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FULL PAPER

Cultivar Evaluation in Multi-Environment Trials of Barley (*Hordeum vulgar* L.) Based On the Principal Coordinate Analysis

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Investigation of genotypes for their yield stability under various environments is important issue in plant breeding programs. Yield stability of 16 barley (Hordeum vulgar L.) genotypes was tested across four locations and three years. The analysis of variance showed that genotype (G), environment (E), and their interaction (G × E) were significant for barley yield. The presence of a large G × E interaction magnitude indicates a significant problem of related to phenotypic expression and makes it difficult for decision making in selection. According to means of environments and total general mean yield (3446.9 kg ha^{-1}), test environments are grouped as H (six high yield) and L (five low yield). The identified most stable genotypes with static stability concept and based on the minimum spanning tree plots and centroid distances were G5 with 3165.4 kg ha^{-1} and G16 with 3191.7 kg ha^{-1}, and therefore could be recommended for unfavorable or poor conditions. Also, genotypes G5 (3165.4 kg ha^{-1}), G13 (3119.1 kg ha^{-1}) and G16 (3191.7 kg ha^{-1}) were located several times in the vertex positions of high cycles according to the principal coordinates analysis. Therefore, genotypes G5 and G16 were found to be the most stable genotypes in both favorable and the favorable conditions and are recommended for commercial release. The principal coordinates analysis provided useful and interesting way of investigating GE interaction of barley genotypes. Finally, the results of principal coordinates analysis in general confirmed the breeding value of the genotypes, obtained on the basis of the yield stability evaluation.

Keywords: centroid distances, minimum spanning tree, yield stability

INTRODUCTION

Selection of barley (Hordeum vulgar L.) genotypes for advancement in crop improvement programs or for planting in farmer fields needs information about genotype performance. Such information is achieved through a series of field experiments designed to sample the target test environments and predict cultivar performance in those environments (Cooper et al. 1993; Kang, 2002). Typically, test results are generated for each test location or for subsets of test locations which is derived from different geographic region, various management systems or a combination of them. Proper testing of genotypes in breeding programs needs a set of test locations that adequately sample environments of interest with minimal duplication (Hamblin et al. 1980). The multi-environment trials used in the crop performance tests are subject to three sources of variation; genotype (G), environment (E), and G × E interaction (Petersen, 1994). Minimizing the G × E interaction component from the combined analysis of variance identifies groups of environments with few genotype rank changes (Park, 1987; Ebdon and Gauch, 2002; Sabaghnia, 2012).

Some authors have used correlation coefficients as measures of similarity for clustering of test environments (Abou-El-Fittouh et al. 1969; Campbell and Lafever, 1977) while Hamblin et al. (1980) associated individual environments or groups of them with state means to determine the better predictors of genotypes' performances. Clustering methods using squared Euclidean distance as the dissimilarity measure have been used extensively (Abdalla et al. 1996; DeLacy et al. 2000). These methods rely on traditional statistical approaches to group genotypes or test environments by analyzing similarity properties. Often the grouping strategies have been used by ordination methods that try to show the proximity of test environments in fewer dimensions by using principal component analysis (PCA) and principal coordinate analysis (DeLacy et al. 1994; Abdalla et al. 1996). PCA is a generalization of joint linear regression that overcomes this difficulty by using the scores of PCA axes as an extra statistic to explain the response pattern of a genotype (Eisemann et al. 1990; Ebdon and Gauch, 2002).

Principal coordinates analysis (PCOA) is a generalization of PCA and involves measurement of similarity between variables (Gower, 1966). This model shows the similarity between variables by Euclidean distance and its main goal is to transform the data from one series of coordinate axes to the other series (Medina et al. 1999). Like PCA, this method preserves most of the original configuration of the dataset in the first axes and so, some initial information is lost. The PCOA can reduce the structure of a two-way dataset of multi-environment trials dimensions in a subspace of fewer dimensions (Ibanmez et al. 2001). Furthermore, the mentioned two-way pattern can be conceptualized as environment points in genotype dimensions. The PCOA may have some limitations; distortions may occur in reduction of dimension, and a lack of correlation between variables prevents few dimensions from explanting for most of the variation (Gower, 1971).

