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PRINCIPAL COORDINATES ANALYSIS OF GENOTYPE × ENVIRONMENT INTERACTION IN GRAIN YIELD OF LENTIL GENOTYPES

SUMMARY

Exploration the genotype × environment (GE) interaction pattern is an important issue in most plant improvement programs. A significant GE interaction for grain yield can limit attempts in selecting the most favorable genotypes for both new cultivar recommendation and improved genotype development. Conventional statistical models of stability analysis provide little or no insight into the pattern of the GE interaction while the principal coordinates analysis can account more effectively for the underlying GE interaction patterns. To characterize 18 lentil genotypes from performance trials, data were obtained from 12 environments (four locations in 3 years). Combined analysis of variance indicated that effects of genotype (G), environment (E) and GE interaction were highly significant. The genotypes accounted for 6.8% of the sum of squares of G+E+GE, with environment responsible for 70.4% and interaction for 22.7%. According to grand means of test environments and total mean yield (1230 kg ha-1), environments are classified to two main groups as H (seven high mean yield) and L (five low mean yield). The identified most stable and high mean yield genotypes based on the minimum spanning tree plots and centroid distances were G2 with 1366 kg ha-1 and G11 with 1374 kg ha-1, and therefore could be recommended for unfavorable or poor conditions. Also, genotypes G5 (1324 kg ha-1), G9 (1329 kg ha-1) and G14 (1402 kg ha-1) were located four, five and six times in the vertex positions of seven high cycles, respectively according to the principal coordinates analysis and so these genotypes were the most stable ones with high mean yielding properties. The principal coordinates analysis provided useful and interesting ways of investigating GE interaction of lentil genotypes.

Key words: Adaptation, multi-environment trials, Lens culinaris Medik., yield stability

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INTRODUCTION

Lentil (*Lens culinaris* Medik.) is the one of the important pulse crops which is grown mainly in rain fed regions. It is one of the important oldest known protein rich food legumes which its mean value is at about 28.5% (Stoilova and Pereira, 1999). Since lentil is a rain fed crop, yield stability is an important objective in most breeding program. This could be achieved through a better understanding of the genotype × environment (GE) interaction impact of grain yield. The importance of GE interaction has led new improved genotypes to be assessed in multi-environment trials. Among the objectives of multi-environment trials are the establishment of adaptation strategies for breeding programs and definition of cultivar recommendation strategies (Gauch et al., 2008). The GE effects should not be ignored, rather analyzed using suitable procedures, in order to explore the potential opportunities and disadvantages.

The adaptation strategies maybe focus on responses of a set of genotypes across different environments to obtain predictions relative to future breeding material (Annicchiarico, 2002). These plant materials may be produced from the genetic bases of which the tested genotypes are assumed to be a representative sample. Also, the adaptation strategies maybe focus on cultivar recommendation which is involves the most important information that concerns the response of tested genotypes, their comparison, and deification of high yielding genotypes (Annicchiarico, 2002). Several statistical methods including parametric univariate, nonparametric univariate, and multivariate procedures have been developed to assess yield stability (Flores et al., 1998). Between them the most widely used is the joint regression model (Finlay and Wilkinson, 1963). The linear regression method uses only one statistic, the regression coefficient, to describe the pattern of response of a genotype across environments and, most of the information is wasted in accounting for deviation. Principal components analysis (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).

Principal coordinates analysis is a generalization of famous PCA and involves with measurement of similarity between variables (Gower, 1966; Westcott, 1987). This method assumes that the original variables define a Euclidean space and so the similarity between them is modeled by Euclidean distance. The main target of the principal coordinates analysis is to transform the data from one series of coordinate axes to the other series (Medina et al., 1999). Like PCA, this analysis preserves most of the original configuration of the dataset in the first axes and so, some original information is inevitably lost. The principal coordinates analysis can effectively reduce the pattern of a two-way dataset of MET dimensions in a subspace of fewer dimensions (Ibanmez et al., 2001). Also the mentioned two-way structure can be conceptualized as environment points in genotype dimensions.

Ordination approaches such as the principal coordinates analysis may have some limitations. In dimension reduction of dataset, distortions may occur. In other word, if the percentage of variance explanted by the first axes is small, individuals that are really far part may be indicated by points that are close together (Gower, 1971). Also, a lack of association between variables prevents few dimensions from explanting for most of the observed variation. In contrast to ANOVA (additive model), multivariate methods such as the principal coordinates analysis assumes a multiplicative model without any explanation of the main effects (Zobel et al., 1988). In some cases the first axes of multivariate methods do not have any clear association to environmental factors (Gauch et al., 2008). Finally, the nonlinear relationships prevent from effective explanation of the real relationships between genotypes through multivariate methods (Gower, 1971). The aim of the present study was to quantify and interpret the GE interaction on performance stability of lentil genotypes using principal coordinates analysis. This should help to interpreting genotypes adaptability for grain yield, which is a complex trait particularly susceptible to GE interaction.

