Evaluation of seed yield stability of barley promising genotypes using principal coordinates analysis

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Abstract

Analysis of the structure of genotype by environment (GE) interaction is essential in crop stability programs. To study the effects of GE interaction on the seed yield and identify stable genotypes of barley for warm and humid regions, 16 barley genotypes with two check cultivars were assayed in a randomized complete block design with four replications in Gachsaran, Moghan, Khorramabad and Gonbad regions for three years (2017-2019). Combined analysis of variance for yield data of 12 environments (year/location combined) showed significant differences among environments and genotypes and significant GE interaction. The GE interaction was examined using principal coordinates analysis (PCoA). Based on the deviation from the grand mean, 12 environments were divided into two main groups: five environments with higher mean yield and seven environments with lower mean yield. The most stable genotypes based on the minimum spanning tree and distance from the center of plots were G13 (2.43 kg/ha), G2 (2.38 kg/ha), G14 (2.29 kg/ha), which could be recommended for environments with a yield lower than the average mean of all studied environments. The results of the PCoA showed that the genotype G18 (2.32 kg/ha) was also located five times in the vertex positions of high cycles and so it can be recommended for favorable or high yielding environments.

Keywords: Barley promising genotypes; GE interaction; Principal coordinates analysis; Stability

Introduction

Cultivation of grain crops is increasing in the world, but this increase will not be enough in the future due to the world population growth. Therefore, increasing diversity and development of introduced cultivars with high yield potential, sustainable and adapted to environmental stresses is one of the most effective ways to compensate for the global grain demand (Reynolds *et al.* 2016). Highly adaptable and stable genotypes are needed under varying environmental conditions. Although this goal is simple, it is very complicated (Elias *et al.* 2016).

In most plant breeding programs GE interaction is said to occur when the responses of different genotypes or cultivars are different in diverse environments. Several statistical methods have been used for the investigation of the GE interaction and exploiting its positive side in cultivar development (Ahmadi *et al.* 2012; Karimizadeh *et al.* 2013; Karimizadeh *et al.* 2016). The production of high-yielding, high-quality and compatible genotypes for a wide range of environments is one of the ultimate goals of the plant breeding programs.

There are some genotypes that perform well in a wide range of environments (extensively adaptive genotypes), and in contrast, there are also genotypes that perform merely in a special set of

environments. (Akcura *et al.* 2009). The inconsistency between phenotypic and genotypic values has caused the breeders to perform incomplete, selective phenotypic compatibility tests and not be able to accurately evaluate and identify the best stable genotype (Yan *et al*. 2007).

Several methods have been proposed to evaluate stability in multi-environment trials. These methods are divided into parametric, nonparametric and multivariate types. Due to the complexity of GE interaction, nowadays multivariate methods are mostly used (Yan 2012).

Different multivariate methods are used to explore the GE interaction, such as principal coordinates analysis (PCoA), principal component analysis (PCA), genotype + GE interaction biplot (GGE) analysis and additive main effects and multiplicative interactions (AMMI). Using PCoA for stability analysis was first suggested by Westcott (1987). A year later, this method was developed by Crossa (1988). The PCoA is a multivariate method that geometrically illustrates the relationships of the original data in different dimensions (Medina *et al*. 1999). PCoA visualizes similarities or dissimilarities of the data. It calculates a series of eigenvalues and eigenvectors. PCoA is a generalization of principal components analysis, but there are fundamental differences between the two methods. The PCA converts several correlated variables into some independent variables and these variables are called the principal components. PCoA starts by projecting the distances into Euclidean space in a larger number of dimensions. The distance among points in a two-dimensional diagram reflects the relationship

between items in the original observed matrix (Zuur *et al*. 2007; Tabachnick and Fidell 2012). Flores *et al*. (1996) among 11 genotypes of Mung (*Vicia faba* L.), Crossa (1988) among 27 corn genotypes, Karimizadeh *et al.* (2019) among 20 durum wheat genotypes and Mohebuddini *et al.* (2012) among 18 lentil cultivars identified suitable cultivars for different regions using the PCoA.