Table 1. Geographical properties of test locations

Location	Longitude Latitude	Altitude (m)	Soil Type	Rainfall (mm)
Gachsaran	50° 50° E 30° 20° N	710	Regosols	460.8
Gonbad	55° 12° E 37° 16° N	45	Regosols	367.5
Khoramabad	23° 26° E 48° 17° N	1148	Regosols	433.1
Moghan	48° 03° E 39° 01° N	1100	Cambisols	271.2

Similar to the ordination strategies, in some cases the first axes of multivariate procedures do not have any clear correlation to environmental factors (Gauch et al. 2008). Also, the nonlinear association prevent from proper description of the relationships between genotypes or environments through multivariate methods (Gower 1971). The main objective of this investigation was to quantify and interpret the G × E interaction on performance stability of barley genotypes using PCOA which could help to understanding genotypes adaptability for grain yield, which is a complex characteristic particularly susceptible to G × E interaction.

Materials and Methods

The barley multi-environmental trials were performed over three years to evaluate the performance of sixteen barley genotypes. The genotypes planted in randomized complete block design layout with four replications during three growing seasons, and were evaluated under four test locations; Gachsaran, Gonbad, Khoramabad and Moghan. Some agro-geographic properties of test locations are given in Table 1. Fourteen of these genotypes were obtained from the breeding activities and two were cultivars which their names are given in Table 2. All of the field plots were prepared by ploughing to a depth of 0.25 m. Each plot measured 4 m^2 (four rows 0.25 m separation) and the sowing rate was about 200 seeds m^{-2}. Weeds were handly controlled, and all of the fields were machine planted and harvested. All trials were fertilized with 60 kg of N ha^{-1} and 60 kg of P_2O_5 during sowing and 60 kg of N ha^{-1} was applied at the beginning of the stem elongation stage. Grain yield (kg ha^{-1}) was determined according to harvested plot in all environments and corrected to 12% moisture basis. The dataset of location Moghan in the third year was not good mode for analysis and so deleted from total data analysis.

Single analysis of variance for individual test environments, identification of outliers, the Anderson-Darling normality test and the Levene variances homogeneity test were performed. The location and genotype were considered as fixed variables while three years were regarded as random variables and combined ANOVA was conducted. The PCOA (Westcott, 1987) was computed for stability analysis using calculation a measure of similarity between two genotypes, m and n, in a given test environment as blow:

$$S_{i(m,n)} = [H_i - (m_i + n_n)/2]/(H_i - L_i)$$

Table 2. Pedigree of 16 barley genotypes

Code	Pedigree or Name
G1	Wi2291/Wi2269//ER/Apm ICB86-0629-0AP-2APH-0AP
G2	Pld10342//Cr.115/Por/3/Bahtim/4/Ds/Apro/5/ wi2291/Wi2291/Wi2269/7/ Wi2291/Wi2291/Wi2291/Wi2269//Wi2291/Bgs ICB94-0402-0AP
G3	7028/2759/3/6982//Ds/Apro/4/H272//Wi2198/ ID601810/5/ Mazurka ICB95 –0437-0AP
G4	Zanbaca/3/H.Spont.21-3/Arar 84//Wi2291/Bgs ICB94-0314-0AP
G5	Hml/WI2291/4/Zanbaca/3/Er/Apm/Lignee131 ICB94 –0587-0AP
G6	Er/Apm//Cerise/3/lignee131/3/Er/Apm ICB83-1985-2AP-0AP
G7	Lignee 124/Hml 024 ICB 82-0757-10AP-0AP-23AP-0AP
G8	Alanda/Harma01/7/Gustoe/6/M6476/Bon//Jo/ York/3/Ms/Colt/As46/4/ Hy3480/Astrix/5/NK1272 ICB95 –0791-0AP-0AP
G9	IPA7//As46/Rhn-05 ICB95 –0162-0AP-0AP
G10	Weahll/Wi2291/Bgs/3/Er/Apm//Ac253 ICB 94 – 0707-0AP-0AP
G11	Roho Alger/Ceres 362 1-1/3/Kantara/4/Bowman ICB93 –0791-21AP-0AP
G12	Mari/Aths×2//Avt/Attiki/3/Aths/Lignee 686 ICB 91 –0368-3AP-0TR-3AP-0AP
G13	IPA 265/PA 7 ICB95 –0127-0AP
G14	Lignee 131/ArabiAbiad/3/Chiem/An57//Albert
G15	Izeh
G16	Gachsaran

where Hi is the highest mean yield of a genotype in test environment i ; Li is the lowest mean yield of a genotype in test environment i ; m_i is the mean yield of genotype m in test environment i and n_i is the mean yield of genotype n in test environment i. Similarity index between two genotypes (m and n) was defined as the average of $S_{i(m,n)}$ across test environments when more than one test environment was used. Each analysis produced a two-dimensional plot based on the first two PCOA scores. centrIn the