MATERIAL AND METHODS

Experimental protocol

Two check cultivars (Cabralia and Gachsaran) and 16 new lentil genotypes were used as plant materials. These genotypes were from the ICARDA's (International Center for Agricultural Research in the Dry Areas) lentil improvement program. These lentil genotypes were planted in a randomized complete block design with four replications, in plots of 4 rows, each 4 m long and spaced 25 × 2.5 cm. Harvest area was 1.75 m^2 each plot after removing border effects. The plots were fertilized according to local recommendations. Appropriate pesticides were used to control insects, weeds and diseases for each environment. Lentil genotypes were evaluated in four locations across three years (2007-2009). The locations were: Gorgan, Gachsaran, Kermanshah and Shirvan. The test locations were selected as sample of lentil growing areas of Iran and to vary in latitude, rainfall, soil types, temperature and other agro-climatic factors. The properties and the location of the experimental environments are given in Table 1.

Table 1. Geographical properties of test locations.

Code	Location	Altitude (meter)	Longitude Latitude	Soil Texture	Rainfall (mm)	Yield (kg ha^{-1})
1	Gorgan	45	55° 12´ E 37° 16´ N	Silty Clay Loam	367	767
2	Kermanshah	1351	47° 19´ E 34° 20´ N	Clay Loam	455	1923
4	Gachsaran	710	50° 50´ E 30° 20´ N	Silty Clay Loam	460	1747
5	Shirvan	1131	58° 07´ E 37° 19´ N	Loam	267	384

Statistical methods

Analysis of variance was performed for individual environments to plot residuals and identify outliers. The Anderson-Darling normality test and the Levene variances homogeneity test were assessed. Each of the four location and 18 genotypes were regarded as fixed variables while three years were regarded as random variables. Combined analysis of variance was conducted using by SAS 9.1 program (SAS, 2004). The principal coordinate analysis (Westcott, 1987) was used for stability analysis. A measure of similarity between two genotypes, *m* and *n*, in a given test environment is:

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

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. The analysis was based on the sequential accumulation of the test environments according to their rank order, the environments being ranked in ascending order according to their overall means. Each analysis produced a two-dimensional plot based on the first two principal coordinates scores. Also, the minimum spanning tree plots were drawn and the most stable genotypes with high mean yield performance were those that across sequential cycles were observed most distant from the centre of the plot. All calculations and plots of the principal coordinate analysis were performed by GENSTAT 12.1 software (VSN International, 2009).

RESULTS

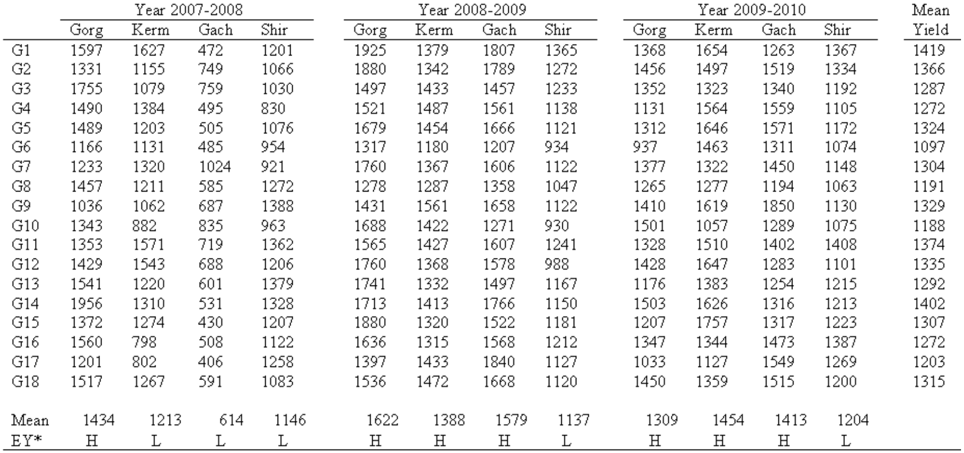
The results of combined analysis of variance (Table 2) revealed significant ($P< 0.01$) GE interaction. The location and year main effects were not significant but their interaction (location × year) was highly significant ($P< 0.01$). The genotype main was highly significant ($P< 0.01$) but its interaction with year was not significant ($P>0.05$). The genotype × location interaction as well as genotype × location × year interaction was highly significant ($P< 0.01$). The location and year main effects explained 14.9 and 21.1 % of the total variation due to G+E+GE. The environment (L+Y+YL) effect explained most (up to 70.4 %) of the G+E+GE variation. Observed variations due to G or GE interactions are measure of how genotypes respond across test environments or differently in different environmental conditions. The environment effects show how the genotype means are different between test environments. Several investigations have indicate that environment typically accounts for >80% of total observed variation (Yan et al., 2000; Sabaghnia et al., 2008b), which is expected regarding the average effect that location has on plant growth; however, traits with high heritability are influenced less by environment (Signor et al., 2001).

