

DOI 10.2478/v10129-011-0069-z

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USING ADDITIVE MAIN EFFECT AND MULTIPLICATIVE INTERACTION
MODEL FOR EXPLORATION OF YIELD STABILITY IN SOME LENTIL
(*LENS CULINARIS* MEDIK.) GENOTYPES

ABSTRACT

The additive main effect and multiplicative interaction (AMMI) analysis has been indicated to be effective in interpreting complex genotype by environment (GE) interactions of lentil (*Lens culinaris* Medik.) multi-environmental trials. Eighteen improved lentil genotypes were grown in 12 semiarid environments in Iran from 2007 to 2009. Complex GE interactions are difficult to understand with ordinary analysis of variance (ANOVA) or conventional stability methods. Combined analysis of variance indicated the genotype by location interaction (GL) and three way interactions (GYL) were highly significant. F_{GH1} and F_{GH2} tests indicated the five significant components; F_{Ratio} showed three significant components and F-Gollob detected seven significant components. The RMSPD (root mean square predicted difference) values of validation procedure indicated seven significant components. Using five components in AMMI stability parameters (EVFI, SIPCFI, AMGEFI and DFII) indicated that genotypes G5 and G6 were the most stable genotypes while considering three components in of AMMI stability parameters (EVFII, SIPCFII, AMGEFII and DFII) showed that genotypes G8 and G18 were the most stable genotypes. Also genotypes G2, G5 and G18 were the most stable genotypes according to AMMI stability parameters which calculated from seven components (EVFIII, SIPCFIII, AMGEFIII and DFIII). Among these stable genotypes, only genotypes G2 ($1365.63 \text{ kg} \times \text{ha}^{-1}$), G11 ($1374.13 \text{ kg} \times \text{ha}^{-1}$) and G12 ($1334.73 \text{ kg} \times \text{ha}^{-1}$) had high mean yield and so could be regarded as the most favorable genotype. These genotypes are therefore recommended for release as commercial cultivars.

Key words: adaptation; AMMI stability parameters; genotype by environment (GE) interactions

INTRODUCTION

The differential response of a genotype for yield across environments is defined as the genotype by environment (GE) interaction which is an important component of plant breeding programs. Breeding for yield stability is done with repetitive field testing and selection of genotypes that performs at or near the top of the individual trials conducted across a range of locations and years (Gauch, 2006; Crossa *et al.*, 2010). Lentil (*Lens culinaris* Medik.) breeders are aware of differences in yield performance among improved genotypes, both location and yearly, indicating the presence of genotype by environment (GE) interactions. Large magnitude of GE interactions slow down selection progress in breeding programs and makes genotype recommendations difficult in multi-environmental trials (Goyal *et al.*, 2011). Most of the plant breeders desire stable genotypes with good yield performance under various conditions of the target regions. Many statistical approaches have been used to analyze GE interaction and assessing yield stability. Exploring GE interaction can help plant breeders to determine whether to develop genotypes specific to an environment or for a range of environments (Gauch *et al.*, 2008).

Williams (1952) indicated the importance of principal component analysis (PCA) in genotypic performances evaluation. Multiplicative approaches using PCA have been used to determine the number of dimensions needed to study the variation pattern (Yan and Tinker, 2006). This approach would be more beneficial than linear regression model when deviations from regression are considerable. Although each statistical procedure gave an indication of genotype stability, most plant breeders preferred to use more than one procedure for accurate assessment of yield stability (Yan *et al.*, 2011). Considering the three conventional methods for GE interaction exploration, ANOVA fails to detect a significant interaction component, PCA fails to identify and separate the significant effects of G and E, linear regression models account for only a small portion of the GE interaction variance (Zobel *et al.*, 1988). The additive main effect and multiplicative interaction (AMMI) model is proposed for achieving these targets and integrates both ANOVA and PCA approaches into a unique procedure.

