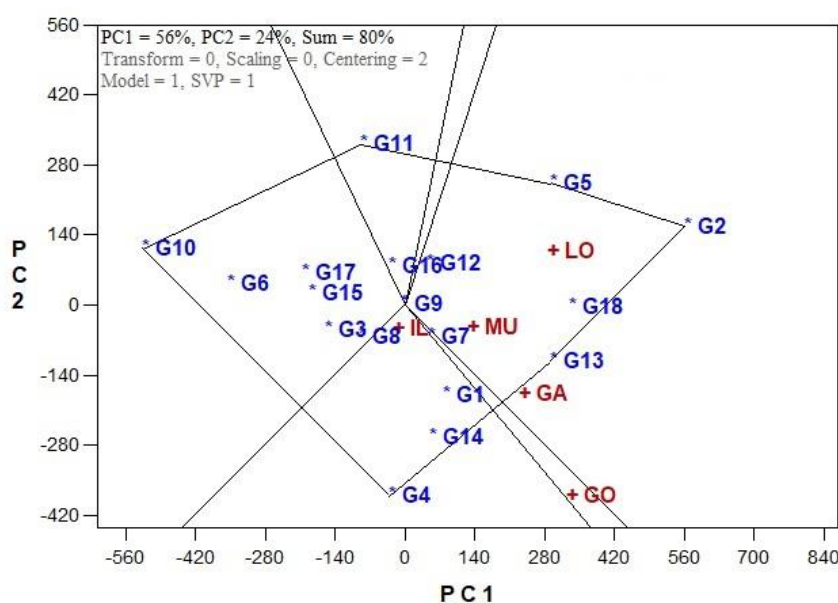


Figure 5. The convex-hull view of the GGE biplot for mean values of three years. The biplot was based on the genotype-focused scale. The test locations were Ghachsaran (GA), Gonbad (GO), Ilam (IL), Lorestan (LO) and Mughan (MU).

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تجزیه اثر متقابل ژنوتیپ \times محیط برای عملکرد دانه جو با استفاده از روش GGE biplot

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چکیده

شناسایی مطلوبترین رقم‌های پرمحصول با عملکرد پایدار معمولاً از طریق تجزیه اثر متقابل ژنوتیپ \times محیط انجام می‌گیرد. در این پژوهش پایداری عملکرد ۱۶ لاین جو به همراه دو رقم شاهد در قالب طرح بلوک‌های کامل تصادفی با چهار تکرار در طی سه سال و پنج مکان به صورت آزمایش‌های چند-محیطی مطالعه شد. داده‌ها با استفاده از روش GGE-biplot (اثر اصلی ژنوتیپ + اثر متقابل ژنوتیپ و محیط) تجزیه و تحلیل شدند. نتایج نشان داد که دو مولفه اول تجزیه به مولفه‌های اصلی ۸۱، ۷۸ و ۷۱ درصد از تغییرات مجموع مربعات GGE را به ترتیب در سال‌های زراعی ۱۳۹۶، ۱۳۹۷ و ۱۳۹۸ توجیه نمودند. بر اساس محور محیط متوسط، ژنوتیپ‌های G2، G13 و G18 به عنوان بهترین ژنوتیپ‌ها از نظر عملکرد در سال‌های ۱۳۹۷ و ۱۳۹۶ منظور شدند. در حالی که G2، G14 و G7 پرمحصولترین ژنوتیپ‌ها در سال ۱۳۹۸ بودند. زمانی که هر دو مقوله عملکرد و پایداری به طور هم‌زمان لحاظ شدند، ژنوتیپ‌های G2 و G13 در سال ۱۳۹۶ و ژنوتیپ‌های G2، G8 و G13 در سال ۱۳۹۷ به موقعیت ژنوتیپ ایده‌آل نزدیک بودند. در سال ۱۳۹۸ ژنوتیپ‌های G2، G7 و G14 از نظر عملکرد و پایداری در حد مطلوبی بودند. در الگوی چی؟ برتر؟ کجا؟ ۵ مکان مربوط به سال ۱۳۹۶ در ۴ بخش مختلف قرار گرفتند و ژنوتیپ‌های راس برتر شامل G2، G5، G14 و G13 بودند. در سال ۱۳۹۷، ۵ مکان در ۳ بخش مختلف واقع شدند و ژنوتیپ‌های راس برتر پرمحصول شامل G2، G4 و G14 بودند. در حالی که در سال ۱۳۹۸ مکان‌ها در ۴ بخش قرار گرفتند و ژنوتیپ‌های G2، G7، G10 و G13 به عنوان ژنوتیپ‌های مطلوب شناسایی شدند. در عین حال، الگوی چی؟ برتر؟ کجا؟ بر اساس میانگین ژنوتیپ‌ها در سه سال برای ۵ مکان نیز ترسیم شد و نتایج شش ابرمحیط را آشکار کرد که با کمی اغماض در مجموع می‌توان یک ابرمحیط را در نظر گرفت و ژنوتیپ G2 (رقم شاخد خرم) بهترین ژنوتیپ در مجموعه این محیط‌ها بود.

واژه‌های کلیدی: آزمایش‌های چند-محیطی؛ تجزیه به مقادیر منفرد؛ جو؛ عملکرد دانه؛ GGE biplot