The contribution of genotype's main effect as well as GL, GY, and GLY interaction effects appeared to be relatively small (Table 2). Moreover, the significant GL effects showed that genotypes responded differently to different locations, confirming the importance of testing lentil genotypes at multi-locations in Iran. When genotypes are tested in multi-environment trials, usually a crossover GE interaction occurs (Ceccarelli et al., 2006; Sabaghnia et al. 2006) and complicates recommendation issue in breeding programs. The high significance of GLY interaction for grain yield variations in lentil genotypes indicated the importance of further analysis for adaptation pattern, genotypes' response and their stability for better exploitation of the GE interaction. The relative large magnitude of GE interaction effects in comprising to genotypic main effects in grain yield of lentil which was found in this study is similar to those found in other multi-environmental trials studies of lentil in rain-fed conditions (Mohebodini et al. 2006; Dehgahni et al., 2008; Sabaghnia et al. 2008a).

Table 2. Combined analysis of variance of lentil performance trial yield data

Source	DF	MS	% of G+E+GE
Year (Y)	2	8400774^{ns}	21.1
Location (L)	3	3962077^{ns}	14.9
Y*L	6	4579496^{**}	34.4
R (Y*L)	36	38152	0.0
Genotype (G)	17	320003^{**}	6.8
Y*G	34	80769^{ns}	3.4
L*G	51	134137^{*}	8.6
Y*L*G	102	84021^{**}	10.7
Error	612	31713	

Table 3. Mean yield data (kg ha-1) of 18 lentil genotypes tested in four locations of Iran during three years



	Year 2007-2008				Year 2008-2009				Year 2009-2010				Mean
	Gorg	Kerm	Gach	Shir	Gorg	Kerm	Gach	Shir	Gorg	Kerm	Gach	Shir	Yield
G1	1597	1627	472	1201	1925	1379	1807	1365	1368	1654	1263	1367	1419
G2	1331	1155	749	1066	1880	1342	1789	1272	1456	1497	1519	1334	1366
G3	1755	1079	759	1030	1497	1433	1457	1233	1352	1323	1340	1192	1287
G4	1490	1384	495	830	1521	1487	1561	1138	1131	1564	1559	1105	1272
G5	1489	1203	505	1076	1679	1454	1666	1121	1312	1646	1571	1172	1324
G6	1166	1131	485	954	1317	1180	1207	934	937	1463	1311	1074	1097
G7	1233	1320	1024	921	1760	1367	1606	1122	1377	1322	1450	1148	1304
G8	1457	1211	585	1272	1278	1287	1358	1047	1265	1277	1194	1063	1191
G9	1036	1062	687	1388	1431	1561	1658	1122	1410	1619	1850	1130	1329
G10	1343	882	835	963	1688	1422	1271	930	1501	1057	1289	1075	1188
G11	1353	1571	719	1362	1565	1427	1607	1241	1328	1510	1402	1408	1374
G12	1429	1543	688	1206	1760	1368	1578	988	1428	1647	1283	1101	1335
G13	1541	1220	601	1379	1741	1332	1497	1167	1176	1383	1254	1215	1292
G14	1956	1310	531	1328	1713	1413	1766	1150	1503	1626	1316	1213	1402
G15	1372	1274	430	1207	1880	1320	1522	1181	1207	1757	1317	1223	1307
G16	1560	798	508	1122	1636	1315	1568	1212	1347	1344	1473	1387	1272
G17	1201	802	406	1258	1397	1433	1840	1127	1033	1127	1549	1269	1203
G18	1517	1267	591	1083	1536	1472	1668	1120	1450	1359	1515	1200	1315
Mean	1434	1213	614	1146	1622	1388	1579	1137	1309	1454	1413	1204	
EY*	H	L	L	L	H	H	H	L	H	H	H	L	