Using AMMI model is more useful in the analysis of multi-environmental trials, because it provides an analytical tool of diagnosing other models as sub cases when these are better for particular data sets (Gauch and Zobel, 1996). Also, AMMI model clarifies the GE interaction and summarizes patterns of genotypes and environments (Zobel and Gauch, 1988). AMMI model is used to improve the accuracy of yield estimates in two-way dataset. AMMI model has received attention in dealing with GE interactions and quantifying the contribution of a genotype variation to GE interaction variance explained is important to know the yield stability of

genotype and to determine which genotype performs well in which environment(s). The significant number of AMMI model interaction PCs and their related components were allocated following the F-Gollob approach (Gollob, 1968), F_{Ratio} Cornelius *et al.* (1992), and F_{GH1} and F_{GH2} tests (Cornelius, 1993) has shown that the degrees of freedom in the conventional AMMI model are incorrect. The proposed tests require values for the expectation and standard deviation of the largest eigenvalue of a central Wishart matrix of the specific dimension and degrees of freedom (Cornelius, 1980). Also, RMSPD (root mean square predicted difference) was proposed as validation procedure for fitted model and to determine the number of significant interaction PCAs (Gauch and Zobel, 1988).

Zobel (1994) introduced two AMMI stability parameters (EV1 and EVF) as averages of the squared eigenvector values. Sneller *et al.* (1997) suggested AMGE1, AMGEF, SIPC1 and SIPC2 stability parameters of AMMI model to describe the contribution of environments to GE interaction. Purchase (1997) proposed a stability parameter called AMMI stability value (ASV) derived from first two interaction PCAs of AMMI model to quantify and rank genotypes according their yield stability. The Euclidean distance from the origin of significant interaction PCAs axes as D parameter was suggested by (Annicchiarico, 1997). Since the interaction PC axes are orthogonal, they add pieces of information uncorrelated to each other and could be reflecting the different aspects of GE interaction and yield stability. The objectives of the this investigation have been (i) application different F-tests approaches AMMI model (ii) using seventeen stability parameters of the AMMI model for the yield stability and adaptability of improved lentil genotypes, (iii) and explore the advantages and disadvantages of different AMMI stability parameters in selecting more stable and better-adapted genotypes.

MATERIALS AND METHODS

In this investigation the yield performances of 18 lentil genotypes across 12 environments (four locations across three years), including rain-fed environments was studied. The individual experiments were performed in the 2007-2008, 2008-2009 and 2009-2010 growing seasons in different locations: Gorgan, Kermanshah, Gachsaran and Shirvan. Gorgan in the north-east of Iran is characterized by semi-arid conditions with sandy loam soil. Kermanshah in the west of Iran is characterized by semi-arid conditions with clay loam soil. Gachsaran, in southern Iran, is relatively arid and has silt loam soil. Shirvan in the north-east of Iran is characterized by moderate conditions, relatively high rainfall and have clay loam soil. 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 and mean yield of the 18 lentil genotypes, studied in 4 locations

Code	Location	Altitude [m]	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

The investigation was carried out in Randomized Complete Block Design (RCBD) with 4 replications. Sixteen improved lentil genotypes with two cultivars (Gachsaran and Cabralia) were analyzed. Sowing was carried out manually in rows 25 cm apart. The seeds were sown in 1 × 4 m plots consisting of 4 rows. The planted plot size was 4 m² and the harvested plot size was 1.75 m² (two 3.5 m rows at the center of each plot). Plots were not irrigated because the lentil is grown in rain-fed conditions. Control by hand weeding was carried out twice when the weed density was high, in the pre-flowering and post-flowering stages. The plots were fertilized with 20 kg N × ha⁻¹ and 80 kg P₂O₅ × ha⁻¹ at planting.

The obtained dataset of each trail was analyzed as RCBD (data and results not presented) to plot residuals and identify outliers. Bartlett's test was used to determine the homogeneity of variances among experiments to determine the validity of the combined analysis of variance. A combined analysis of variance was done from the mean data from each environment, to create the means data for the different statistical analyses methods. The model AMMI model which is used to investigate the GE interactions is:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^N \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij}$$

Where Y_{ij} is the yield of the i th genotype in the j th environment; μ is the grand mean; g_i and e_j are the genotype and environment deviations from the grand mean, respectively; λ_n is the eigenvalue of the IPC analysis axis n ; γ_{in} and δ_{jn} are the genotype and environment eigenvectors for axis n ; n is the number of principal components retained in the model and ρ_{ij} is the error term.