The objectives of this study were to identify high-yielding and stable genotypes under different environments using the PCoA.

Material and Methods

This study was conducted in three years (2017-2019) and warm zone stations of Gachsaran, Moghan, Khorramabad and Gonbad to identify stable genotypes of barley for warm and humid regions using a randomized complete block design with four replications, 16 genotypes and two selected check cultivars of Mahoor and Khorram (Table 1). The seed rate for each genotype was 350 seeds per m^2. The seeds were planted with an experimental planter. Each plot consisted of six rows of 6m long with a row spacing of 20 cm. Weeds were controlled by a chemical herbicide (Granstar).

Analysis of variance was carried out for each test environment. Homogeneity of residual variances was verified by Bartlett's homogeneity test, before carrying out the combined analysis of variance. In this analysis, years were assumed as random and locations and genotypes as fixed factors.

In each environment, the similarity between genotypes m and n was measured by $Si(m,n)=[H_i-$

Table 1. List and pedigree of the studied barley genotypes.

Number	Pedigree of the genotypes
1	Mahoor as check
2	Khorram as check
3	HART-BAR/CANELA//MSEL CBSS01Y00777T-Z-0Y-10M-0M-1M-0Y(PRBYT2010-11-44)
4	CANELA/CHERI CBSS01Y00007S-0Y-6M-0M-1M-0Y(PRBYT2010-11 -28)
5	Moroc9-75//WI2291/WI2269 ICB93-1132-0AP-31AP-0AP-5TR-8AP-0AP(PRBYT2010-11-81)
6	6B89.2027/5/ATACO/BERMEJO//HIGO/3/CLNB/80.5138//GLORIABAR/COPAL/4/CHEVRONBAR/6/LEGACY CBSS01Y00858T-B-0Y-9M-0M-2M-0Y(PRBYT2010-11-31)
7	Moroc9-75//WI2291/WI2269 ICB93-1132-0AP-31AP-0AP-6TR-38AP-0AP(PRBYT2010-11-85)
8	MNS1//CALI92/ROBUST CBSS01Y00154S-0Y-10M-0M-3M-0Y(PRBYT2010-11-33)
9	Moroc9-75//WI2291/WI2269 ICB93-1132-0AP-31AP-0AP-5TR-20AP-0AP(PRBYT2010-11-82)
10	MSEL//CLI18/E.QUEBRACHO CBSS01Y00023S-0Y-10M-0M-1M-0Y(PRBYT2010-11-26)
11	Giza127/4/Gloria'S'/Saida//Mtn'S'/EH165/3/LBIran/Una80//Lignee640 ICB97-0488-0AP-21AP-6TR-0AP(PRBYT2010-11-20)
12	MSEL//CLI18/E.QUEBRACHO CBSS01Y00023S-0Y-10M-0M-1M-0Y(PRBYT2010-11-42)
13	WI2291//Apm/PI000046/3/Hml-02/4/Arda/Moroc9-75 ICB01-0006-0AP-28AP-0AP(PRBYT2010-11-99)
14	WI2291/4/7028/2759/3/6982//Ds/Apro/5/Zanbaka/3/ER/Apm//Lignee131I CB94-0590-0AP-9A-0AP-0AP-14AP-0AP-9AP-0AP(PRBYT2010-11-93)
15	Moroc9-75//WI2291/WI2269 ICB93-1132-0AP-33AP-0AP-18TR-41AP-0AP(PRBYT2010-11-88)
16	Moroc9-75//WI2291/WI2269 ICB93-1132-0AP-31AP-0AP-6TR-46AP-0AP(PRBYT2010-11-86)
17	Moroc9-75//WI2291/WI2269 ICB93-1132-0AP-13AP-0AP-19AP-0AP(PRBYT2010-11-122)
18	Hml-02//WI2291/Bgs ICB83-1554-1AP-1AP-6AP-0AP-23AP-0AP-13AP-0AP(PRBYT2010-11-121)

