UDC 575:635
DOI: 10.2298/GENSR1203457S
Original scientific paper

GROUPING GENOTYPES AND TEST ENVIRONMENTS BY SOME CLUSTER METHODS REGARDING GENOTYPE × ENVIRONMENT INTERACTION IN MULTI-ENVIRONMENT TRIALS

Naser SABAGHNIA[1*], Rahmatollah KARIMIZADEH[2], Mohtasham MOHAMMADI[2]

Department of Agronomy and Plant Breeding, Faculty of Agriculture, University of Maragheh, Maragheh, Iran.
[2]Dryland Agricultural Research Institute (DARI), Gachsaran, Iran

Sabaghnia N., R. Karimizadeh, and M. Mohammadi (2012): *Grouping genotypes and test environments by some cluster methods regarding genotype × environment interaction in multi-environment trials.* - Genetika, Vol 44, No. 3, 457 - 473.

Lentil (*Lens culinaris* Medik.) is an important source of protein and carbohydrate food for people of developing countries and is popular in some developed countries where they are perceived as a healthy component of the diet. Ten lentil genotypes were tested for grain yield in five different environmental conditions, over two consecutive years to classify these

Corresponding author: Naser Sabaghnia, Department of Agronomy and Plant Breeding, Faculty of Agriculture,University of Maragheh,Maragheh, P.O. Box 55181-83111, Iran,Tel: +98-421-2273070,Fax: +98-421-2276060, E-mail sabaghnia@maragheh.ac.ir, sabaghnia@yahoo.com

genotypes for yield stability. Seed yield of lentil genotypes ranged from 989.3 to 1.367 kg ha^{-1} and the linear regression coefficient ranged from 0.75 to 1.18. The combined analysis of variance showed that the effect of environment (E) and genotype by environment (GE) interaction were highly significant while the main effect of genotype (G) was significant at 0.05 probability level. Four different cluster procedures were used for grouping genotypes and environments. According to dendograms of regression methods for lentil genotypes there were two different genotypic groups based on G plus GE or GE sources. Also, the dendograms of ANOVA methods indicated 5 groups based on G and GE sources and 4 groups based on GE sources. According to dendograms of regression methods for environments there were 5 different groups based on G plus GE sources while the dendograms of ANOVA methods indicated 9 groups based on G and GE sources and 3 groups based on GE sources. The mentioned groups were determined via F-test as an empirical stopping criterion for clustering. The most responsive genotypes with high mean yield genotypes are G2 (1145.3 kg ha^{-1}), G8 (1200.2 kg ha^{-1}) and G9 (1267.9 kg ha^{-1}) and could be recommended as the most favorable genotypes for farmers.

Key words: GE interaction, dendogram, grouping methods, seed yield

INTRODUCTION

Lentil (*Lens culinaris* Medik.), an annual diploid, is an annual cool-season food legume that was among the early domesticates in the Near East. It is predominantly grown in South and West Asia and East and North Africa and as a staple legume, provides nutritional security to the poor, who cannot afford animal protein (SARKER *et al.,* 2009). Lentil seed is a rich source of good protein (up to 33%), micronutrients and vitamins (SARKER *et al.,* 2009), and thus contributes to nutritional security in South Asia and North Africa. Lentil straw is in high demand as an animal feed (SARKER and ERSKINE, 2006), and in West Asia, farmers earn similar income from straw as they receive from seed. Lentil cultivation improves soil health by enriching soil carbon, nitrogen, and organic matter status, and thus provides sustainable cropping systems wherever it is grown in rotation with winter cereals (SARKER *et al.,* 2009).

Due to high importance of lentil, the International Center for Agricultural Research in the Dry Areas (ICARDA) has put emphasis on lentil research, and has been assigned a world mandate for its improvement in important traits such as yield performance (SARKER *et al.,* 2009). Iran has had several important lentil breeding programs in recent decade, supported by ICARDA and increasing the potential of yield performance is an important goal of lentil improvement program (SABAGHNIA *et al*., 2006). The new improved lentil genotypes are evaluated in multi-environment trials to test their performance across different environmental conditions and to select the best genotypes in specific environments. In most trials, genotype × environment (GE) interaction is observed, complicating selection for yield

(ANNICCHIARICO *et al.,* 2010). Effective interpretation of GE interaction and yield stability can be aided by statistical modeling in multi-environment trials (MET).

The major goal of MET is to estimate yield stability, to evaluate the performance of new improved genotypes under different test environments, and to effective interpret GE interaction such that the best genotypes across test environments are selected. The major problem in the selection process is the effect of GE interaction, and the degree of uncertainty in identification of genotypes with broad or specific adaptation to the target environments (GAUCH *et al*., 2008; STEFANOVA and BUIRCHELL, 2010). Therefore, efficient analysis of MET dataset decreases the uncertainty and aides in understanding the GE interaction nature. Several statistical methods can be used to achieve some or all of these objectives based on yield stability concept or GE interaction investigation (YAN et al., 2007; SABAGHNIA, 2012).

For partitioning of GE interaction, the GE interaction effects for each genotype could be squared and summed across all environments, as a stability measure. Another method for interpreting the GE interaction is the joint linear regression method. The regression model has been extensively used in plant breeding for determining yield stability of different genotypes (MOHEBODINI *et al*., 2006; YAN and HOLLAND, 2010). The additive main effects and multiplicative interaction (AMMI) model use the ANOVA, where after the AMMI model separates the additive variance from the multiplicative GE interaction, and then applies principal component analysis to the GE interaction portion from the ANOVA analysis to extract a new set of coordinate axes which account for the GE interaction pattern (GAUCH *et al*., 2008).