Different F-tests including F-Gollob (Gollob, 1968), F_{Ratio} (Cornelius *et al.*, 1992), F_{GH1} and F_{GH2} tests (Cornelius, 1993) were used to determine of significant numbers of interaction PCs in AMMI model. The validation procedure used to determine the number of interaction PCAs to retain in the AMMI method used 1000 validation runs, each using three replications to build

a model and one replication to validate the model. The AMMI model that produced the minimum root mean square predicted difference (RMSPD; Gauch and Zobel, 1988) was selected. RMSPD calculations for AMMI were performed by the open source software MATMODEL Version 3.0 (Gauch, 2007). Zobel (1994) suggested the two EV1 and EVF stability parameters of AMMI according to the below relation:

$$EV = \sum_{n=1}^N \gamma_{in}^2 / n$$

In this formula N=1 for EV1; for EVF, N was the number of IPC that were retained in the AMMI procedure via F test. The AMGE1 and AMGEF parameters according to Sneller *et al.* (1997) are expressed as:

$$AMGE = \sum_{n=1}^N \sum_{g=1}^M \lambda_n \gamma_{in} \delta_{jn}$$

Where M is the number of environments; for $AMGE1$, N was one, for $AMGEF$, N was the number of IPC which were significant. The lower the IPC scores, the more stable a genotype is to environments and so $SIPC1$ and $SIPCF$ stability parameters of AMMI are sums of the absolute value of the IPC scores for each genotype.

$$SIPC = \sum_{n=1}^n \lambda_n^{0.5} \gamma_{in}$$

In this equation N=1 for $SIPC1$; for $SIPCF$, N was the number of PC that were retained in the AMMI procedure via F test. Another stability parameter of AMMI according to the below equation was proposed by Annicchiarico (1997).

$$D = \sqrt{\sum_{n=1}^N (\lambda_n \gamma_{in})^2}$$

where for $D1$, N was one, for DF , N was the number of IPC which were significant. AMMI's stability value (ASV) was calculated using as suggested by Purchase (1997):

$$ASV = \sqrt{\frac{SSIPC}{SSIPC} \frac{1}{2} (PC 1)^2 + (PC 2)^2}$$

Where, *ASV* is the AMMI's stability value, SS, sum of squares, IPC1, interaction of principal component analysis one, IPC2, interaction of principal component analysis two. The AMMI stability parameters were compared using their ranks for each genotype via calculating Spearman's rank correlation. All analyses were performed using the statistical package Genstat release 12.0 (Genstat, 2010) and SAS release 9.1 (SAS, 2004).

RESULTS

Analysis of variance was conducted to determine the effects of year, location, genotype, and interactions among these factors, on grain yield of lentil genotypes. The main effects of years (Y) and locations (L) were not significant, but their interactions ($Y \times L$) were highly significant (results are not shown). Therefore we combined Y and L into macro environment (E) which would be more meaningful and accurate (Table 2). The main effect of environment (E) and genotype (G) were significant ($P < 0.01$), and the genotype by environment interaction ($G \times E$) was highly significant ($P < 0.01$). (Table 2). The high significance of GE interactions is indicating the studied genotypes exhibited both crossover and non-crossover types of GE interaction. Usually grain yield indicate important sources of genetic variation attributed to GE interactions (Gauch and Zobel, 1996). Complexity of grain yield is a result of diverse processes that occur during plant development. The relative large contributions of GE interaction effects in grain yield of lentil which 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; Sabaghnia *et al.*, 2008a).

Table 2

Combined ANOVA of lentil performance trial yield data

Source	DF	Mean Squares
Environment (E)	11	5105886.8**
R (E)	36	38152.0 ^{ns}
Genotype (G)	17	320003.0**
G×E	187	97097.7**
Error	612	31713.0 ^{ns}

** , * and ^{ns}, respectively significant at the 0.01 and 0.5 probability level and non-significant

F_{GH1} and F_{GH2} tests (Cornelius, 1993) were used to measure significant of interaction PCs components and indicated that the first four components were significant at the 0.01 probability level and the fifth component was significant at the 0.05 probability level (Table 3). Results of F_{Ratio} (Cornelius *et al.*, 1992) showed that only three interaction PCs components were significant at the 0.01 probability level while based on F-test Gollob

(1968), seven interaction PCAs components were significant. The validation procedure and RMSPD values indicated that similar to F-test Gollob (1968), seven interaction PCAs components were significant and so AMMI7 is the best model for interpreting GE interaction and yield stability in this dataset (Table 3). Considering different numbers of significant interaction PCAs (5, 3 and 7), different stability parameters of AMMI (EVF, AMGEF, SIPCF and DF) were calculated. Like the results obtained from AMMI models used in multi-environmental trials of lentil (Sabaghnia *et al.*, 2008b) or other crops like soybean (Zobel *et al.*, 1988), the AMMI model used in the this investigation showed a more complex interaction which required as many as seven interaction PCAs.