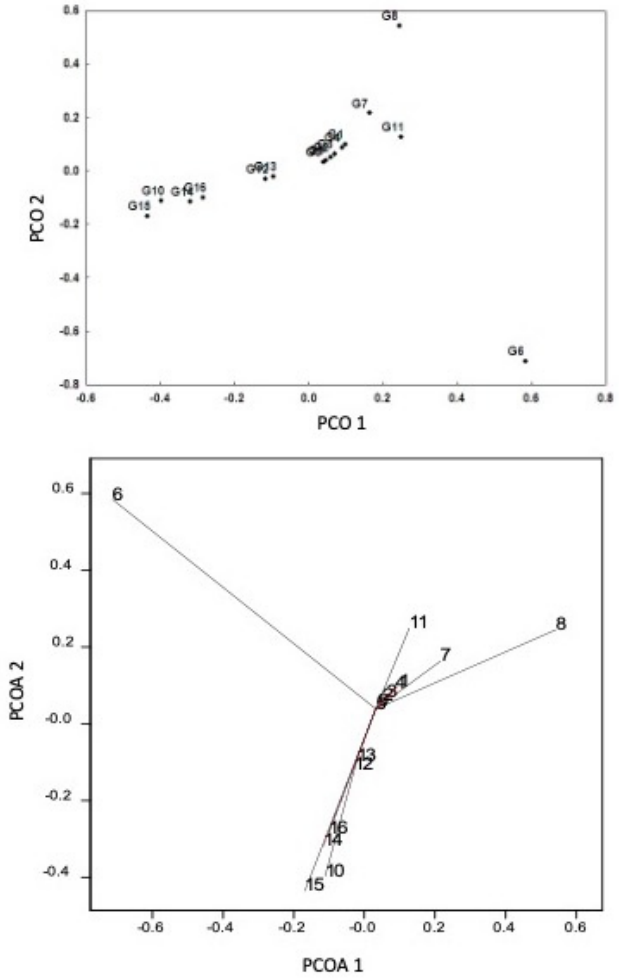

Figure 1. Plot of the first two principal coordinate analysis axes of 16 barley genotypes in eleven environments, scatter plot (up) and the minimum spanning tree in cycle H1 (down)

minimum spanning tree plots, the most stable genotypes (with high mean yield) were those located across sequential cycles and were observed most distant from the plot center. All calculations and plots were generated by GENSTAT 12.1 package (VSN International, 2009).

RESULTS AND DISCUSSION

The grain yield of barley genotypes varied from 1623.8 kg ha^{-1} in genotype G7 grown at Gonbad in the third year to 5719.0 kg ha^{-1} at Gachsaran in genotype G1 grown in the second year. Average mean yields varied from 3119.1 kg ha^{-1} in G13 to 3804.8 kg ha^{-1} in G1 (Table 3). Maximum mean yields varied from 4409.0 kg ha^{-1} in G14 to 5719.0 kg ha^{-1} in G1, while minimum mean yield varied from 1623.8 kg ha^{-1} in genotype G7 to 2931.8 kg ha^{-1} in G2 (Table 3). Average yield was positively correlated with maximum mean yield (r=0.59, P<0.05), but it did not showed any correlation with maximum and amplitude yield. Minimum yield was negatively associated with amplitude yield (r=-0.76, P<0.01), but it did not showed any correlation with maximum yield whereas maximum yield was positively correlated with amplitude yield (r=0.73, P<0.01). Yield amplitudes

Table3. Average, maximum, minimum and amplitude of grain yield in 16 barley genotypes