$(m_i+n_i)/2]/(H_i-L_i)$ (Westcott, 1986), where $S_i(m,n)$ is the similarity index between two genotypes, H_i and L_i are the highest and lowest genotype yields in the test environment i; mi is the mean yield of the mth genotype in the ith test environment, and n_i is the mean yield of the nth genotype in the ith test environment. This index was measured as the average of all $S_i(m,n)$ across test environments. Using this similarity index, the PCoA was performed for stability analysis of the studied genotypes based on the method of Westcott (1986). The environments were first divided into two groups based on their mean grain yield. The first and second groups consisted of the environments with a mean yield lower and higher than the grand mean of all environments, respectively. Then environments were examined in cycles. For the first group, in the cycle L_1, the lowest-yielding environment was analyzed. In the second cycle (L_2), the two lowest-yielding environments were analyzed and so on. Also, cycles H_1, H_2, etc. included the highest-yielding environment, the two highest yielding environments, etc., respectively. In each cycle, a two-dimensional picture (minimum spanning tree - MST) was produced and the first two principal coordinates were plotted for each genotype. The distance between two points showed the dissimilarity between the corresponding genotypes and high yielding genotypes were more dissimilar to low yielding genotypes. Each MST has a natural center from which all the branches radiated. The better genotypes are the furthest from the center and the stable genotypes are the ones that are consistently better over cycles.

The GENSTAT v.12 (Committee 2009) software was used to do the analysis of variance and PCoA.

Results and Discussion

The results of the combined analysis of variance showed significant GE interaction (p ≤ 0.01) (Table 2). This result indicates that the barley genotypes respond differently to the different environmental conditions. The effects of genotypes and environments were also significant (p ≤ 0.01). The average mean yield varied from 1.99 ton/ha for G6 to 2.43 tons/ha for G13 (Table 3). The minimum mean yield varied from 1.053 ton/ha for genotype G10 to 1.583 ton/ha for G14, while the maximum mean yield varied from 2.510 ton/ha for G6 and G10 to 3.395 ton/ha for G18. The yield range varied from 1.272 ton/ha for G6 to 2.192 ton/ha for G1 (Table 3). As was mentioned before, the test environments were grouped into two main high yielding (H) and low yielding groups. There were five H test environments and seven L test environments, which were analyzed in sequential cycles. In the MST plots for L cycles, the genotypes that had the highest performance were those with the furthest distance from the center such as genotypes G8, G2 and G14 (Figure 1-A), G9, G14 and G8 (Figure 1-B), G2, G14 and G13 (Figure 1-C), G8, G14 and G13 (Figure 1-D), G2, G13 and G14 (Figure 1-E), G14, G13 and G2 (Figure 1-F), G14, G13 and G2 (Figure 1-G). The number of top positions and ranking of the superior genotypes based on distance from the center in low cycles is presented in Table 4. Based on these ranks in all L cycles, the genotypes G14, G13 and G2 (Khorram as the check variety) were the most favorable genotypes with high mean yield and good stability and could be recommended for environments with

a mean yield lower than the grand mean of the studied environments.

In the MST plots for H cycles, high-yielding genotypes were those that were farther from the center. Therefore, the genotypes G18, G9 and G4 (Figure 2-A), G11, G17 and G18 (Figure 2-B), G17, G18 and G3 (Figure 2-C), G17, G18 and G2 (Figure 2-D), G13, G18, and G2 (Figure 1-E) detected as the high-yielding genotypes. The number of top positions and ranking of superior genotypes resting on the distance from the center in high cycles is presented in Table 5. Thus, G18 is regarded as the most favorable genotype with a higher mean yield and better stability and could be recommended for environments with a yield higher than the grand mean of all environments.

Various stability criteria have been used by different researchers for quantifying genotype stability for yield. Almost all researchers believe that both yield and stability should be examined simultaneously to counteract the effects of GE interaction and to achieve a more accurate and refined genotype selection. In the present study, the PCoA was used to interpret GE interaction. Flores *et al.* (1996) in *Faba bean*, Sabaghnia *et al.* (2013) in bread wheat and Karimizadeh *et al.* (2019) in durum wheat used PCoA to select for the stable genotypes. Medina *et al.* (1999) reported that the use of PCoA when some environments are different from others provides more reliable results than other methods. Mohebodini *et al.* (2012) in a study conducted to investigate the stability of 18 lentil cultivars reported that the PCoA offers a better interpretation of the GE interaction than univariate

Table 2. Combined analysis of variance of the barley genotypes for the yield data.