Table 3

Computation of different F-tests and cross validation for interaction principal components of AMMI model

Components	U ₁	U ₂	V ₁	V ₂	F _{GH1}	F _{GH2}	F _{Ratio}	F _{Gollob}	RMSPD
IPC1	46.50	6.96	30483.11	33902.44	3.396**	3.407**	2.589**	5.82**	215.63
IPC2	42.65	6.76	27793.09	31516.44	2.653**	2.661**	2.228**	4.50**	214.90
IPC3	38.79	6.55	25133.08	29153.6	2.544**	2.552**	1.801**	4.27**	210.13
IPC4	34.94	6.32	22501.85	26802.41	1.823**	1.829**	1.515 ^{ns}	3.01**	209.37
IPC5	31.08	6.08	19897.77	24449.24	1.653*	1.658*	1.199 ^{ns}	2.69**	207.36
IPC6	27.21	5.81	17318.52	22077.27	1.328 ^{ns}	1.332 ^{ns}	0.313 ^{ns}	2.11**	206.30
IPC7	23.33	5.52	14760.47	19664.93	1.180 ^{ns}	1.184 ^{ns}	0.166 ^{ns}	1.78*	<u>204.57</u>
IPC8	19.43	5.19	12217.22	17183.03	0.535 ^{ns}	0.537 ^{ns}	0.107 ^{ns}	0.80 ^{ns}	206.90

U₁, U₂, V₁ and V₂ are computed by approximations for calculating F_{GH1} and F_{GH2} according to Cornelius (1980) and Cornelius (1993).

RMSPD, the root mean square prediction differences in cross validation, the minimum value of RMSPD is underlined

The values of the EV1, SIPC1, AMGE1 and D1 parameters for each genotype could be useful in identifying its stability in AMMI procedure (Table 4). The genotypes G3, G5 and G6 had the lowest absolute values of stability parameters and so could be considered as the most stable genotypes. The most unstable genotype according to the mentioned parameters, were G1, G9 and G17. The first interaction PCA (IPCA1) accounted 27.7 percent of GE interaction which it seems that this magnitude could not be sufficient for yield stability analysis. According to ASV parameter, genotypes G5, G8 and G18 were identified as the most stable genotypes while genotypes G9, G10 and G17 were recognized as the most unstable genotypes (Table 4). Considering first two IPCs in ASV parameter, 47.5% of GE interaction is used in yield stability analysis. The two IPCAs have different values and meanings and the ASV parameter using the Pythagoras theorem and to get estimated values between IPCA1 and IPCA2 scores to produce a balanced parameter between the two IPCA scores (Purchase, 1997).

Table 4

Mean yields in $\text{kg} \times \text{ha}^{-1}$ (MY) and some AMMI stability parameters estimates for lentil yields of 18 genotypes tested in 12 environments

Genotypes	MY	EV1	SIPC1	AMGE1	D1	ASV	EVFI	EVFII	EVFIII
G1	1418.71	0.1766	-14.07	-5.92	471.05	16.94	0.2970	0.1963	0.3854
G2	1365.63	0.0142	3.99	1.68	133.58	4.76	0.2583	0.0250	0.2622
G3	1287.27	0.0007	0.91	0.38	30.39	12.05	0.2700	0.1679	0.3510
G4	1272.04	0.0111	-3.52	-1.48	117.99	6.97	0.4451	0.0498	0.5135
G5	1324.42	0.0001	-0.38	-0.16	12.59	4.64	0.1405	0.0264	0.1848
G6	1096.52	0.0026	-1.72	-0.73	57.67	6.99	0.1193	0.0709	0.3972
G7	1304.13	0.0124	3.73	1.57	125.01	6.81	0.3607	0.3182	0.4435
G8	1191.13	0.0035	-1.97	-0.83	65.86	4.09	0.3302	0.0181	0.3337
G9	1329.46	0.2117	15.40	6.48	515.65	22.55	0.4722	0.4243	0.6589
G10	1187.94	0.0632	8.42	3.54	281.72	19.47	0.4362	0.4242	0.4919
G11	1374.13	0.0107	-3.46	-1.46	115.83	6.55	0.2214	0.0570	0.3381
G12	1334.73	0.0857	-9.80	-4.12	328.15	11.63	0.1795	0.1662	0.3294
G13	1292.13	0.0166	-4.31	-1.81	144.36	5.66	0.1906	0.0458	0.2362
G14	1401.85	0.0744	-9.13	-3.84	305.75	12.27	0.2735	0.2456	0.4709
G15	1307.33	0.0638	-8.46	-3.56	283.11	12.19	0.2141	0.1164	0.4201
G16	1272.38	0.0449	7.10	2.99	237.62	9.99	0.2647	0.2164	0.3618
G17	1203.25	0.2035	15.10	6.35	505.58	19.22	0.4660	0.4224	0.6278
G18	1314.60	0.0042	2.17	0.92	72.81	3.26	0.0606	0.0089	0.1934