	Average	Minimum	Maximum	Amplitude
G1	3804.8	1990.8	5719	3728.3
G2	3689.6	2931.8	5079	2147.3
G3	3473.8	2193.5	4458.8	2265.3
G4	3392.8	2238.5	4518	2279.5
G5	3165.4	1672.5	4739.5	3067
G6	3591.3	1814.8	5015	3200.3
G7	3367	1623.8	4697.8	3074
G8	3482.6	1940.8	5068.8	3128
G9	3347.1	2179.5	5024.5	2845
G10	3560.8	2547.5	4767	2219.5
G11	3549.2	2278.8	5067.8	2789
G12	3439.8	2460.8	4637.5	2176.8
G13	3119.1	2157.5	4547.5	2390
G14	3488	2588.8	4409	1820.3
G15	3487.8	2427.5	4962.3	2534.8
G16	3191.7	2165.8	4852.3	2686.5

were very large, from 1820.3 kg ha^{-1} for G14 to 3728.3 kg ha^{-1} for G1 (Table 3). The combined analysis of variance was conducted to determine the effects of environment, genotype, and their interaction on grain yield of barley genotypes (Results are not shown). The main effects of environment (E) and genotypes (G) were highly significant. The GE interaction was highly significant at 1% probability level which indicates the studied barley genotypes exhibited complicated GE interaction regarding additive and crossover aspects. According to Cooper et al. (1995), the large GE interaction magnitude cause to the more dissimilarly in the plant genetic systems which controlling the physiological processes conferring yield stability at different environments. The relative contributions of GE interaction for grain yield found in this investigation are similar to those found in other researches in rain-fed areas (Dehghani et al. 2006; Sabaghnia et al. 2008).

According to grand means and total mean yield (3446.9 kg ha^{-1}), test environments were grouped as High mean yield (H) and Low mean yield (L). There were six H test environments and five L test environments which entered in the sequential analysis cycles. Grain yields are analyzed for the highest test environment (cycle H1); the second cycle (H2) involves analyzing the two highest environments, and so on. A typical plot for the cycles is shown in Figure 1A where the scatter point diagram indicates the results of analysis for the first high cycle (H1). Plot of first two PCOA axes in cycle H1 showed genotype G6 was completely different from the other genotypes. Also, genotypes G10, G12, G13, G14, G15 and G16 were distinguished from the other genotypes considering the scores of first two PCOA. The above plot uses only first two PCOA axes and so ignoring some information of the other PCOA axes.

Table 4. Values of centroid distances for the barley genotypes in the high and low cycles

	High Cycles						Low Cycles				
	H1	H2	H3	H4	H5	H6	L1	L2	L3	L4	L5
G1	0.776	0.771	0.836	0.867	0.874	0.874	0.95	0.857	0.89	0.84	0.778
G2	0.601	0.703	0.669	0.694	0.732	0.774	0.749	0.789	0.794	0.776	0.805
G3	0.67	0.761	0.703	0.688	0.749	0.76	0.613	0.8	0.667	0.661	0.639
G4	0.753	0.738	0.711	0.717	0.754	0.732	0.671	0.692	0.573	0.611	0.601
G5	0.186	0.189	0.426	0.552	0.599	0.605	0.335	0.432	0.532	0.532	0.488
G6	0.954	0.791	0.797	0.796	0.815	0.822	0.404	0.531	0.635	0.704	0.649
G7	0.865	0.837	0.782	0.788	0.796	0.773	0.563	0.598	0.576	0.533	0.485
G8	0.907	0.772	0.788	0.75	0.754	0.781	0.541	0.4	0.488	0.598	0.568
G9	0.414	0.663	0.715	0.728	0.706	0.679	0.637	0.584	0.63	0.693	0.665
G10	0.63	0.731	0.747	0.751	0.742	0.734	0.715	0.65	0.647	0.644	0.66
G11	0.543	0.677	0.72	0.753	0.753	0.752	0.696	0.598	0.631	0.657	0.692
G12	0.434	0.645	0.681	0.685	0.698	0.7	0.874	0.815	0.773	0.709	0.704
G13	0.412	0.593	0.634	0.576	0.547	0.52	0.5	0.459	0.535	0.551	0.635
G14	0.616	0.745	0.709	0.675	0.65	0.671	0.68	0.647	0.697	0.719	0.751
G15	0.763	0.86	0.84	0.82	0.797	0.764	0.283	0.424	0.481	0.629	0.654
G16	0.582	0.596	0.498	0.61	0.551	0.614	0.227	0.43	0.539	0.544	0.538

Table 5. Rank of barley genotypes based on magnitudes of centroid distances for the high and low cycles