Stability methods involving the linear regression strategy and related yield stability statistics cannot be recommended, nor can the defects of these procedures be overcome by the use of the cluster analysis (SABAGHNIA *et al*., 2012). The use of the particular cluster strategy in cluster analysis could lead to a result in different cluster groups and the acceptance or rejection of any particular choice may be difficult to justify.

LIN and THOMPSON (1975) used cluster analysis to extend conventional approaches of cluster analysis and indicated that this dissimilarity measure equaled the mean of the measures for all possible pairs of genotypes in the subset. LIN (1982) used the GE interaction mean square as dissimilarity index through a slight adjustment of distance coefficient. LIN and BUTLER (1990) studied cluster analyses for analyzing two-way classification data and introduced two new dissimilarity measures. The objectives of present study were to (i) evaluate yield performance of lentil genotypes over several locations in Iran via cluster analysis, and (ii) classifying test environments using different clustering methods.

MATERIALS AND METHODS

For this investigation, seed yield data recorded from ten lentil international nurseries and yield trials over two year's period were examined. Plant materials mostly consisted of new breeding lines developed through crossbreeding using

genotypes originating from geographically diverse locations of world (Table 1). The trials were conducted in Gonbad, Kermanshah, Ilam, Gachsaran and Shirvan research stations of Iran. Key climatic and geographic parameters related to lentil production in these locations are highly variable (Table 2). The trials were conducted in a randomized complete block designs with four replicates for ten genotypes including a local check (Gachsaran). Each genotype was planted in 4 m long, 4 rows. In each plot, two rows distance of 25 cm and two plants distance of 5 cm were maintained. To avoid border effect in plots, all genotypes were planted continuously with no extra space between two genotypes. The seed yield magnitude was recorded from harvested plants from 3 m long rows in each plot, and then plot seed yield was converted to kg ha^{-1} for analysis.

Table 1. Name and origin of the studied lentil genotypes

Code	Name	Origin
G1	FLIP 97-1L	ICARDA
G2	FLIP 82-1L	ICARDA
G3	FLIP 92-15L	ICARDA
G4	FLIP 96-9L	ICARDA
G5	FLIP 92-12L	Jordan and Cyprus
G6	FLIP 96-4L	Chile and Syria
G7	ILL 7946	ICARDA
G8	ILL 6037	Canada and Argentina
G9	ILL6199	ICARDA and Chile
G10	Gachsaran	Iran

Individual ANOVA, Anderson-Darling normality test and Bartlett's test for homogeneity of residuals were done for each environment's dataset. A combined ANOVA was performed on the total dataset to partition out the effects of environment (E), genotype (G) and GE interaction. Genotype and replication was regarded as fixed factor while environment was regarded as random factor. The GE interaction of two-way classification data can often be identified if the data are stratified into homogeneous subsets. Four cluster methods, 2 new and 2 originally developed for investigating GE interaction, are used for this purpose. The 4 methods differ in the dissimilarity indices depending on whether the joint linear regression model or conventional ANOVA model is performed, and whether the similarity is specified with respect to the GE interaction alone or with respect to the genetic effect

and GE interaction combined. The link between the cluster analysis and conventional ANOVA provides a suitable way of determining the cutoff point based on the F-ratio of the smallest dissimilarity index and the error estimate. The cluster analysis of LIN and THOMPSON (1975) based on the intercept and slope of linear regression model (Method 1), the procedure of LIN (1982) based on the similarity of GE interaction (Method 4) and two new methods of Lin and Butler (1990) according to the slope of linear regression model (Method 2) and based on the similarity of G effect and GE interaction (Method 3) were used. Details of these clustering procedures are given in LIN and BUTLER (1990) and the statistical package Sl16 is used for all four methods of cluster analysis.

Table 2. Geographical properties of 5 test locations

Location	Code		Longitude Latitude	Rainfall (mm)	Soil Texture	Altitude (meter)
	Second year	First year				
Gonbad	GO1	GO2	55˚ 12´ E 37˚ 16´ N	367	Silty Clay Loam	45
Kermanshah	KE1	KE2	47˚ 19´ E 34˚ 20´ N	455	Clay Loam	1351
Ilam	IL1	IL2	46˚ 36´ E 33˚ 47´ N	350	Clay Loam	975
Gachsaran	GA1	GA2	50˚ 50´ E 30˚ 20´ N	460	Silty Clay Loam	710
Shirvan	SH1	SH2	58˚ 07´ E 37˚ 19´ N	267	Loam	1131

RESULTS AND DISCUSSION

The combined ANOVA was conducted to determine the effects of E, G and GE interaction on seed yield of lentil genotypes (Table 3). The effect of E and GE interaction were highly significant while the main effect of genotype was significant at 0.05 probability level. The GE interaction would greatly decrease the significance of the association between phenotypic and genotypic values (DEHGHANI *et al*., 2008). When GE interaction is due to unpredictable environmental factors such as rainfall, the plant breeder maybe improve widely adaptable genotypes. Nevertheless, the significant GE interaction is frequently reported, the linear model is not completely satisfactory (HILL *et al*., 1998; ANNICCHIARICO, 2010). However, since the environment effect was highly significant as well, it indicates to some extent further examination of yield stability parameters for each grouped test environments separately. Therefore, it seems that classifying of test environments through cluster analysis was essential.

The results of the joint linear regression model for both genotypes and environments are shown in Table 4. The pooled error estimate is 40525670.1 and 1351211.4 for genotypes and environments, respectively. These values are the sum of deviation variance from linear regression model of all studied variables and was

used to performing F-test for cutoff point determination. The coefficient of determination (R^2) values of the joint linear regression model ranged from 73.6 to 99.2% for genotypes and ranged from 7.8 to 61.1% for environments (Table 4). Therefore, it seems that genotypes with high R^2 values could be evaluated adequately via the joint linear regression model and the response of the genotypes to different environments is predictable (ANNICCHIARICO, 2010). In contrast, environments with low R^2 values could not be evaluated sufficiently through the joint linear regression model and the response of the environments to different genotypes is unpredictable.