The EVFI parameter based on five IPCs introduced genotypes G5, G6 and G18 as the most stable genotypes while genotypes G2, G8 and G18 were the most favorable genotypes according to the EVFII parameter which uses only first three IPCs (Table 5). The genotype G2 was as a high-yielding genotype among these stable genotypes. The EVFIII stability parameter according to seven IPCs identified genotypes G6, G13 and G18 as the most stable genotypes. According to explanation of different IPCs, EVFI parameter benefits from 84.9%, EVFII parameter benefits from 64.8% and EVFIII parameter benefits from 96.5% of total GE interaction variance. Regarding the complex nature of GE interaction in this research, it is reasonable to conclude that EVF stability parameter based on F-test results are more useful for selecting the most adaptable genotype. Similar to EVF parameter, various SIPC values based on different F-tests and RMSPD of validation procedure were computed (Table 5). Genotypes G5, G11 and G12 were the most favorable genotypes according to the SIPCFI parameter. Also, genotypes G8, G12 and G16 were the most stable genotypes based to the SIPCFFII statistic while genotypes G4, G5 and G18 were the most adaptable genotypes according to the SIPCFFIII parameter

(Table 5). The stable genotypes G11 and G12 had good mean yield and so can be regarded as the most favorable genotypes with both stability and yield. The EVF and SIPCF parameters differ by standardization and indicate the general pattern of GE interaction using IPCs-based parameters of AMMI model which are attributable to genotypes.

Table 5
Some other AMMI stability parameters estimates for lentil yields of 18 genotypes tested in 12 environments

Genotypes	SIPCFI	SIPCFII	SIPCFIII	AMGEFI	AMGEFII	AMGEFIII	DFI	DFII	DFIII
G1	-31.53	-20.07	-40.71	-14.36	-9.84	-1.04	535.41	488.49	557.28
G2	-8.30	7.70	-10.24	-2.67	3.69	-0.36	377.32	162.46	378.57
G3	20.42	9.20	23.05	8.73	4.37	1.8	440.01	386.67	460.87
G4	6.77	-6.87	3.21	1.78	-3.37	0.67	458.38	219.33	478.64
G5	-3.81	-6.82	-0.65	-2.1	-3.15	-0.47	269.58	152.88	291.69
G6	3.92	-4.06	15.90	1.12	-2.02	3.71	292.08	249.58	382.33
G7	17.97	24.61	10.41	8.69	11.32	-0.32	529.29	508.84	551.17
G8	12.02	-0.12	10.17	4.83	-0.11	-0.24	417.51	131.26	418.61
G9	13.21	6.88	18.84	6.28	3.74	-1.17	691.67	673.95	728.10
G10	29.09	32.78	34.40	14.01	15.43	-0.05	633.79	629.77	646.28
G11	-3.71	-4.49	-9.86	-1.82	-2.29	0.51	358.48	230.07	402.08
G12	-2.61	-2.50	-4.54	-1.69	-1.69	-2.26	420.74	413.49	461.54
G13	-12.39	-6.32	-7.11	-5.29	-3.04	1.49	323.91	210.89	339.06
G14	-8.21	-14.24	-10.75	-4.46	-6.81	-2.64	494.29	481.67	539.84
G15	-27.80	-16.45	-13.51	-12.43	-7.96	1.92	416.77	356.84	477.26
G16	-4.87	1.38	4.25	-1.4	1.10	2.00	467.99	441.13	491.33
G17	-10.66	-4.12	-22.76	-3.64	-1.12	-1.19	672.06	658.48	704.39
G18	10.49	3.50	-0.10	4.42	1.72	-2.36	175.63	97.33	247.67