Source of variation	df	SS	MS
Genotype	17	11.470	0.675**
Environment	11	188.033	17.094**
Genotype × Environment	187	57.451	0.307**
Error	612	66.569	0.109
Total	864	4572.934	

Table 3. Average, maximum, minimum and range of grain yield for 18 barley genotypes.

Genotype	Average	Minimum	Maximum	Range
G1	2.34	1.063	3.255	2.192
G2	2.38	1.475	3.195	1.720
G3	2.19	1.105	2.793	1.688
G4	2.17	1.120	3.288	2.168
G5	2.27	1.320	3.230	1.910
G6	1.99	1.233	2.505	1.272
G7	2.14	1.175	3.073	1.898
G8	2.18	1.428	3.090	1.662
G9	2.24	1.335	3.370	2.035
G10	2.00	1.053	2.505	1.452
G11	2.25	1.200	2.633	1.433
G12	2.26	1.265	2.988	1.723
G13	2.43	1.313	3.088	1.775
G14	2.29	1.583	3.230	1.647
G15	2.18	1.103	2.873	1.770
G16	2.09	1.155	2.555	1.400
G17	2.13	1.308	2.745	1.437
G18	2.32	1.355	3.395	2.040

methods. The better relative efficiency of this method as compared to other stability analyses has been suggested elsewhere (Flores *et al*., 1996; Ibanmez *et al*. 2001).
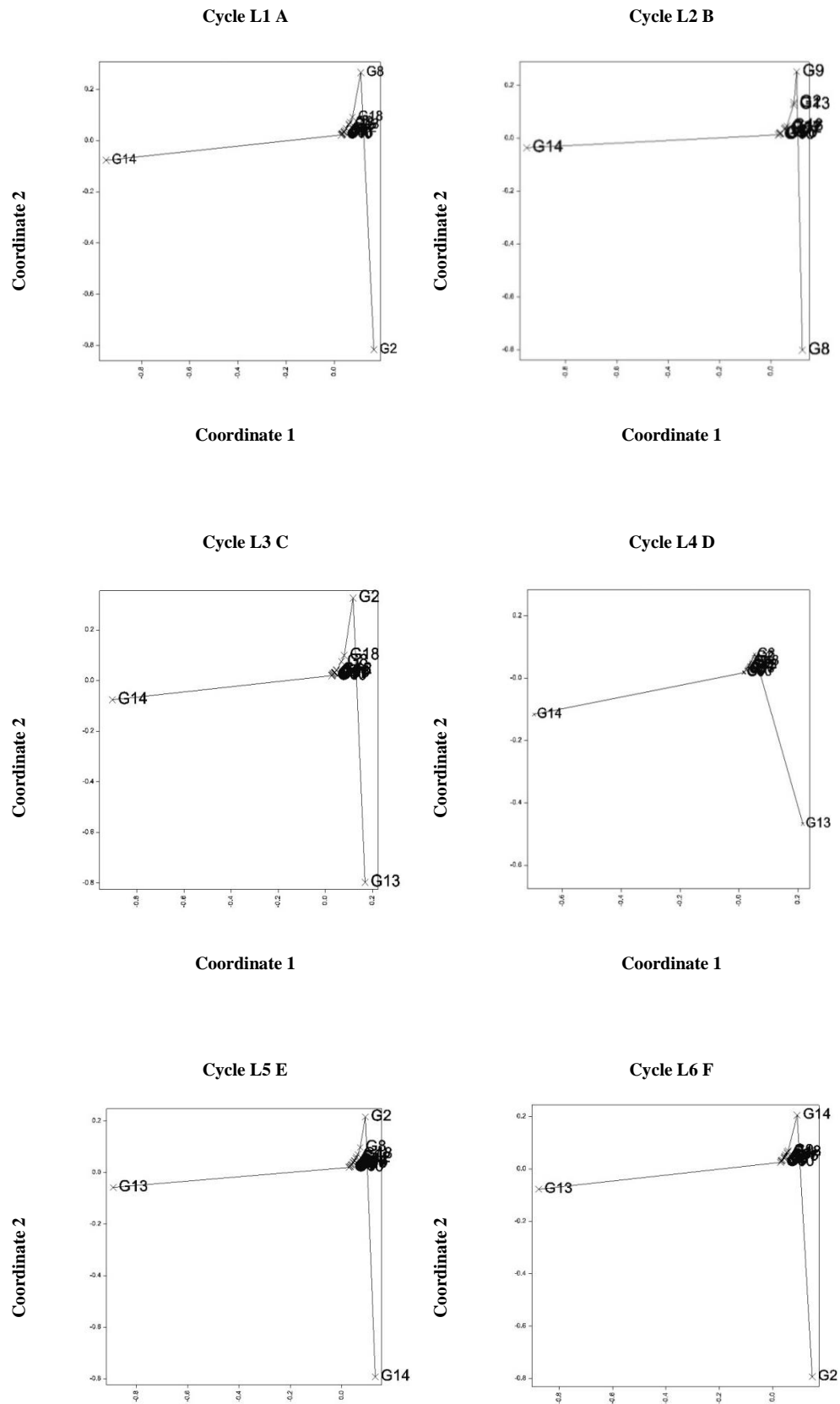
Conclusion.