Gorg, Gorgan; Kerm, Kermanshah; Gach, Gachsaran; Shir, Shirvan

* EY, Environmental type; H, high yielding from average; L, low yielding from average

The actual mean yield of the lentil genotypes at four test locations and across three years are given in Table 3 and the grand mean yield values at each environment are determined. According to these grand means and total mean yield (1230 kg ha^{-1}), test environments are classified to two main groups as H (high mean yield) and L (low mean yield). There are seven H test environments and five test environments in the Table 3 which were analyzed in the sequential cycles. Grain yield performances were first analyzed for the lowest test environment (cycle L1); the second cycle (L2) involves analyzing the two lowest environments, and so on. A typical plot for the cycles is shown in Figure 1 where the scatter point diagram indicates the results of analysis for the first low cycle (L1). Plot of first two principal coordinates analysis axes in cycle L1 (Figure 1) indicated genotypes G7 and G10 were different from the other genotypes. This plot uses only first two principal coordinates analysis axes and so ignoring some information of the other principal coordinates axes. Considering this comment, a minimum spanning tree plot could be useful. The high-yielding genotypes are those which are furthest from the centre, and so genotypes G1, G2 and G11 were detected as the high yielding genotypes in L5 cycle (Figure 2).

The differences in the lengths of the branches are grotesque relative to the differences between studied 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) proposed using a parameter as centroid distances which is benefits from all principal coordinates dimensions. Rather than including all five scatter diagrams of L cycles, the stability patterns of the genotypes are described in the text and only centroid distances (Table 4), corresponding to all L cycles are presented. Ranking genotypes based on the maximum values of centroid distances for each L cycle is given in Table 5. According to centroid distances values, genotypes G2, G3 and G7 were the favorable genotypes in cycles L1 and L2 while genotypes G1, G2, G11 and G12 were the favorable genotypes in cycles L3, L4 and L5 (Table 5). According to obtained results for all low cycles, genotypes G1, G11 and G14 were the favorable stable ones. Among these genotypes only G2 and G11 were located three times in the vertex positions of five low cycles and so these genotypes (G2 and G11) were the most stable ones with high mean yielding properties. The most stable genotypes are the ones that are consistent over cycles (Westcott, 1987; Flores et al., 1996). The identified most stable and high mean yield genotypes had acceptable mean yield; G2 with 1366 kg ha^{-1} and G11 with 1374 kg ha^{-1}, and therefore could be recommended for unfavorable or poor conditions.

According to the results presented in Table 3, seven test environments were as H (high mean yield) which were analyzed in the sequential cycles. Lentil yield performances are first analyzed for the highest test environment (cycle H1); the second cycle (H2) involves analyzing the two highest test environments, and so on. According to scatter point diagram of the first high cycle (H1), genotypes G9, G10, G14 and G18 were different from the other genotypes (Figure 3). Similar to L cycles, minimum spanning tree plot was used and showed that genotypes G5, G9 and G14 were high-yielding genotypes because they were furthest from the centre in H5 cycle (Figure 4).