AMGEF parameters are a function of both genotype and environment GE interaction pattern components. AMGEF calculation according to the first five IPCs (AMGEFI) indicated that genotypes G6, G12 and G16 were the most stable genotypes (Table 5). Genotypes G8, G16 and G17 were the most stable genotypes based on AMGEFII while AMGEFIII parameter detected genotypes G9, G10 and G12 as the most stable genotypes (Table 5). The most stable genotypes according to DFI, were genotypes G5, G6 and G18; according to DFII, were genotypes G5, G8 and G18; and according to DFIII, were genotypes G5, G13 and G18 (Table 5). Using five IPCs in computations of AMMI stability parameters indicated that genotypes G5 and G6 were the most stable genotypes while considering three IPCs in calcula-

tions of AMMI stability parameters showed that genotypes G8 and G18 were the most stable genotypes. Also genotypes G2, G5 and G18 were the most stable genotypes according to AMMI stability parameters which calculated from seven IPCs. Simultaneous selection of mean yield and stability caused to selection of genotype G2 as the most favorable genotype. Also genotypes G5 and G18 could be regarded as the other most favorable genotypes.

Table 6

Spearman's correlation coefficients among ranks of 18 lentil genotypes at 12 environments based on AMMI stability parameters

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	-0.30*																
2	-0.30	1.00															
3	-0.30	1.00	1.00														
4	-0.30	1.00	1.00	1.00													
5	-0.01	0.74	0.74	0.74	0.74												
6	0.17	0.47	0.47	0.47	0.47	0.56											
7	0.04	0.66	0.66	0.66	0.66	0.89	0.63										
8	0.24	0.54	0.54	0.54	0.54	0.78	0.78	0.78									
9	0.11	0.29	0.29	0.29	0.29	0.42	0.46	0.36	0.34								
10	-0.24	0.24	0.24	0.24	0.24	0.46	0.37	0.45	0.41	0.65							
11	0.08	0.41	0.41	0.41	0.41	0.75	0.49	0.65	0.58	0.67	0.57						
12	-0.11	0.28	0.28	0.28	0.28	0.38	0.38	0.33	0.23	0.94	0.72	0.62					
13	-0.27	0.20	0.20	0.20	0.20	0.43	0.30	0.42	0.37	0.63	0.99	0.53	0.71				
14	-0.09	0.12	0.12	0.12	0.12	0.15	-0.48	0.02	-0.04	-0.29	-0.33	-0.10	-0.33	-0.28			
15	0.03	0.70	0.70	0.70	0.70	0.81	0.89	0.87	0.81	0.47	0.42	0.62	0.41	0.37	-0.22		
16	-0.01	0.72	0.72	0.72	0.72	0.90	0.64	0.99	0.78	0.38	0.45	0.68	0.34	0.41	0.01	0.89	
17	0.05	0.74	0.74	0.74	0.74	0.86	0.83	0.90	0.87	0.44	0.43	0.63	0.38	0.38	-0.15	0.98	0.92

Critical values of correlation $P < 0.05$ and $P < 0.01$ (D.F. 16) are 0.47 and 0.59, respectively

Numbers of parameters:

0 – MY	9 – SPCFI
1 – EVI	10 – SPCFII
2 – SPC1	11 – SPCFIII
3 – AMGE1	12 – AMGEFI
4 – D1	13 – AMGEFII
5 – ASV	14 – AMGEFIII
6 – EVFI	15 – DFI
7 – EVFII	16 – DFII
8 – EVFIII	17 – DFIII