There are several methods to analyze the GE interaction for choosing stable and high-yielding cultivars. PCoA is one of the methods that can make it possible to achieve this goal. The results of the PCoA analysis in this study were useful for comparing different barley genotypes and show which ones are stable in different environmental conditions. Genotypes G13 (2.43 kg/ha), G2 (2.38 kg/ha) and G14 (2.29 kg/ha) had high stability in the poor environmental conditions. Also, genotype G2 (2.32 kg/ha) is an ideal candidate for favorable environments due to its higher stability and grain yield.

Conflict of Interest

The authors declare that they have no conflict of interest with any organization concerning the subject of the manuscript.

Cycle L1 A

Coordinate 1

Cycle L2 B

Coordinate 1

Cycle L3 C

Coordinate 1

Cycle L4 D

Coordinate 1

Cycle L5 E

Cycle L6 F

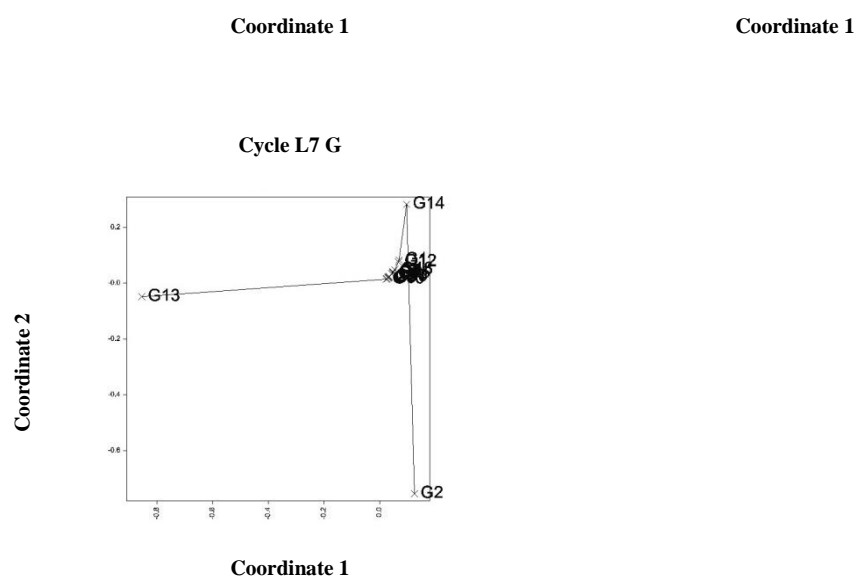**Coordinate 1**   **Coordinate 1**

Cycle L7 G

Figure 1. Minimum spanning tree of the first two principal coordinate axes for the seven low cycles (L).