	High Cycles							Low Cycles					
	H1	H2	H3	H4	H5	H6	VG*	L1	L2	L3	L4	L5	VG
G1	13	12	15	16	16	16	0	16	16	16	16	15	0
G2	7	7	4	7	7	13	0	14	13	15	15	16	0
G3	10	11	6	6	9	10	0	8	14	12	10	7	0
G4	11	9	8	8	11.5	7	0	10	12	6	6	5	0
G5	1	1	1	1	3	2	6	3	4	3	1	2	4
G6	16	14	14	14	15	15	0	4	6	10	12	8	0
G7	14	15	12	13	13	12	0	7	8.5	7	2	1	2
G8	15	13	13	10	11.5	14	0	6	1	2	5	4	2
G9	3	5	9	9	6	5	1	9	7	8	11	11	0
G10	9	8	11	11	8	8	0	13	11	11	8	10	0
G11	5	6	10	12	10	9	0	12	8.5	9	9	12	0
G12	4	4	5	5	5	6	0	15	15	14	13	13	0
G13	2	2	3	2	1	1	6	5	5	4	4	6	0
G14	8	10	7	4	4	4	0	11	10	13	14	14	0
G15	12	16	16	15	14	11	0	2	2	1	7	9	3
G16	6	3	2	3	2	3	5	1	3	5	3	3	4

Considering above comment, usage of a minimum spanning tree plot could be useful. In this plot, the high-yielding genotypes are those which are furthest from the centr, and so genotypes G6, G8 and G15 were detected as the high yielding genotypes in H1 cycle (Figure 2B).

The scatter point diagram for the second high cycle (H2) indicates genotypes G7 and G15 were completely different from the other barley genotypes. Also, genotypes G10, G11, G12, G14 and G16 were distinguished from the other genotypes considering the magnitudes of the first two PCOA in the high cycle H2 (Figure 2A). In the related minimum spanning tree plot, the high-yielding genotypes were those furthest from the centrcenter, and so genotypes G7, G11 and G15 were detected as the high yielding genotypes in H2 cycle (Figure 2B). The differences in the lengths of the branches are grotesque relative to the differences between genotypes, because the minimum spanning tree is represented in two dimensions ignoring information in the next principal coordinates axis. Regarding this limitation, Flores et al. (1996) suggested using a parameter as centroid distances which benefits from all PCOA dimensions. Rather than including all six scatter diagrams of H cycles, the stability structures of the genotypes are explained in the text and only centroid distances (Table 4), corresponding to all H cycles are shown. Ranking genotypes based on the maximum values of centroid

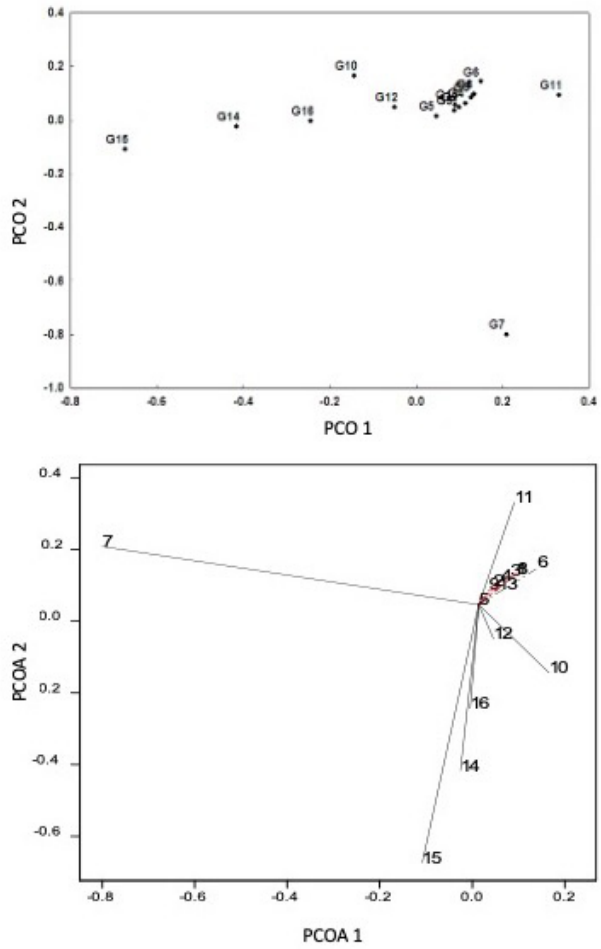

Figure 2. Plot of the first two principal coordinate analysis axes of 16 barley genotypes in eleven environments, scatter plot (up) and the minimum spanning tree in cycle H2 (down)