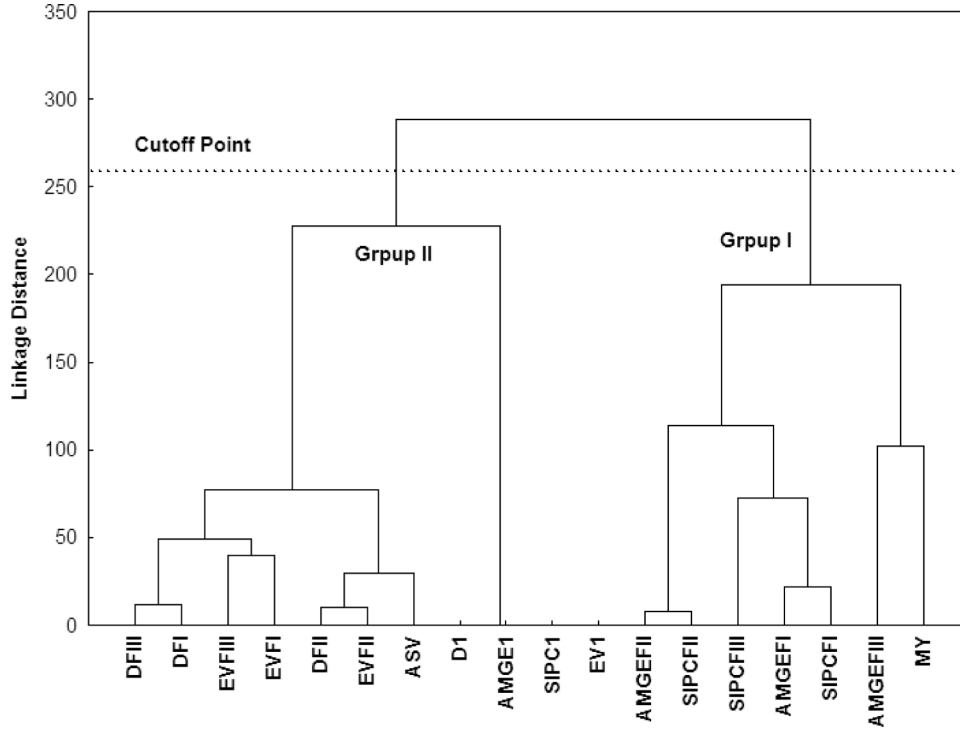


Fig. 1. Hierarchical cluster analysis based on Ward's method using for mean yield and AMMI stability parameters

Each one of the AMMI stability parameters produced a unique genotype ranking. The Spearman's rank correlations between each pair of the AMMI stability parameters were calculated (Table 6). The mean yield had not any positive or negative correlation with the AMMI stability parameters. Some of AMMI statistics including EV1, SIPC1, AMGE1, D1, ASV, EVFI, EVFII, EVFIII, DFI, DFII and DFIII were positively correlated with each other. SPCFI indicated significant positive correlation with SPCFII, SPCFIII, AMGEFI, AMGEFII and DFI parameters while SPCFII showed significant positive correlation with SPCFIII, AMGEFI and AMGEFII parameters. SPCFIII indicated significant positive correlation with ASV, EVFI, EVFII, EVFIII, SPCFI, SPCFII, AMGEFI, AMGEFII, DFI, DFII and DFIII stability parameters. Finally, EVFI, EVFII and EVFIII were positively correlated with each other. To better reveal associations among AMMI stability parameters, the two-way data of ranks matrix, was analyzed further using a clustering method. Ward's hierarchical clustering indicated that the seventeen parameters could be divided into two major groups (Fig. 1). Group I contain SPCFI, SPCFII, SPCFIII, AMGEFI, AMGEFII, AMGEFIII and mean yield; and Group II contain EV1, SIPC1, AMGE1,

D1, ASV, EVFI, EVFII, EVFIII, DFI, DFII and DFIII parameters. Therefore it seems that choosing stable genotypes based on SIPCF and AMGEF parameters cause to simultaneous selection yield and stability.

DISCUSSION

Like many of the multi-environmental trials, remarkable GE interactions including GL and GYL interactions were observed in this research. GE interaction has been an investigation focus among plant breeders for several decades. Although many stability parameters have been proposed but there is a gap in understanding and interpreting of GE interaction between quantitative geneticists versus plant breeders. The magnitude of GE interaction for lentil grain yield found in this study is similar to those found in other crop adaptation studies in rain-fed environments or dry-land areas (Mohebodini *et al.*, 2006; Sabaghnia *et al.*, 2008a). Therefore as an important consideration in plant breeding, GE interaction makes it difficult to select the best performing and most stable genotypes. This considerable amount of variation in the GE interaction could be associated with the nature of the crop, rain-fed properties of semi-arid areas, environmental conditions or diverse genetic background obtained from different sources.