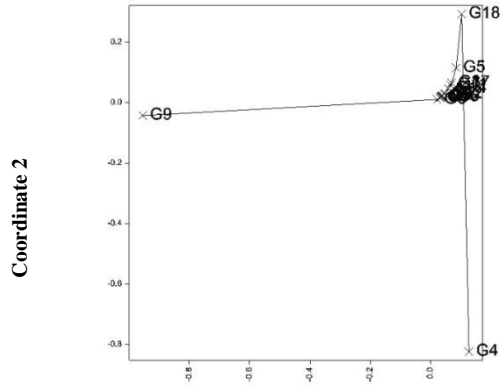Table 4. Ranking of superior genotypes based on distance from the center in the low cycles.

Genotype	Yield	L1	L2	L3	L4	L5	L6	L7	No. of Top Positions
G1	2.34	-	-	-	-	-	-	-	0
G2	2.38	3	-	1	-	1	3	3	5
G3	2.19	-	-	-	-	-	-	-	0
G4	2.17	-	-	-	-	-	-	-	0
G5	2.27	-	-	-	-	-	-	-	0
G6	1.99	-	-	-	-	-	-	-	0
G7	2.14	-	-	-	-	-	-	-	0
G8	2.18	1	3	-	1	-	-	-	3
G9	2.24	-	1	-	-	-	-	-	1
G10	2.00	-	-	-	-	-	-	-	0
G11	2.25	-	-	-	-	-	-	-	0
G12	2.26	-	-	-	-	-	-	-	0
G13	2.43	-	-	3	3	2	2	2	5
G14	2.29	2	2	2	2	3	1	1	7
G15	2.18	-	-	-	-	-	-	-	0
G16	2.09	-	-	-	-	-	-	-	0
G17	2.13	-	-	-	-	-	-	-	0
G18	2.32	-	-	-	-	-	-	-	0

Table 5. Ranking of superior genotypes based on distance from the center in the high cycles.

Genotype	Yield	H1	H2	H3	H4	H5	No. of Top Positions
G1	2.34	-	-	-	-	-	0
G2	2.38	-	-	-	3	3	2
G3	2.19	-	-	3	-	-	1
G4	2.17	3	-	-	-	-	1
G5	2.27	-	-	-	1	1	2
G6	1.99	-	-	-	-	-	0
G7	2.14	-	-	-	-	-	0
G8	2.18	-	-	-	-	-	0
G9	2.24	2	-	-	-	-	1
G10	2.00	-	-	-	-	-	0
G11	2.25	-	1	-	-	-	1
G12	2.26	-	-	-	-	-	0
G13	2.43	-	-	-	-	1	1
G14	2.29	-	-	-	-	-	0
G15	2.18	-	-	-	-	-	0
G16	2.09	-	-	-	-	-	0
G17	2.13	-	1	1	1	-	3

G18	2.32	1	3	2	2	2	5

Cycle H1 A

Cycle H2 B
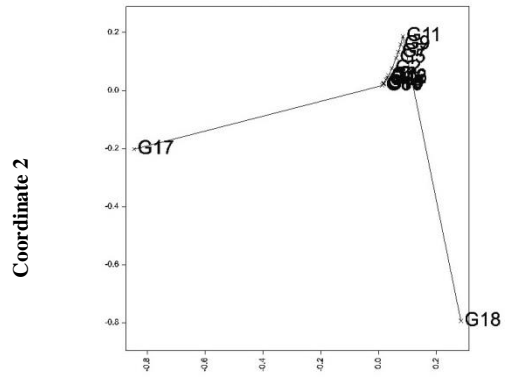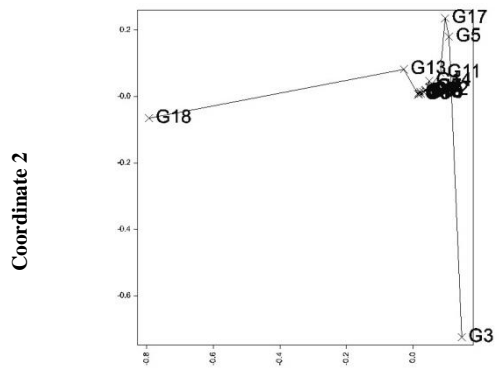
Cycle H3 C