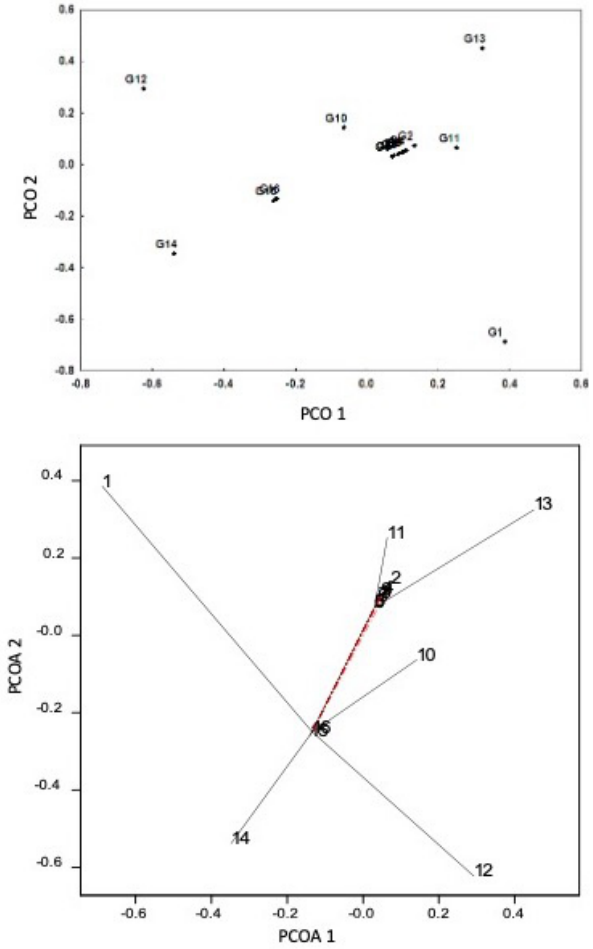

Figure 3. Plot of the first two principal coordinate analysis axes of 16 barley genotypes in eleven environments, scatter plot (up) and the minimum spanning tree in cycle L1 (down)

distances for each H cycle is given in Table 5. Although, according to these values, genotypes G5, G13 and G16 were the most favorable genotypes in most H cycles, but their mean yield were not high. Accordingly, Ibanmez et al. (2001) noted that the results of the PCOA do not completely agree with those obtained using the other multivariate stability analysis such as AMMI (the additive main effects and multiplicative model) model or univariate stability analysis such as linear regression analysis.

There were five L environments which analyzed in the sequential cycles and grain yields were analyzed for the lowest test environment (cycle L1); the second cycle (L2) involves analyzing the two lowest environments, and so on. The scatter point diagram of Figure 3A indicates the results of analysis for the first low cycle (L1). Plot of first two PCOA axes in cycle L1 showed genotypes G1, G12 and G14 were completely different from the other genotypes. Also, genotypes G10, G11, G13, G15 and G16 were distinguished from the other genotypes considering the scores of first two PCOA. Considering minimum spanning tree plot, the high-yielding genotypes were those furthest from the centr, and so genotypes G1, G12, G13 and G14 were detected as the high yielding genotypes in L1 cycle (Figure 3B). The scatter point diagram of Figure 4A indicates the results of analysis for the second low cycle (L2) and demonstrated that genotypes G12, G13 and G14 were completely different from the other genotypes. Also, genotypes G1, G10, G11, G15 and G16 were distinguished from the other genotypes considering the scores of first two PCOA. Considering minimum spanning tree plot, the high-yielding genotypes were those furthest from the centr, and so genotypes G1, G12, G13 and G14 were detected as the high yielding genotypes in L2 cycle (Figure 4B). According to suggestion of Flores et al. (1996) and considering centroid distances of all PCOA dimensions in low cycles, genotypes G5, G7, G8, G15 and G16 were the most stable genotypes in most L cycles. Among these genotypes, only G8 and G15 could be considered as the most favorable genotypes regarding both mean yield and stability.