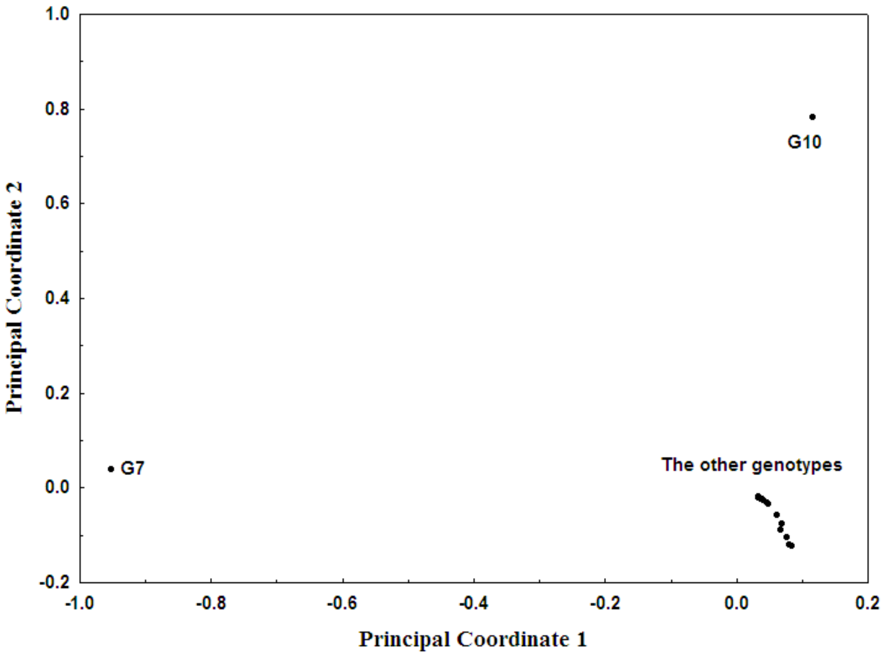


Figure 1. Plot of the first two principal axes from a principal coordinate analysis of 18 lentil genotypes in twelve environments, in cycle L1.

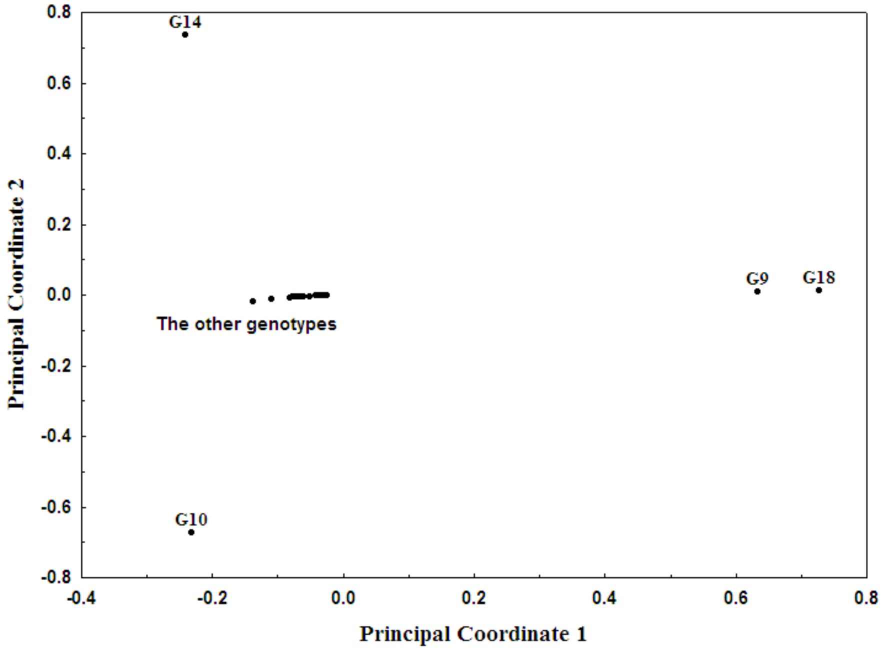


Figure 2. Plot of the first two principal axes from a principal coordinate analysis of 18 lentil genotypes in twelve environments, in cycle H1.

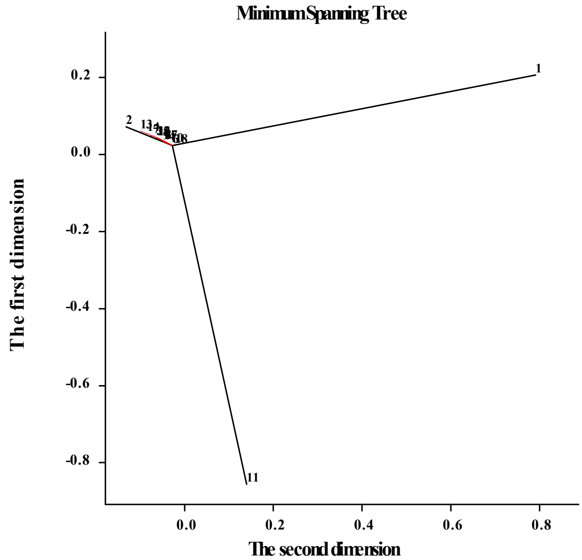


Figure 3. Plot of the first two principal axes from a principal coordinate analysis of 18 lentil genotypes in twelve environments, in cycle L5. Part of the minimum spanning tree is superimposed on the plot.