Table 3. Combined analysis of variance for lentil performance trial yield data

SOV†	DF‡	Mean Squares
Environment (E)	9	17682339.1**
Replication/E	30	120655.0
Genotype (G)	9	369593.3*
GE	81	189553.6**
Error	270	51214.0

† Sources of variation

‡ Degrees of freedom

*, ** Significant at the 0.05 and 0.01 probability level, respectively.

The dissimilarity indexes and calculated F-test statistics of all clustering cycles are given in Table 5. The F-test statistic for method 1 of genotypes was significant in the cycle 9 where the dissimilarity index was 87461.3 (Table 5). In this step, genotypes G2, G8 and G9 were grouped with a cluster which containing other genotypes and so there was significant difference between them due to G and GE sources of linear regression model or intercept and slop parameters (Fig. 1A). According to dendogram Fig. 1A, there were two different genotypic groups; one group as the most responsive genotypes with high mean yield genotypes (G2, G8 and G9) which could be considered as the most favorable genotypes and the other group contain the other remained genotypes (the most stable genotypes with low mean yield or the most unstable genotypes with high mean yield). For improving the effectiveness of this method it has been indicated that most of the variation among genotypes is included in the between group component (Lin and Thompson, 1975). The values of the determination coefficient of linear regression model were high and so it can be concluded that using this clustering method is useful to some extent for this dataset. Applying the usual biometrical model as the linear regression model, it is assumed that the effects are independent of each other. This assumption is performed when regarding all the genotypes together and when no covariance exists between the effects of test environments and of GE interactions. Considering each genotype separately, however, this covariance may be different from zero and the linear

regression model coefficient is a standardized description of the mentioned covariance (YAN and TINKER, 2006; SABAGHNIA *et al.*, 2012).

Table 4. Linear regression parameters and regression analysis of variance statistics

Genotype	Intercept	Slope	SS Total	SS Reg.†	SS Res.‡	R^2
G1	1187.8	0.950	3906481.6	3588277.0	39775.5	91.9
G2	1145.3	1.171	5893758.1	5456418.9	54667.4	92.6
G3	989.3	0.948	3887440.1	3571707.4	39466.6	91.9
G4	997.2	1.000	4245991.6	3976120.4	33734.0	93.6
G5	1168.9	0.749	3032742.9	2233428.9	99914.3	73.6
G6	1153.1	1.024	4524032.9	4174595.4	43679.6	92.3
G7	1107.8	0.936	3708471.6	3487634.0	27604.8	94.0
G8	1200.2	1.179	5618083.6	5526371.2	11464.0	98.4
G9	1267.9	1.183	5609154.9	5564941.5	5526.6	99.2
G10	1002.5	0.861	3195546.5	2946175.4	31171.5	92.2
Environment						
E1	476.7	0.501	34122.1	20857.1	1658.1	61.1
E2	1752.9	1.156	614142.9	111034.5	62888.6	18.1
E3	742.2	0.729	173803.6	44140.9	16207.8	25.4
E4	1852.1	1.783	474476.9	264252.5	26278.1	55.7
E5	486.8	0.271	22195.6	6088.4	2013.4	27.4
E6	1133.9	0.616	135850.9	31578.2	13034.1	23.2
E7	2093.2	1.137	1381583.6	107360.3	159277.8	7.8
E8	791.9	2.578	1420226.9	552464.0	108470.4	38.9
E9	1640.9	1.567	347114.9	203976.4	17892.4	58.8
E10	249.4	-0.337	66812.4	9459.1	7169.2	14.2

†Linear regression model sum of squares

‡ Residual sum of squares

Table 5. The smallest dissimilarity index at each cluster step and the determination of the cutoff point in genotypes and environments clustering

Step	Method 1		Method 2		Method 3		Method 4	
	SDI†	F-test	SDI	F-test	SDI	F-test	SDI	F-test
Genotypes								
1	2866.0	0.07^{ns}	8.1	0.00^{ns}	5536.2	0.54^{ns}	6080.4	0.59
2	7589.8	0.20^{ns}	32.4	0.00^{ns}	8672.4	0.85^{ns}	6116.9	0.59
3	8554.8	0.22^{ns}	137.8	0.00^{ns}	8955.2	0.87^{ns}	7403.8	0.72
4	10051.7	0.26^{ns}	206.2	0.01^{ns}	12372.4	1.21^{ns}	12601.1	1.23
5	12526.1	0.32^{ns}	1207.9	0.03^{ns}	16689.4	1.63^{ns}	14663.6	1.43
6	18926.2	0.49^{ns}	5848.3	0.15^{ns}	21324.7	2.08**	16238.2	1.58
7	33076.1	0.85^{ns}	12844.4	0.33^{ns}	29325.9	2.86**	23352.2	2.28**
8	55833.5	1.44^{ns}	34300.3	0.89^{ns}	33421.6	3.26**	24843.3	2.42**
9	87461.3	2.26**	82580.5	2.13**	51892.8	5.07**	47398.5	4.62**
Environments								
1	1357.1	0.03^{ns}	15.4	0.00^{ns}	2110.5	0.2^{ns}	2288.3	0.22^{ns}
2	32777.4	0.79^{ns}	524.7	0.01^{ns}	22696.4	2.2**	5194.9	0.51^{ns}
3	60043.5	1.45^{ns}	1078.5	0.03^{ns}	33707.6	3.3**	7396.2	0.72^{ns}
4	77246.3	1.86^{ns}	1948.1	0.05^{ns}	42329.2	4.1**	8446.5	0.82^{ns}
5	97900.3	2.36**	3188.0	0.08^{ns}	42685.7	4.2**	12671.6	1.24^{ns}
6	189822.0	4.58**	8397.1	0.20^{ns}	74995.1	7.3**	16085.6	1.57^{ns}
7	277820.0	6.70**	14873.0	0.36^{ns}	92168.0	9.0**	22698.7	2.22**
8	520037.4	12.53**	28962.8	0.70^{ns}	121048.4	11.8**	33635.1	3.28**
9	223903.0	53.97**	57792.8	1.39^{ns}	484685.3	47.3**	47397.9	4.63**

† SDI, smallest dissimilarity index

*, ** and ^{ns} Significant at the 0.05 and 0.01 probability level and non-significant, respectively.