In the present investigation, interpretation of the GE interaction was based on the AMMI model and its different stability parameters. In spite of pervious conventional methods for stability analysis (parametric univariate methods) which attempt to define the GE interactions by one or two parameter, multivariate methods such as AMMI model have not these deficiencies for explaining GE interaction patterns. Also AMMI model adjustment was done through several F-tests including F-Gollob (Gollob, 1968), F_{Ratio} (Cornelius *et al.*, 1992), F_{GH1} and F_{GH2} tests (Cornelius, 1993). The results of these test indicated that at least three IPCs and maximum seven IPCs can explain GE interaction in this research. These special tests are more robust and verify the significance of the residual GE interaction variation in each AMMI model, beginning with AMMI0. The RMSPD values of validation procedure via MATMODEL indicated seven IPCs needed for AMMI model of lentil dataset. Thus, our AMMI model exhibited a more complex interaction which required many IPCs. Regarding this complex GE interaction, multivariate statistical methods such as AMMI can explore multi-directionality aspects of dataset pattern and attempt to extract more information from this component. According to Ebdon and Gauch (2002) the AMMI model is an effective multivariate procedure which extracts a reduced model by fitting a model to the GE interaction dataset. The AMMI uses all the data as relevant in predicting future performance of genotypes; discovers GE interaction pattern and discards the noise that in-

roduces discrepancies between the estimate value and the corresponding mean of two-way dataset (Gauch, 2006).

For better use of AMMI model, several concepts of stability based on IPCs scores of genotypes and environments were computed. Our results showed that AMMI stability parameters which based on SIPCF and AMGEF statistics were as the most favorable parameters because were grouped with mean yield. Sabaghnia *et al.* (2008b) reported SIPCF parameter can select both mean yield and stability simultaneously and Dehghani *et al.* (2010) declared similar properties for SIPCF and AMGEF parameters. But these authors used only F-Gollob in their studies and did not use other F-tests or validation procedure. The AMMI model provided a better description of static and dynamic concepts of stability for interpreting GE interaction. In static concept, genotypes have a minimal variance over different environments while in dynamic concept; it is not needed that the genotypic response to environmental conditions should be equal for all genotypes (Becker and Leon, 1988). AMMI stability parameters clearly influenced by high mean yield were SIPCFI, SIPCFII, SIPCFIII, AMGEFI, AMGEFII, AMGEFIII and selection for the most favorable genotypes according to these methods results in the high performance genotypes being introduced as the most stable genotypes. Considering all AMMI stability parameters and specially parameters which benefits significant IPCs via F-tests, genotypes G2, G5, G8, G11, G12 and G18 were identified as the most stable genotypes. Among these stable genotypes, only genotypes G2, G11 and G12 had high mean yield and so could be regarded as the most favorable genotype. The mean yield of these genotypes were $G2 = 1365.63 \text{ kg} \times \text{ha}^{-1}$, $G11 = 1374.13 \text{ kg} \times \text{ha}^{-1}$ and $G12 = 1334.73 \text{ kg} \times \text{ha}^{-1}$. These genotypes are therefore recommended for release as commercial cultivars by the Dry Land Agricultural Research Institute of Iran.

Several statistical methods are available for analysis of complex GE interaction data matrix into a simpler and more meaningful component. These range from univariate parametric models and nonparametric procedures to multivariate models. The advantages and disadvantages of these statistical methods, as well as the relationships between them have been reviewed by several authors (Lin *et al.*, 1986; Flores *et al.*, 1998). The investigation targets of plant breeders conducting multi-environmental trials need partitioning main effects of genotype and environment and GE interaction because they present different challenges and opportunities (Gauch, 2006). The AMMI separates these effects before applying singular value decomposition to GE interaction matrix. Different F-tests are available for determining significant and sufficient numbers of IPCs in AMMI model. Also, the cross validation can help breeders to select the best AMMI model. According to Gauch *et al.* (2008), the important reason AMMI is appropriate for plant breeding programs is that the ANOVA part of AMMI can separate the

main effects and PCA part of AMMI can interpret GE interaction. Therefore, the AMMI model offers good opportunities for analysis of GE interaction in multi-environmental trials.

ACKNOWLEDGMENT

The authors thank the Dryland Agricultural Research Institute (DARI) and its research stations (Gorgan, Kermanshah and Shirvan) for making available the plant materials, experimental locations and technical assistance.

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