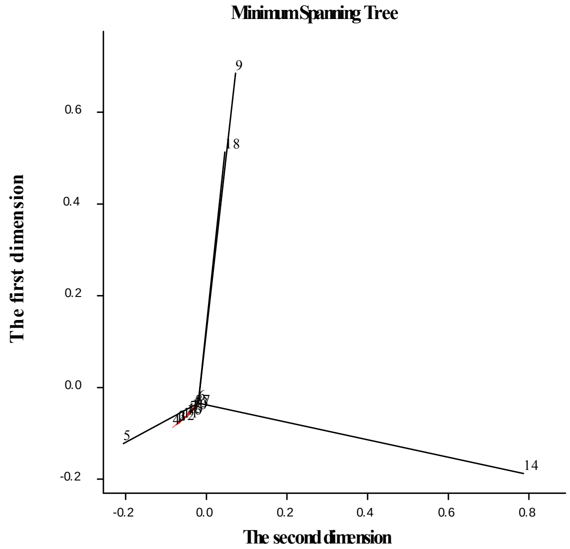


Figure 4. Plot of the first two principal axes from a principal coordinate analysis of 18 lentil genotypes in twelve environments, in cycle H5. Part of the minimum spanning tree is superimposed on the plot.

Table 4. Lengths of the entire minimum spanning tree (centroid distances values) for the five low cycles.

Genotypes	L1	L2	L3	L4	L5
G1	0.3402	0.7173	0.7417	0.7836	0.8211
G2	0.7163	0.7867	0.7402	0.7685	0.7444
G3	0.7263	0.7657	0.7122	0.6848	0.6637
G4	0.3853	0.5469	0.4579	0.4353	0.5314
G5	0.4031	0.5378	0.5778	0.5709	0.5939
G6	0.3667	0.2898	0.3631	0.3328	0.4065
G7	0.9533	0.8145	0.7076	0.6599	0.6823
G8	0.5264	0.5202	0.6522	0.5694	0.5942
G9	0.6375	0.6563	0.7729	0.7116	0.6884
G10	0.7980	0.5749	0.5490	0.4889	0.4631
G11	0.6861	0.7518	0.8181	0.8540	0.8686
G12	0.6523	0.5336	0.6320	0.5735	0.6542
G13	0.5488	0.6368	0.7562	0.7293	0.7220
G14	0.4466	0.5804	0.7064	0.6902	0.7042
G15	0.2346	0.5441	0.6384	0.6433	0.6621
G16	0.4079	0.6199	0.6493	0.7281	0.6552
G17	0.1408	0.4728	0.6214	0.6538	0.5900
G18	0.5177	0.5989	0.6222	0.6276	0.6541

Table 5. Lentil genotypes ranks based on centroid distances values for the five low cycles.

Genotypes	L1	L2	L3	L4	L5	VG*
G1	16	5	4	2	2	2
G2	4	2	5	3	3	3
G3	3	3	6	8	8	2
G4	14	12	17	17	16	0
G5	13	14	15	14	14	0
G6	15	18	18	18	18	0
G7	1	1	7	9	7	2
G8	9	16	9	15	13	0
G9	7	6	2	6	6	1
G10	2	11	16	16	17	1
G11	5	4	1	1	1	3
G12	6	15	12	13	11	0
G13	8	7	3	4	4	1
G14	11	10	8	7	5	0
G15	17	13	11	11	9	0
G16	12	8	10	5	10	0
G17	18	17	14	10	15	0
G18	10	9	13	12	12	0

*The number of vertex genotypes

Table 6. Lengths of the entire minimum spanning tree (centroid distances values) for the seven high cycles.

Genotypes	H1	H2	H3	H4	H5	H6	H7
G1	0.8454	0.7783	0.6654	0.6879	0.7324	0.7701	0.7994
G2	0.9230	0.7950	0.7589	0.7133	0.7245	0.7609	0.7862
G3	0.8300	0.8099	0.7146	0.7498	0.7236	0.7073	0.6895
G4	0.5858	0.7392	0.7327	0.7197	0.7412	0.7391	0.7208
G5	0.7916	0.8063	0.7817	0.7572	0.7838	0.7906	0.7862
G6	0.1957	0.1888	0.2904	0.3166	0.4354	0.4042	0.3892
G7	0.8535	0.7743	0.7230	0.6671	0.6555	0.6760	0.7000
G8	0.7441	0.6470	0.5354	0.5676	0.5656	0.5544	0.5169
G9	0.8654	0.9011	0.9062	0.7939	0.8088	0.8099	0.7775
G10	0.9605	0.8722	0.7467	0.7056	0.6360	0.5979	0.6251
G11	0.8075	0.7940	0.7225	0.6881	0.7071	0.7181	0.7085
G12	0.8989	0.7997	0.6885	0.6754	0.7218	0.7257	0.7413
G13	0.6436	0.6334	0.5496	0.5950	0.6102	0.6193	0.6507
G14	0.9625	0.8668	0.7507	0.8065	0.8192	0.8340	0.8278
G15	0.6794	0.6412	0.5806	0.5827	0.6751	0.6775	0.7178
G16	0.8257	0.7173	0.6905	0.6999	0.6862	0.6944	0.6981
G17	0.4354	0.6376	0.6625	0.6120	0.5688	0.6506	0.6244
G18	0.9016	0.8602	0.7885	0.7726	0.7492	0.7621	0.7489

Table 7. Lentil genotypes ranks based on centroid distances values for the seven high cycles.