The F-test statistic of method 2 similar to the method 1 for genotypes was significant in the cycle 9 where the dissimilarity index was 82580.5 (Table 5). In this step, genotypes G2, G8 and G9 were grouped with the cluster of the other remained genotypes and so there was significant difference between these two groups due to GE source of linear regression model or slop parameter (Fig. 1B). Like to method 1, the dendogram of Fig. 1B showed that there were two different genotypic groups; one cluster with genotypes G2, G8 and G9 and one cluster with the other remained genotypes. In other word, the most favorable genotypes were distinguished from the unfavorable genotypes. Due to the high values of the R^2 of linear regression model, it could be concluded that using this clustering method is useful. Results of these two methods were similar and effective in clustering genotypes in MET and regarding yield stability. The linear regression model major contributes to model an environment effect using an environmental index and clustering procedures using this strategy was developed by LIN and THOMPSON (1975) and LIN and BUTLER (1990) to group genotypes for similarity of GE+G or GE interaction. KARIMIZADEH

et al. (2006) showed that this cluster analysis based on regression analysis has good ability for distinguish of similarities and dissimilarities. Regression models of MET data analysis have Type II stability concept and a genotype is considered to be stable if its response to environment is parallel to the mean response of all genotypes in the trial and this type of stability beside Type III are very popular among plant breeders (MOHAMMADI *et al*., 2012).

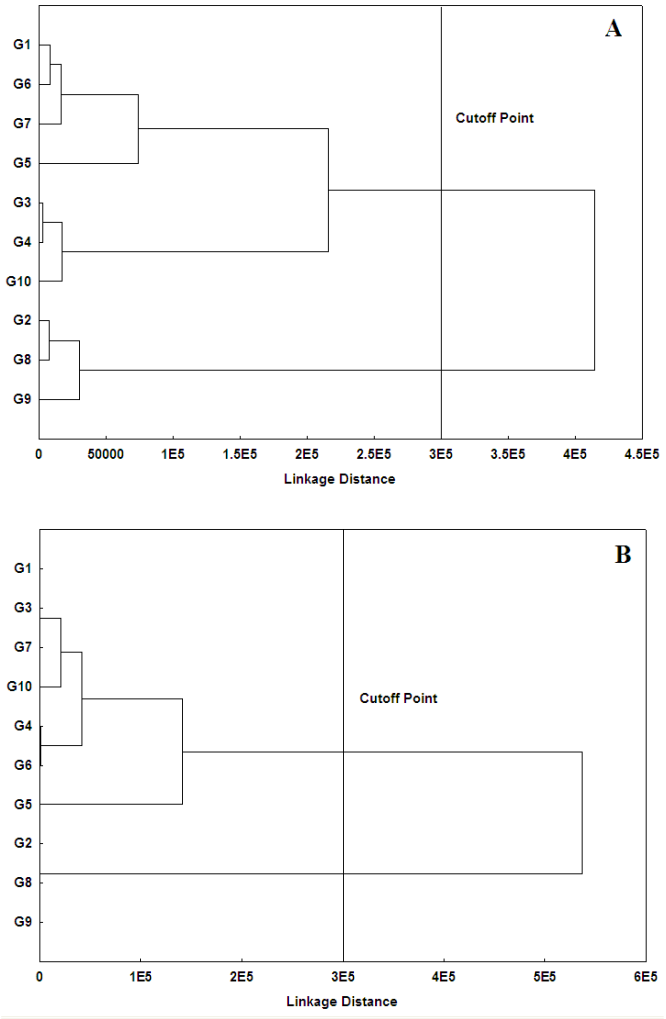
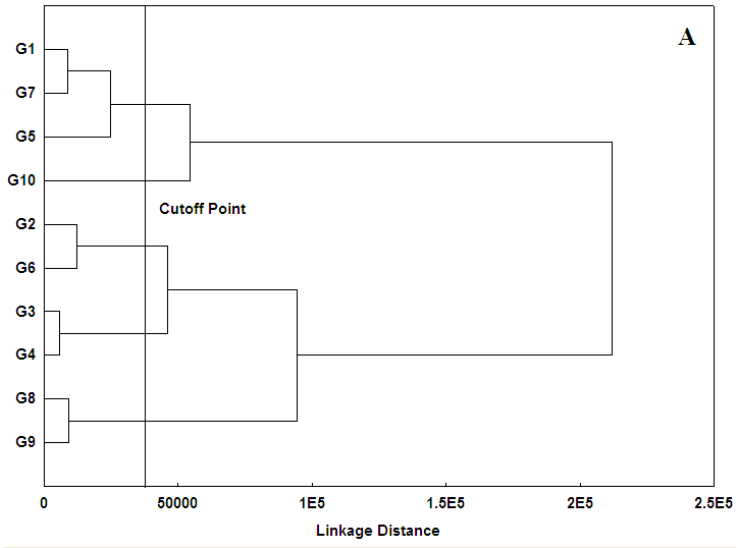


Figure 1. Dendrogram of dissimilarity indices based on (A) line slope and intercept and (B) line slope of regression model for 10 lentil genotypes.