The mentioned PCOA results are useful for comparing the merits of different barley genotypes, and show which ones are capable of stability across different environmental conditions. Flores et al. (1996) found that both AMMI and PCOA approaches obtained equally satisfactory results, but Medina et al. (1999) reported that PCOA might be more straightforward than AMMI model when there are values that are conspicuously separated from the majority of other values. For the barley genotypes analyzed in this study, the PCOA seems necessary

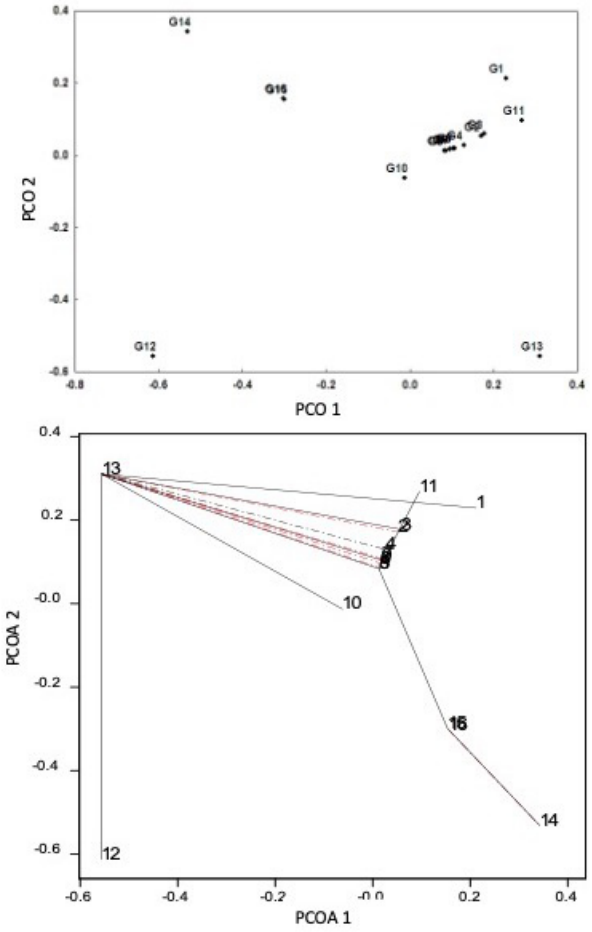

Figure 4. Plot of the first two principal coordinate analysis axes of 16 barley genotypes in eleven environments, scatter plot (up) and the minimum spanning tree in cycle L2 (down)

for an adequate description of the GE interaction. The present dataset and other similar studies (Flores et al. 1998; Ibanmez et al. 2001) encountered problems, because conventional methods confound GE interaction and main effects and are unable to explain non-linear genotypic response to the environments. In addition, the identified most favorable genotypes in both cycles (favorable versus unfavorable conditions) especially in Low cycles, were relatively the most high yielding genotypes. However in the semi-arid regions and rain fed condition, where fluctuations in growing conditions are unpredictable, additional investigations are needed to obtain an integration of GE interaction analysis with environmental factors. The yield stability refers to a genotype's ability to perform relatively consist (high or low) across a range of environmental conditions. The stability approaches relate to either of two contrasting concepts of stability as static and dynamic (Becker and Leon, 1988). In the dynamic concept of stability, a stable genotype indicates relatively similar performance in different test environments and its responses are parallel to the mean response of the tested genotypes. It seems that the results of PCOA are mostly associated with the static or biological concept of stability.

CONCLUSION

Genotypes G5 (3165.4 kg ha^{-1}) and G16 (3191.7 kg ha^{-1}) showed static stability concept while genotypes G8 (3482.6 kg ha^{-1}) and G15 (3487.8 kg ha^{-1}) had dynamic stability concept in poor environmental conditions. In addition, genotypes G5 (3165.4 kg ha^{-1}), G13 (3119.1 kg ha^{-1}) and G16 (3191.7 kg ha^{-1}) are ideal candidates due to high stability with high grain yield for all high (H) environments. Therefore, for future applications, genotypes G5 and G16 were found to be the most stable genotypes in both favorable and in favorable conditions. It seems that recommending of genotypes G8 and G15 for commercial release in favorable environments would be logical. Finally, the PCOA method was found to be useful in detecting the phenotypic stability; and studying G × E interaction and could suggest a breeding strategy of specifically adapted genotypes in homogeneously grouped environments regardless of test environment type (favorable or unfavorable). Such similar PCOA outcome could be used to delineate rigorous recommendation procedures as well as to help definition of stability concepts for barley and other major crops.

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