Genotypes	H1	H2	H3	H4	H5	H6	H7	VG*
G1	8	10	13	11	6	4	2	1
G2	3	8	4	7	7	6	3.5	2
G3	9	5	10	5	8	10	13	0
G4	16	12	7	6	5	7	8	0
G5	12	6	3	4	3	3	3.5	4
G6	18	18	18	18	18	18	18	0
G7	7	11	8	13	13	13	11	0
G8	13	14	17	17	17	17	17	0
G9	6	1	1	2	2	2	5	5
G10	2	2	6	8	14	16	15	2
G11	11	9	9	10	10	9	10	0
G12	5	7	12	12	9	8	7	0
G13	15	17	16	15	15	15	14	0
G14	1	3	5	1	1	1	1	6
G15	14	15	15	16	12	12	9	0
G16	10	13	11	9	11	11	12	0
G17	17	16	14	14	16	14	16	0
G18	4	4	2	3	4	5	6	2

*The number of vertex genotypes

The centroid distances values of H cycles are given in Table 6 and genotypes ranks based on these centroid distances are given in Table 7. Rather than including all seven scatter diagrams of H cycles, the stability patterns of the genotypes are described using centroid distances. According to centroid distances values, genotypes G2, G10 and G14 were the favorable genotypes in cycle H1; genotypes G9, G10 and G14 were the favorable genotypes in cycle H2; genotypes G5, G9 and G18 were the favorable genotypes in cycle H3; genotypes G9, G14 and G18 were the favorable genotypes in cycle H4; genotypes G5, G9 and G14 were the favorable genotypes in cycles H5 and H6; genotypes G1, G2, G5 and G14 were the favorable genotypes in cycle H7. Among these genotypes only G5, G9 and G14 were located four, five and six times in the vertex positions of seven high cycles, respectively and so these genotypes were the most stable ones with high mean yielding properties. The mean yield performances of these favorable genotypes were 1324 kg ha^{-1} (G5), 1329 kg ha^{-1} (G9) and 1402 kg ha^{-1} (G14).

DISCUSSION

In the present investigation interpretation of the GE interaction was based on the principal coordinate analysis. This procedure is a multivariate statistical method which tries to explore multi-directionality aspects of multi-environment trials dataset. The conventional stability method, linear regression model, had shown certain deficiencies for explaining GE interaction patterns and it attempt to define the GE interaction by one or two parameter. However the multiplicative GE interaction component is far too complex to be summarized by one or two stability parameter. Multivariate statistical procedures have been introduced to explore complexity and attempt to extract more information from GE interaction. Crossa (1988) found that the principal coordinate analysis gives more satisfactory results than joint linear regression model in detecting genotypes that perform well and remain stable under different environmental conditions. Crossa (1990) and Hill and Bagler (1983) concluded that joint linear regression model should be used with caution when one of the environments is atypical. In these situations, a weakness of AMMI is that when there are atypical values, this analysis can show a distorted view of both genotypes and environments in the biplot (Medina et al., 1999).

Our results obtained with the principal coordinate analysis are useful for comparing the merits of different genotypes, and indicate which ones are capable of stability across different environments. Although, Flores et al. (1996) reported that both AMMI (the additive main effects and multiplicative model) and principal coordinate models obtained equally satisfactory results, but Medina et al. (1999) mentioned that principal coordinate model might be more straightforward than AMMI analysis when there are values that are conspicuously separated from the majority of other values. The principal coordinate analysis represents an alternative to the linear regression model for multivariate analysis of breeding programs interested in the interpretation of the GE interaction patterns in yield performance. In contrast, Ibanmez et al. (2001)

noted that the results of the principal coordinate analysis do not completely agree with those obtained using the AMMI and regression analysis. They reported that the AMMI method was better than the linear regression model and the principal coordinate analysis in quantifying environment and genotype effects.