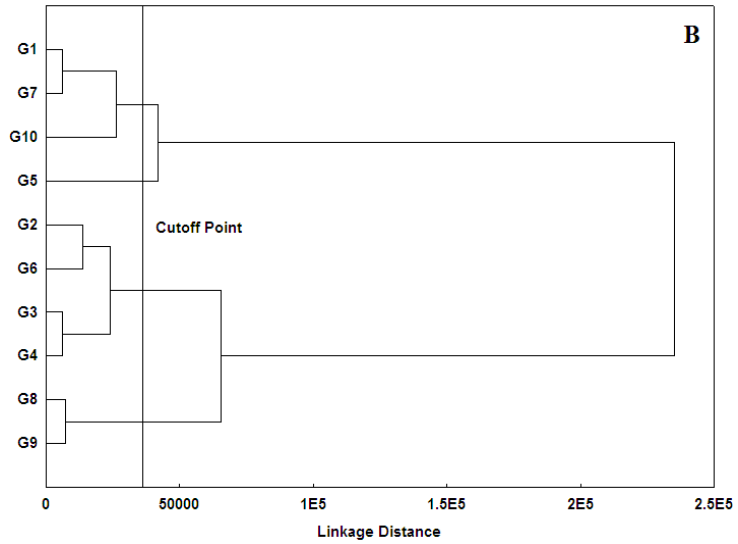


Figure 2. Dendrogram of dissimilarity indices based on (A) genotype plus GE interaction, (B) GE interaction of ANOVA model for 10 lentil genotypes.

In method 3, LIN and BUTLER (1990) introduced a dissimilarity index using G and GE interaction in terms of distance adjusted for the average effects in ANOVA table. The numerical results of the genotypes clustering process (dissimilarity index of each step and F-test statistic) are given in Table 5. According to the obtained results, F-test statistic was significant in cycle 6 where the dissimilarity index was 21324.7 and in this step, genotypes G2 and G6 were grouped with genotypes 3 and 4. Thus, there was significant difference between these clusters based on G and GE sources of ANOVA model. It should be mentioned that, the cutting threshold or cutoff point was fixed 20% of pooled error in combined ANOVA (ROBERT, 1997) and so G and GE interaction within clusters of genotypes must be less than 20% of total variation. According to the dendogram of method 3 (Fig. 2A), there were five different genotypic groups consist on: genotypes G1, G5, G7 and G9 as one group; G2 and G6 as one group; G3 and G4 as one group; G8 and G9 as one group; and G10 as a single group.

The dissimilarity index of method 4 for studied genotypes is defined in terms of distance adjusted for the average effects of genotypes and it to be equivalent to within group MS of GE interaction in ANOVA model. According to the dissimilarity index of each clustering cycle and its related F-test statistic (Table 5), and similar to method 3, 20% of pooled error in combined ANOVA was used to determination of cutoff point. The F-test statistic was significant in cycle 7 where the dissimilarity index was 23352.2 and in this cycle genotypes G5 were grouped with a cluster which containing genotypes G1, G7 and G10. Thus, there was significant difference between these clusters based GE interaction sources of analysis of variance model. The visualization of this groping method via dendogram and position of the significant cutoff point (Fig. 2B) indicated that there were four different genotypic groups including cluster 1; genotypes G1, G7 and G10, cluster 2; genotype G5, cluster 3; genotypes G2, G3, G4 and G6, and cluster 4; genotypes G8 and G9. LIN (1982) reported the genotypes clustering based on similarity of GE interaction is as an effective analytical tool for investigating MET data, provides a logical base to compare the individuals within clusters by their average effect. The most prominent findings according to Fig. 2A are: genotypes G8 and G9 with the relatively high mean yield and high stability were grouped as a same cluster; genotype G5 with the relatively high mean yield and low stability was grouped as individual cluster; genotypes G1, G7 and G10 with the relatively low mean yield and moderate stability were grouped as a same cluster. Similar to method 3, the genotypes clustering based on ANOVA and similarity of GE interaction showed huge variation among lentil genotypes.

The clustering of test environments based on method 1 indicated that the F-test statistic was significant in the cycle 5 where the dissimilarity index was 97900.3 (Table 5). In this step, environment KE2 was grouped with a cluster which containing GA1, GA2 and KE1 environments and so there was significant difference between them due to G and GE interaction of linear regression model (intercept and slop parameters). According to dendogram Fig. 3A, there were five different environment groups. The first and second years of Gachsaran (GA1 and GA2), Ilam

(IL1 and IL2) and Shirvan (SH1 and SH2) were grouped in same clusters while two years of Gonbad and Kermanshah were grouped in different clusters (Fig. 3A). The values of the determination coefficient of linear regression model were relatively moderate or low and so it could be concluded that using this clustering method is not more useful. The test environments grouping based on method 2 showed that the F-test statistic was not significant in any cycles (Table 5). Thus, there was not significant difference between test environments due to GE interaction of linear regression model (linear slop). According to dendogram Fig. 3B, there were not any different environmental groups and so all test environments were similar to each other. It could be mentioned that due to moderate or low values of R^2 in the linear regression model, this clustering procedure in not suitable. The joint linear regression model attempts to quantify an environment effect using an environmental index. LIN and THOMPSON (1975) and LIN and BUTLER (1990) developed types of cluster methods to group genotypes or environments for similarity of GE interaction plus G effect or only GE interaction via linear regression model.