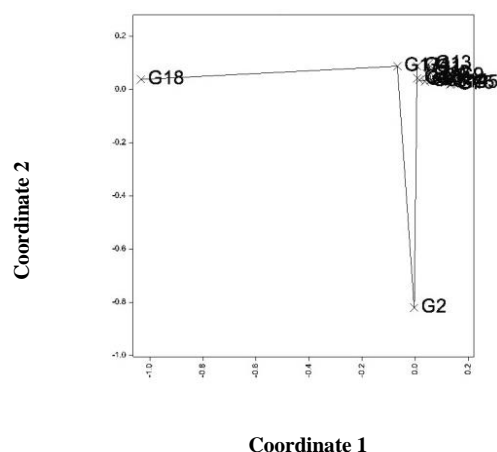**Cycle H4 D**

Cycle H5 E

Coordinate 1

Figure 2. Minimum spanning tree of the first two principal coordinate axes for the five high cycles (H).

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ارزیابی پایداری عملکرد دانه‌ی ژنوتیپ‌های امید بخش جو با استفاده از تجزیه به مولفه‌های هماهنگ اصلی

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چکیده

تجزیه ساختار اثر متقابل ژنوتیپ و محیط در بررسی پایداری گیاهان ضروری می‌باشد. به منظور بررسی اثر متقابل ژنوتیپ و محیط روی عملکرد دانه و شناسایی ژنوتیپ‌های پایدار جو در مناطق گرم و مرطوب، ۱۶ ژنوتیپ جو به همراه دو رقم شاهد در قالب طرح بلوک‌های کامل تصادفی با چهار تکرار در چهار منطقه گچساران، مغان، خرم‌آباد و گنبد به مدت سه سال (۹۸-۱۳۹۶) ارزیابی شدند. تجزیه مرکب داده‌های عملکرد در ۱۲ محیط نشان داد که ژنوتیپ‌ها و محیط‌ها اختلاف معنی‌دار داشتند و اثر متقابل ژنوتیپ و محیط نیز معنی‌دار بود. معنی‌دار بودن اثر متقابل نشان می‌دهد که عملکرد ژنوتیپ‌ها در محیط‌ها یکسان نبوده است. اثر متقابل ژنوتیپ و محیط با استفاده از روش چند متغیره تجزیه به مولفه‌های هماهنگ اصلی مورد تجزیه قرار گرفت. با در نظر گرفتن میانگین کل، ۱۲ محیط به دو گروه با عملکرد بالاتر از میانگین کل (H) و پایین‌تر از میانگین کل (L) تقسیم شدند. با استفاده از نمودارهای MST و فاصله از مرکز نمودار، ژنوتیپ‌های G13 (۲/۴۳ تن در هکتار)، G2 (۲/۳۸ تن در هکتار) و G14 (۲/۲۹ تن در هکتار) برای مناطق با عملکرد کمتر از میانگین کل آزمایش مناسب و قابل توصیه بودند. در مناطق با عملکرد بالاتر از میانگین کل، ژنوتیپ‌های G2 (۲/۳۸ تن در هکتار)، G9 (۲/۲۴ تن در هکتار)، G18 (۲/۳۲ تن در هکتار) و G14 (۲/۲۹ تن در هکتار) چندین بار در راس نمودارهای MST قرار گرفتند و قابل توصیه برای مناطق با عملکرد بیشتر از میانگین کل بودند.

واژه‌های کلیدی: اثر متقابل GE؛ پایداری؛ تجزیه به مولفه‌های هماهنگ اصلی؛ ژنوتیپ‌های امیدبخش جو