For the lentil genotypes and test environments analyzed in this investigation, the principal coordinate analysis seems necessary 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 contrast, the principal coordinate analysis appears to be able to extract a large portion of the GE interaction and thus it is more efficient in analyzing GE interaction pattern in different crops, as demonstrated by Flores et al. (1996), Medina et al. (1999) and Ibanmez et al. (2001). Also the detected most favorable genotypes in both cycles or condition (favorable versus unfavorable) are relatively the most high yielding genotypes and so it seems that this strategy can select the most stable genotypes based on the dynamic stability concept. 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. In conclusion, genotypes G2 (1366 kg ha^{-1}) and G11 (1374 kg ha^{-1}) are ideal candidates in this regard as they had the desirable characteristics of high stability with high grain yield for all low (L) environments. Also, genotypes G5 (1324 kg ha^{-1}), G9 (1329 kg ha^{-1}) and G14 (1402 kg ha^{-1}) are ideal candidates due to high stability with high grain yield for all high (H) environments.

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CONCLUSIONS

To characterize 18 lentil genotypes from performance trials, data were obtained from 12 environments (four locations in 3 years). Combined analysis of variance indicated that effects of genotype (G), environment (E) and GE interaction were highly significant. The genotypes accounted for 6.8% of the sum of squares of G+E+GE, with environment responsible for 70.4% and interaction for 22.7%. According to grand means of test environments and total mean yield (1230 kg ha^{-1}), environments are classified to two main groups as H (seven high mean yield) and L (five low mean yield). The identified most stable and high mean yield genotypes based on the minimum spanning tree plots and centroid distances were G2 with 1366 kg ha^{-1} and G11 with 1374 kg ha^{-1}, and therefore could be recommended for unfavorable or poor conditions. Also, genotypes G5 (1324 kg ha^{-1}), G9 (1329 kg ha^{-1}) and G14 (1402 kg ha^{-1}) were located four, five and six times in the vertex positions of seven high cycles, respectively according to the principal coordinates analysis and so these genotypes were the most stable ones with high mean yielding properties. The principal coordinates analysis provided useful and interesting ways of investigating GE interaction of lentil genotypes.

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ANALIZA OSNOVNIH KOORDINATA INTERAKCIJE GENOTIP × OKOLINA U POGLEDU PRINOSA ZRNA GENOTIPOVA SOČIVA

Ispitivanje obrasca interakcije genotip × okolina (GE) predstavlja važno pitanje u većini programa oplemenjivanja bilja. Značajna interakcija GE u pogledu prinosa zrna može ograničiti pokušaje odabira najpovoljnijih genotipa i u cilju preporučivanja novog kultivara i u cilju razvoja boljih genotipova. Konvencionalni statistički metodi analize stabilnosti daju ili malo ili nimalo uvida u obrazac interakcije GE, dok je analiza osnovnih koordinata efikasnija za osnovne obrasce interakcije GE. U cilju karakterizacije 18 genotipova sočiva iz ispitivanja performansi, prikupljeni su podaci iz 12 sredina (četiri lokacije u period od 3 godine). Kombinovana analiza varijansi pokazala je da su efekti genotipa (G), sredine (E) i interakcije GE veoma značajni. Genotipovi su činili 6,8% sume kvadrata G+E+GE, dok je okolina odgovorna za 70,4% a interakcija za 22,7%. Prema ukupnoj srednjoj vrijednosti ispitivanih okolina (1230 kg ha-1), okoline se klasifikuju u dvije glavne grupe, a to su H (sedam sa visokom srednjom vrijednošću prinosa) i L (pet sa niskom srednjom vrijednošću prinosa). Identifikovani najstabilniji genotipovi sa visokom srednjom vrijednošću prinosa zasnovani su na grafu minimalnog razapinjućeg stabla, a razmaci težišta (centroida) su bili G2 sa 1366 kg ha-1 i G11 sa 1374 kg ha-1, i stoga bi se mogli preporučiti za nepovoljne ili loše uslove. Takođe, genotipovi G5 (1324 kg ha-1), G9 (1329 kg ha-1) i G14 (1402 kg ha-1) locirani su četiri, odnosno, pet, odnosno, šest puta u vrhovima sedam visokih ciklusa, u skladu sa analizom osnovnih koordinata, tako da su ovi genotipovi bili najstabilniji sa visokim srednjim vrijednostima prinosa. Analiza osnovnih koordinata dala je korisne i interesantne načine ispitivanja GE interakcije genotipova sočiva.

Ključne riječi: Prilagođavanje, ogledi u više sredina, Lens culinaris Medik., stabilnost prinosa