The grouping of test environments according to dissimilarity index using G and GE interaction of ANOVA (method 3) indicated that the related F-test statistic was significant in cycle 2 where the dissimilarity index was 22696.4. In this cycle, environments SH1 and GO1 were grouped with environment SH2. Thus, there was significant difference between these clusters based on G and GE sources of ANOVA model. According to the dendogram of method 3 (Fig. 3A), there were eight different environmental groups. The dissimilarity index of method 4 for test environments is defined in terms of GE interaction in ANOVA model. According to the dissimilarity index of each clustering cycle and its related F-test statistic (Table 5), the cycle 7 was significant where the dissimilarity index was 22698.7. In this cycle IL1 was grouped with a cluster which containing environments GA1, GA2, GO1, GO2, SH1, SH and IL2. Thus, there was significant difference between these groups based GE interaction sources of analysis of variance model. The visualization of this groping method via dendogram and position of the significant cutoff point (Fig. 4B) indicated that there were three different environment groups.

There are several clustering methods for classification of genotypes or test environments (LIN, 1982) and whatever method is selected, the question concerning the determination of cutoff point is raised. The suitable link between the cluster analysis and the ANOVA in the clustering procedures provides a comfortable way of determining the cutoff point based on the F-test. The all mentioned clustering methods (LIN and THOMPSON, 1975; LIN, 1982; LIN and BUTLER, 1990) enable plant breeders to describe the dataset into homogeneous subsets. These procedures have been reported to be useful not only for two-way data classification, but also for multi-way classification data (SABAGHNIA *et al*., 2012). In this investigation and considering R^2 values of linear regression model, it seems that methods 1 and 2 were suitable for clustering of genotypes while methods 3 and 4 were suitable for clustering of environments. LIN and BUTLER (1990) suggested that for grouping variables, the similarity of both G and GE may be more suitable; but for grouping environments, the similarity of GE alone is more proper. Therefore, it seems that the

results of method 1 (intercept and slope of regression) are valid for genotypes grouping while results of method 4 (GE interaction of ANOVA model) are valid for environments grouping.

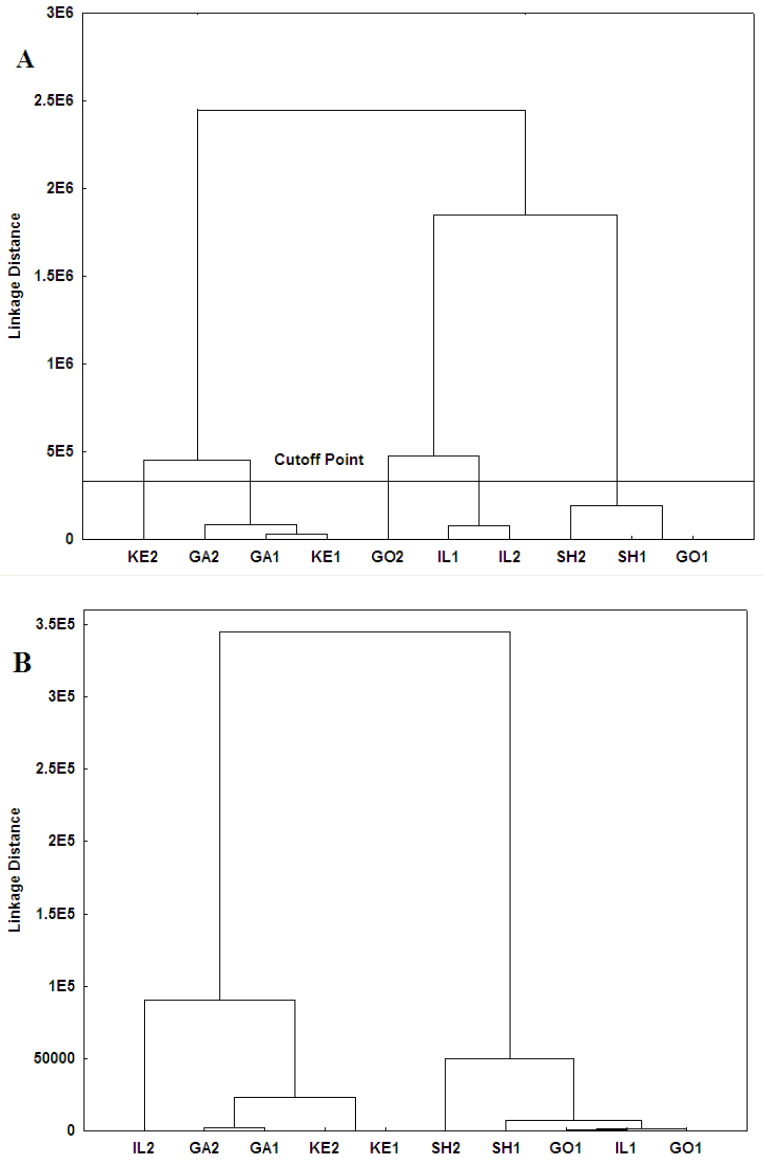


Figure 3. Dendrogram of dissimilarity indices based on (A) line slope and intercept and (B) line slope of regression model for 10 test environments.

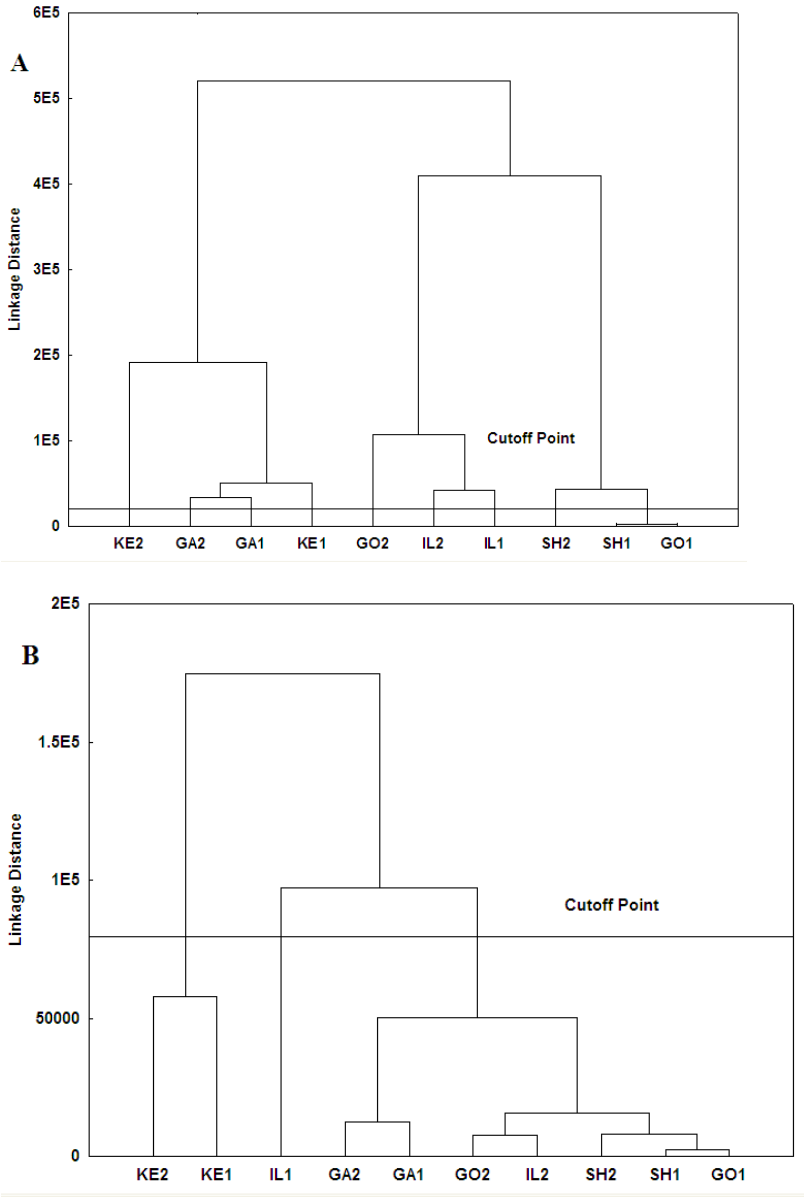


Figure 4. Dendrogram of dissimilarity indices based on (A) genotype plus GE interaction, (B) GE interaction of ANOVA model for 10 test environments.

Therefore, there were eight different environmental groups which indicate considerable differences among test environments and presence high GE interaction. The relative contributions GE interaction effects found in this research is similar to those found in other MET studies in rain-fed environments (BERTERO *et al*., 2004; SABAGHNIA *et al*. 2008). The GE interaction makes difficult to select the best performing and most stable genotypes and reduces the progress from selection in plant breeding programs (YAN and KANG, 2003; YAN FREGEAU-REID, 2008). Finally, the most responsive genotypes with high mean yield genotypes are G2 (1145.3 kg ha^{-1}), G8 (1200.2 kg ha^{-1}) and G9 (1267.9 kg ha^{-1}) and could be recommended as the most favorable genotypes. Such a similar outcome could be applied in the future to delineate predictive, more rigorous recommendation strategies as well as to help define stability concepts for recommendations of new lentil genotypes and other crops in the other areas of the world.

ACKNOWLEDGEMENTS

Sincere gratitude goes to Iran's Research and Education Organization (AREO) and its Agricultural Research Stations for providing plant materials, experimental locations, and technical assistance.

Received July 30th, 2012
Accepted November 06th, 2012

REFERENCES

ANNICCHIARICO, P., N. HARZIC, A.M. CARRONI (2010): Adaptation, diversity, and exploitation of global white lupin (*Lupinus albus* L.) landrace genetic resources. Field Crops Research *119*: 114-124.

BERTERO, H.D., A.J. DE LA VEGA, G. CORREA, S.E. JACOBSEN, A. MUJIC (2004): Genotype and genotype-by-environment interaction effects for grain yield and grain size of quinoa (*Chenopodium quinoa* Willd.) as revealed by pattern analysis of international multi-environment trials. Field Crops Res. *89*, 299–318.

DEHGHANI, H., S.H. SABAGHPOUR, N. SABAGHNIA (2008): Genotype × environment interaction for grain yield of some lentil genotypes and relationship among univariate stability statistics. Span. J. Agric. Res. *6:* 385–394.

GAUCH, H.G., H.P. PIEPHO, P. ANNICCHIARICO (2008): Statistical Analysis of Yield Trials by AMMI and GGE: Further Considerations Crop Sci. *48*: 866–889.

HILL, J., H.C. BECKER, P.M.A. TIGERSTEDT (1998): Quantitative and ecological aspects of plant breeding. Chapman and Hall. London.

KANG, m.s. (1998): Using genotype-by-environment interaction for crop cultivar development. Adv. Agron. 62, 199–252.

KARIMIZADEH R., M. MOHAMMADI, N. SABAGHNIA, M.K. SHEFAZADEH (2012a): Genotype × environment interaction and yield stability analysis of new improved bread wheat genotypes. Turk. J. Field Crops *17:* 67–73.

KARIMIZADEH R., M. MOHAMMADI, N. SABAGHNIA, M.K. SHEFAZADEH (2012b): Using different aspects of stability concepts for interpreting genotype by environment interaction of some lentil genotypes. Aust. J. Crop Sci. *6*: 1017–1023.

KARIMIZADEH, R., H. DEHGHANI, Z. DEHGHANPOUR (2006): Using Cluster Analysis for Stability of Maize Hybrids. J. Crop Produc. Process. *10:* 337–348.

MOHAMMADI, M., R. KARIMIZADEH T. HOSSEINPOUR M. KALATEHARABI H. KHANZADEH N. SABAGHNIA (2012): Analysis of genotype, environment and genotype × environment interaction in bread wheat in warm rainfed areas of Iran. Crop Breed. J. *2*: 63–70.

MOHEBODINI, M., H. DEHGHANI, S.H. SABAGHPOUR (2006): Stability of performance in lentil (*Lens culinaris* Medik.) genotypes in Iran. Euphytica *149*: 343–352.

ROBERT, n. (1997): Structuring genotype × environment interaction for quality traits in bread wheat, in two multi-location series of trials Euphytica *97:* 53–66.

SABAGHNIA, n. (2012): Multivariate statistical analysis of genotype × environment interaction in multi-environment trials of breeding programs. Agric. Fores. *56:* 19–38.

SABAGHNIA, N., H. DEHGHANI, S.H. SABAGHPOUR (2006): Nonparametric methods for interpreting genotype × environment interaction of lentil genotypes. Crop Sci. *46:* 1100–1106.

SABAGHNIA, N., H. DEHGHANI, S.H. SABAGHPOUR (2008): Graphic analysis of genotype × environment interaction of lentil yield in Iran. Agron. J. *100:* 760–764.

SABAGHNIA, N., R. KARIMIZADEH, M. MOHAMMADI (2012): Model selection in additive main effect and multiplicative interaction model in durum wheat. Genetika *44:* 325–339.

SARKER, A., A. AYDOGAN, S. CHANDRA, M. KHARRAT S.H. SABAGHPOUR (2009): Genetic enhancement for yield and stability. p. 102–120. *In* W. ERSKINE, F. MUEHLBAUER, A. SARKER, B. SHARMA (ed.) The lentil: Botany, production and uses. CAB Int., Wallingford, UK.

SARKER, A., W. ERSKINE (2006): Recent developments in the ancient lentils. J. Agric. Sci. *144:* 19–29.

STEFANOVA, K.T., B. BUIRCHELL (2010): Multiplicative mixed models for genetic gain assessment in Lupin breeding. Crop Sci. *50:* 880–891.

YAN, W., J. FREGEAU-REID (2008): Breeding line selection based on multiple traits. Crop Sci.48:417−423.

YAN, W., J.B. HOLLAND (2010): A heritability−adjusted GGE biplot for test environment evaluation. Euphytica *171:* 355−369.

YAN, W., M.S. KANG (2003): GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, FL.

YAN, W., M.S. KANG, B. MA, S. WOODS, P.L. CORNELIUS (2007): GGE Biplot vs. AMMI Analysis of Genotype-by-Environment Data. Crop Sci. *47:* 643−653.

YAN, W., N.A. TINKER (2006): Biplot analysis of multi-environment trial data: principles and applications. Can. J. Plant Sci. *86:* 623–645.

GRUPISANJE GENOTIPOVA I USLOVA ŽIVOTNE SREDINE KORIŠĆENJEM KLASTER METODA KOJE SE ODNOSE NA INTERAKCIJU GENOTIP x ŽIVOTNA SREDINA U RAZLIČITIM USLOVIMA SREDINE

Naser SABAGHNIA[1*], Rahmatollah KARIMIZADEH[2], Mohtasham MOHAMMADI[2]

[1] Odelenje za poljprivredu i oplemenjivanje biljaka, Poljoprivredni fakultet, Maragheb
Univerzitet, Maragheh, Iran.
[2] Dryland Poljoprivredni istraživački Institut (DARI), Gachsaran, Iran

Sočivo (*Lens culinaris* Medik.) je značajan izvor protein i ugljenih hidrata u hrani stanovništva zemalja u razvoju a popularno je u razvijenim zemljama kao komponenta zdrave hrane. Deset genotipova sočiva je testirano na prinos u pet različitih uslova gajenja u toku dve uzastopne godine u cilju klasifikacije genotipova prema stabilnosti prinosa. Prinos semena je varirao od 989,3 do 1367,00 kg ha^{-1} a koeficijent linearne regresije je varirao od 0,75 – 1.18. Kombinovana analiza variance pokazuje da su efekti okoline (E) i interakcija genotipa i okoline (GE) bile visoko značajne dok je nivo statističke značajnosti glavnog efekta genotipa (G) bio 0.05. Korišćene su četiri različite metode grupisanja genotipova i okoline (klaster analiza) . Prema dobijenim dendrogramima grupisanja rezultata analize regresije genotipova dobijene su dve različite grrupe genotipova zasnovane na rezultatima ispitivanja genotipa (G) plus genopip x okolina (GE) i samo GE (genopip x okolina). Dendogrami dobijeni ANOVA metodom analize ukazuju na 5 grupa zasnovanih na G i GE i četiri grupe zasnovane na rezultatima ispitivanja GE. Also, the dendograms of ANOVA methods indicated 5 groups based on G and GE sources and 4 groups based on GE sources. Prema dendogramima metoda analize regresije okoline utvrđeno je 5 različitih grupa zasnovanih na G plus GE dok rezultati ANOVA metoda ukazuje na 9 grupazasnovanih na G I GE I 3 grupe zasnovane na analizi GE. Pomenute grupe su određene i korišćenjem F- testa, empirijskog kriterijuma za grupisanje (klastering). Genotipovi sa visokim prosečnim prinosom su G2 (1145,3 kg ha^{-1}), G8 (1200.2 kg ha^{-1}) I G9 (1267.9 kg ha^{-1}) mogu da se preporuče kao najbolji genotipovi za gajenje.

Primljeno 30. VII. 2012.
Odobreno 06. XI. 2012.